

Gln	Ala	Thr	Val	Gln	Thr	Asp	Lys	Val	Asp	Gly	Lys	Leu	Phe	Ala	Leu	625	630	635	640
Ala	Pro	Lys	Ala	Leu	Tyr	Glu	Thr	Ser	Trp	Gln	Lys	Ile	Thr	Ile	Pro		645	650	655
Ala	Asn	Ser	Ser	Lys	Gln	Val	Thr	Ile	Pro	Ile	Asp	Val	Ser	Gln	Phe		660	665	670
Ser	Lys	Asp	Leu	Leu	Ala	Pro	Met	Lys	Asn	Gly	Tyr	Phe	Leu	Glu	Gly		675	680	685
Phe	Val	Arg	Phe	Lys	Gln	Asp	Pro	Thr	Lys	Glu	Glu	Leu	Met	Ser	Ile		690	695	700
Pro	Tyr	Ile	Gly	Phe	Arg	Gly	Asp	Phe	Gly	Asn	Leu	Ser	Ala	Leu	Glu	705	710	715	720
Lys	Pro	Ile	Tyr	Asp	Ser	Lys	Asp	Gly	Ser	Ser	Tyr	Tyr	His	Glu	Ala		725	730	735
Asn	Ser	Asp	Ala	Lys	Asp	Gln	Leu	Asp	Gly	Asp	Gly	Leu	Gln	Phe	Tyr		740	745	750
Ala	Leu	Lys	Asn	Asn	Phe	Thr	Ala	Leu	Thr	Thr	Glu	Ser	Asn	Pro	Trp		755	760	765
Thr	Ile	Ile	Lys	Ala	Val	Lys	Glu	Gly	Val	Glu	Asn	Ile	Glu	Asp	Ile		770	775	780
Glu	Ser	Ser	Glu	Ile	Thr	Glu	Thr	Ile	Phe	Ala	Gly	Thr	Phe	Ala	Lys	785	790	795	800
Gln	Asp	Asp	Asp	Ser	His	Tyr	Tyr	Ile	His	Arg	His	Ala	Asn	Gly	Lys		805	810	815
Pro	Tyr	Ala	Ala	Ile	Ser	Pro	Asn	Gly	Asp	Gly	Asn	Arg	Asp	Tyr	Val		820	825	830
Gln	Phe	Gln	Gly	Thr	Phe	Leu	Arg	Asn	Ala	Lys	Asn	Leu	Val	Ala	Glu		835	840	845
Val	Leu	Asp	Lys	Glu	Gly	Asn	Val	Val	Trp	Thr	Ser	Glu	Val	Thr	Glu		850	855	860
Gln	Val	Val	Lys	Asn	Tyr	Asn	Asn	Asp	Leu	Ala	Ser	Thr	Leu	Gly	Ser	865	870	875	880
Thr	Arg	Phe	Glu	Lys	Thr	Arg	Trp	Asp	Gly	Lys	Asp	Lys	Asp	Gly	Lys		885	890	895
Val	Val	Ala	Asn	Gly	Thr	Tyr	Thr	Tyr	Arg	Val	Arg	Tyr	Thr	Pro	Ile		900	905	910
Ser	Ser	Gly	Ala	Lys	Glu	Gln	His	Thr	Asp	Phe	Asp	Val	Ile	Val	Asp		915	920	925
Asn	Thr	Thr	Pro	Glu	Val	Ala	Thr	Ser	Ala	Thr	Phe	Ser	Thr	Glu	Asp		930	935	940
Arg	Arg	Leu	Thr	Leu	Ala	Ser	Lys	Pro	Lys	Thr	Ser	Gln	Pro	Val	Tyr	945	950	955	960
Arg	Glu	Arg	Ile	Ala	Tyr	Thr	Tyr	Met	Asp	Glu	Asp	Leu	Pro	Thr	Thr		965	970	975
Glu	Tyr	Ile	Ser	Pro	Asn	Glu	Asp	Gly	Thr	Phe	Thr	Leu	Pro	Glu	Glu		980	985	990
Ala	Glu	Thr	Met	Glu	Gly	Ala	Thr	Val	Pro	Leu	Lys	Met	Ser	Asp	Phe		995	1000	1005
Thr	Tyr	Val	Val	Glu	Asp	Met	Ala	Gly	Asn	Ile	Thr	Tyr	Thr	Pro		1010	1015	1020	
Val	Thr	Lys	Leu	Leu	Glu	Gly	His	Ser	Asn	Lys	Pro	Glu	Gln	Asp		1025	1030	1035	
Gly	Ser	Asp	Gln	Ala	Pro	Asp	Lys	Lys	Pro	Glu	Thr	Lys	Pro	Glu		1040	1045	1050	
Gln	Asp	Gly	Ser	Gly	Gln	Ala	Pro	Asp	Lys	Lys	Pro	Glu	Thr	Lys		1055	1060	1065	
Pro	Glu	Gln	Asp	Gly	Ser	Gly	Gln	Thr	Pro	Asp	Lys	Lys	Pro	Glu					

1070	1075	1080
Thr Lys Pro Glu Gln Asp Gly	Ser Gly Gln Thr Pro	Asp Lys Lys
1085	1090	1095
Pro Glu Thr Lys Pro Glu Lys	Asp Ser Ser Gly Gln	Thr Pro Gly
1100	1105	1110
Lys Thr Pro Gln Lys Gly Gln	Pro Ser Arg Thr Leu	Glu Lys Arg
1115	1120	1125
Ser Ser Lys Arg Ala Leu Ala	Thr Lys Ala Ser Thr	Lys Asp Gln
1130	1135	1140
Leu Pro Thr Thr Asn Asp Lys	Asp Thr Asn Arg Leu	His Leu Leu
1145	1150	1155
Lys Leu Val Met Thr Thr Phe	Phe Leu Gly Leu Val	Ala His Ile
1160	1165	1170
Phe Lys Thr Lys Arg Thr Glu	Asp	
1175	1180	

		675					680					685			
Leu	Thr	Ser	Leu	Asn	Phe	Ile	Asp	Leu	Ser	Gln	Asn	Asn	Leu	Ala	Leu
	690					695					700				
Leu	Pro	Lys	Thr	Ile	Glu	Lys	Leu	Arg	Ala	Leu	Ser	Thr	Ile	Val	Ala
705					710					715					720
Ser	Arg	Asn	His	Ile	Thr	Arg	Ile	Asp	Asn	Ile	Ser	Phe	Lys	Asn	Leu
				725					730					735	
Pro	Lys	Leu	Ser	Val	Leu	Asp	Leu	Ser	Thr	Asn	Glu	Ile	Ser	Asn	Leu
			740					745				750			
Pro	Asn	Gly	Ile	Phe	Lys	Gln	Asn	Asn	Gln	Leu	Thr	Lys	Leu	Asp	Phe
		755					760					765			
Phe	Asn	Asn	Leu	Leu	Thr	Gln	Val	Glu	Glu	Ser	Val	Phe	Pro	Asp	Val
	770					775					780				
Glu	Thr	Leu	Asn	Leu	Asp	Val	Lys	Phe	Asn	Gln	Ile	Lys	Ser	Val	Ser
785					790					795					800
Pro	Lys	Val	Arg	Ala	Leu	Ile	Gly	Gln	His	Lys	Leu	Thr	Pro	Gln	Lys
				805					810					815	
His	Ile	Ala	Lys	Leu	Glu	Ala	Ser	Leu	Asp	Gly	Glu	Lys	Ile	Lys	Tyr
			820					825					830		
His	Gln	Ala	Phe	Ser	Leu	Leu	Asp	Leu	Tyr	Tyr	Trp	Glu	Gln	Lys	Thr
		835					840					845			
Asn	Ser	Ala	Ile	Asp	Lys	Glu	Leu	Val	Ser	Val	Glu	Glu	Tyr	Gln	Gln
	850					855					860				
Leu	Leu	Gln	Glu	Lys	Gly	Ser	Asp	Thr	Val	Ser	Leu	Leu	Asn	Asp	Met
865					870					875					880
Gln	Val	Asp	Trp	Ser	Ile	Val	Ile	Gln	Leu	Gln	Lys	Lys	Ala	Ser	Asn
				885					890					895	
Gly	Gln	Tyr	Val	Thr	Val	Asp	Glu	Lys	Leu	Leu	Ser	Asn	Asp	Pro	Lys
			900				905					910			
Asp	Asp	Leu	Thr	Gly	Glu	Phe	Ser	Leu	Lys	Asp	Pro	Gly	Thr	Tyr	Arg
	915					920						925			
Ile	Arg	Lys	Ala	Leu	Ile	Thr	Lys	Lys	Phe	Ala	Thr	Gln	Lys	Glu	His
	930					935				940					
Ile	Tyr	Leu	Thr	Ser	Asn	Asp	Ile	Leu	Val	Ala	Lys	Gly	Pro	His	Ser
945				950						955					960
His	Gln	Lys	Asp	Leu	Val	Glu	Asn	Gly	Leu	Arg	Ala	Leu	Asn	Gln	Lys
			965					970					975		
Gln	Leu	Arg	Asp	Gly	Ile	Tyr	Tyr	Leu	Asn	Ala	Ser	Met	Leu	Lys	Thr
		980					985					990			
Asp	Leu	Ala	Ser	Glu	Ser	Met	Ser	Asn	Lys	Ala	Ile	Asn	His	Arg	Val
		995					1000					1005			
Thr	Leu	Val	Val	Lys	Lys	Gly	Val	Ser	Tyr	Leu	Glu	Val	Glu	Phe	
	1010					1015					1020				
Arg	Gly	Ile	Lys	Val	Gly	Lys	Met	Leu							

Ser	Leu	Thr	Thr	Glu	Lys	Ala	Lys	Val	Val	Lys	Glu	Thr	Asn	Asn	
1130						1135					1140				
Pro	Gln	Glu	Asn	Ser	His	Leu	Thr	Ser	Thr	Asp	Gln	Leu	Lys	Gly	
1145						1150					1155				
Pro	Gln	Asn	Arg	Gln	Gln	Glu	Lys	Thr	Pro	Thr	Ser	Pro	Pro	Ser	
1160						1165					1170				
Ala	Ala	Thr	Gly	Ile	Ala	Asn	Leu	Thr	Asp	Leu	Leu	Ala	Lys	Lys	
1175						1180					1185				
Ala	Thr	Gly	Gln	Ser	Thr	Gln	Glu	Thr	Ser	Lys	Thr	Asp	Asp	Thr	
1190						1195					1200				
Asp	Lys	Ala	Glu	Lys	Leu	Lys	Gln	Leu	Val	Arg	Asp	His	Gln	Thr	
1205						1210					1215				
Ser	Ile	Glu	Gly	Lys	Thr	Ala	Lys	Asp	Thr	Lys	Thr	Lys	Lys	Ser	
1220						1225					1230				
Asp	Lys	Lys	His	Arg	Ser	Asn	Gln	Gln	Ser	Asn	Gly	Glu	Glu	Ser	
1235						1240					1245				
Ser	Ser	Arg	Tyr	His	Leu	Ile	Ala	Gly	Leu	Ser	Ser	Phe	Met	Ile	
1250						1255					1260				
Val	Ala	Leu	Gly	Phe	Ile	Ile	Gly	Arg	Lys	Thr	Leu	Phe	Lys		
1265						1270					1275				

<210> SEQ ID NO 3

<211> LENGTH: 1827

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 3

atgtctaaaa	ttattggtat	tgacttaggt	acaacaaact	cagcagtagc	agttcttgaa	60
gggactgaat	caaaaatcat	tgctaaccce	gaaggcaatc	gtacaactcc	ttcagtagta	120
tcattcaaaa	atggtgaaat	tatcgtgggt	gatgctgcaa	aacgtcaagc	agtgacaaac	180
ccagaaacag	taatctctat	taaatctaaa	atgggaactt	ctgaaaaagt	ttctgcaaat	240
ggtaaagaat	atactcctca	agaaatttca	gcaatgattc	ttcaatacct	ttaaaggttat	300
gctgaagact	atccttgaga	aaaagtagaa	aaagcagtta	ttactgttcc	agcttacttc	360
aacgatgcac	aacgtcaggc	aactaaagac	gctggtaaaa	ttgcaggtct	tgaagtagaa	420
cgtatcgtta	acgaaccaac	agcagccgca	cttgcttatg	gtatggataa	gactgacaag	480
gatgaaaaaa	tcttagtttt	tgaccttggt	ggtggtaaca	ttgacgtatc	aatccttgaa	540
ttagggtgatg	gtgtcttcga	cgttcttgca	acagcaggtg	ataacaaact	tgggtggtgac	600
gactttgacc	aaaaaattat	tgatttctta	gtggctgaat	ttaagaaaga	aaatggcatt	660
gacttatcac	aagataagat	ggcacttcaa	cgcttgaaag	atgctgctga	aaaagctaaa	720
aaagatcttt	cagggtgtgac	acaaacacaa	atttcattac	cgttcatcac	tgctggttct	780
gccggtcctc	ttcacttgga	gatgagctta	tctcgtgcta	aatttgacga	tctcactcgc	840
gaccttgtag	aacgtacgaa	aactccagtt	cgtaagcccc	tttcagatgc	aggattgtca	900
ttgtcagaaa	ttgatgaagt	tatccttggt	ggtggatcaa	ctcgtatccc	agcagttgtc	960
gaagctgtaa	aagctgaaac	tggtaaagaa	ccaaataaat	ctgtaaacc	tgatgaagtg	1020
gttgctatgg	gtgctgctat	ccaaggtggt	gttatcactg	gggatgtgaa	agacgttgtc	1080
cttccttgacg	taacaccatt	gtcacttggt	attgaaacaa	tgggtggtgt	cttcactaaa	1140
ttgatcgacc	gcaatacaac	tatccaaca	tctaaatcac	aagtcttctc	aacagcagca	1200
gacaaccaac	cagctgttga	tatccatgtt	cttcaagggt	aacgccaat	ggcagcagat	1260
aacaagactc	ttggtcgctt	ccaattgact	gatatcccag	ctgcacctcg	tggaatccca	1320
caaattgaag	taacatttga	tatcgataaa	aacggtattg	tttctgtaaa	agctaaagac	1380
cttggtacgc	aaaaggaaca	acacatcggt	atcaaatcaa	acgacggact	ttctgaagaa	1440
gaaattgatc	gcatgatgaa	agacgctgaa	gctaagcccg	aagccgatgc	gaaacgtaaa	1500
gaagaagttg	accttaaaaa	cgaagttgac	caagctatct	ttgctactga	aaaaacaatc	1560
aaagaaactg	aaggtaaaag	ctttgataca	gaacgcgatg	cagcgcaatc	agctcttgac	1620
gagttaaaaa	ctgcgcaaga	atctggcaac	cttgacgaca	tgaagctaa	acttgaagca	1680
ttaaatagaa	aagcgcaagc	tttggctggt	aaaatgtacg	agcaagctgc	agcagctcaa	1740
caagcagcac	aaggtgcaga	aggtgcacaa	gctaattgatt	cagcaataaa	tgatgatggt	1800
gtagatggcg	aatttacaga	aaagtaa				1827

<210> SEQ ID NO 4

<211> LENGTH: 608

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 4

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Met Ser Lys Ile Ile Gly Ile Asp Leu Gly Thr Thr Asn Ser Ala Val
1      5      10      15
Ala Val Leu Glu Gly Thr Glu Ser Lys Ile Ile Ala Asn Pro Glu Gly
20      25      30
Asn Arg Thr Thr Pro Ser Val Val Ser Phe Lys Asn Gly Glu Ile Ile
35      40      45
Val Gly Asp Ala Ala Lys Arg Gln Ala Val Thr Asn Pro Glu Thr Val
50      55      60
Ile Ser Ile Lys Ser Lys Met Gly Thr Ser Glu Lys Val Ser Ala Asn
65      70      75      80
Gly Lys Glu Tyr Thr Pro Gln Glu Ile Ser Ala Met Ile Leu Gln Tyr
85      90      95
Leu Lys Gly Tyr Ala Glu Asp Tyr Leu Gly Glu Lys Val Glu Lys Ala
100     105     110
Val Ile Thr Val Pro Ala Tyr Phe Asn Asp Ala Gln Arg Gln Ala Thr
115     120     125
Lys Asp Ala Gly Lys Ile Ala Gly Leu Glu Val Glu Arg Ile Val Asn
130     135     140
Glu Pro Thr Ala Ala Ala Leu Ala Tyr Gly Met Asp Lys Thr Asp Lys
145     150     155     160
Asp Glu Lys Ile Leu Val Phe Asp Leu Gly Gly Gly Thr Phe Asp Val
165     170     175
Ser Ile Leu Glu Leu Gly Asp Gly Val Phe Asp Val Leu Ala Thr Ala
180     185     190
Gly Asp Asn Lys Leu Gly Gly Asp Asp Phe Asp Gln Lys Ile Ile Asp
195     200     205
Phe Leu Val Ala Glu Phe Lys Lys Glu Asn Gly Ile Asp Leu Ser Gln
210     215     220
Asp Lys Met Ala Leu Gln Arg Leu Lys Asp Ala Ala Glu Lys Ala Lys
225     230     235     240
Lys Asp Leu Ser Gly Val Thr Gln Thr Gln Ile Ser Leu Pro Phe Ile
245     250     255
Thr Ala Gly Ser Ala Gly Pro Leu His Leu Glu Met Ser Leu Ser Arg
260     265     270
Ala Lys Phe Asp Asp Leu Thr Arg Asp Leu Val Glu Arg Thr Lys Thr
275     280     285
Pro Val Arg Gln Ala Leu Ser Asp Ala Gly Leu Ser Leu Ser Glu Ile
290     295     300
Asp Glu Val Ile Leu Val Gly Gly Ser Thr Arg Ile Pro Ala Val Val
305     310     315     320
Glu Ala Val Lys Ala Glu Thr Gly Lys Glu Pro Asn Lys Ser Val Asn
325     330     335
Pro Asp Glu Val Val Ala Met Gly Ala Ala Ile Gln Gly Gly Val Ile
340     345     350
Thr Gly Asp Val Lys Asp Val Val Leu Leu Asp Val Thr Pro Leu Ser
355     360     365
Leu Gly Ile Glu Thr Met Gly Gly Val Phe Thr Lys Leu Ile Asp Arg
370     375     380
Asn Thr Thr Ile Pro Thr Ser Lys Ser Gln Val Phe Ser Thr Ala Ala
385     390     395     400
Asp Asn Gln Pro Ala Val Asp Ile His Val Leu Gln Gly Glu Arg Pro
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<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 6

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Met Lys Ile Gly Lys Lys Ile Val Leu Met Phe Thr Ala Ile Val Leu
1      5      10      15
Thr Thr Val Leu Ala Leu Gly Val Tyr Leu Thr Ser Ala Tyr Thr Phe
20      25      30
Ser Thr Gly Glu Leu Ser Lys Thr Phe Lys Asp Phe Ser Thr Ser Ser
35      40      45
Asn Lys Ser Asp Ala Ile Lys Gln Thr Arg Ala Phe Ser Ile Leu Leu
50      55      60
Met Gly Val Asp Thr Gly Ser Ser Glu Arg Ala Ser Lys Trp Glu Gly
65      70      75      80
Asn Ser Asp Ser Met Ile Leu Val Thr Val Asn Pro Lys Thr Lys Lys
85      90      95
Thr Thr Met Thr Ser Leu Glu Arg Asp Thr Leu Thr Thr Leu Ser Gly
100      105      110
Pro Lys Asn Asn Glu Met Asn Gly Val Glu Ala Lys Leu Asn Ala Ala
115      120      125
Tyr Ala Ala Gly Gly Ala Gln Met Ala Ile Met Thr Val Gln Asp Leu
130      135      140
Leu Asn Ile Thr Ile Asp Asn Tyr Val Gln Ile Asn Met Gln Gly Leu
145      150      155      160
Ile Asp Leu Val Asn Ala Val Gly Gly Ile Thr Val Thr Asn Glu Phe
165      170      175
Asp Phe Pro Ile Ser Ile Ala Glu Asn Glu Pro Glu Tyr Gln Ala Thr
180      185      190
Val Ala Pro Gly Thr His Lys Ile Asn Gly Glu Gln Ala Leu Val Tyr
195      200      205
Ala Arg Met Arg Tyr Asp Asp Pro Glu Gly Asp Tyr Gly Arg Gln Lys
210      215      220
Arg Gln Arg Glu Val Ile Gln Lys Val Leu Lys Lys Ile Leu Ala Leu
225      230      235      240
Asp Ser Ile Ser Ser Tyr Arg Lys Ile Leu Ser Ala Val Ser Ser Asn
245      250      255
Met Gln Thr Asn Ile Glu Ile Ser Ser Arg Thr Ile Pro Ser Leu Leu
260      265      270
Gly Tyr Arg Asp Ala Leu Arg Thr Ile Lys Thr Tyr Gln Leu Lys Gly
275      280      285
Glu Asp Ala Thr Leu Ser Asp Gly Gly Ser Tyr Gln Ile Val Thr Ser
290      295      300
Asn His Leu Leu Glu Ile Gln Asn Arg Ile Arg Thr Glu Leu Gly Leu
305      310      315      320
His Lys Val Asn Gln Leu Lys Thr Asn Ala Thr Val Tyr Glu Asn Leu
325      330      335
Tyr Gly Ser Thr Lys Ser Gln Thr Val Asn Asn Asn Tyr Asp Ser Ser
340      345      350
Gly Gln Ala Pro Ser Tyr Ser Asp Ser His Ser Ser Tyr Ala Asn Tyr
355      360      365
Ser Ser Gly Val Asp Thr Gly Gln Ser Ala Ser Thr Asp Gln Asp Ser
370      375      380
Thr Ala Ser Ser His Arg Pro Ala Thr Pro Ser Ser Ser Ser Asp Ala
385      390      395      400
Leu Ala Ala Asp Glu Ser Ser Ser Ser Gly Ser Gly Ser Leu Val Pro
405      410      415
Pro Ala Asn Ile Asn Pro Gln Thr
420
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<210> SEQ ID NO 7
<211> LENGTH: 2166
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 7
gtgattacaa ttaaaaatcc aaaaatcctt aagtggctaa agtatgtatt aagtgcaatt      60
cttagcctta ttatccttgt tattattatt ggtgggtcttt tgtttacctt ctacattagc      120
agtgtccga aactgtcaga agcccagtta aaatcaacaa actctagctt ggtttatgac      180
ggtaataaca atctgattgc tgatttgggt tctgaaaagc gtgaaaatgt aacagctgat      240
agtatcccta ttaatctagt taatgctatt acctcaattg aagataaacg tttctttaac      300
catcgtggag tagatcttta tcgtattttt ggtgctgcct ttcataatct aacgagtcag      360
accactcaag gggggtcaac gcttgatcag caactcatta aactagccta tttttctact      420
aatgaatctg atcaaacctt aaaacgtaag gctcaagaag tttggcttgc ttttcaaagt      480
gagcgaaaat atactaaaca agaaatcctg actttttaca tcaacaaagt atatatgggt      540
aatggcaact atgggtatgct gacagccgct aagtcttatt atggcaagga tcttaaggat      600
ttatcttatg cccaactagc cctattggct ggaatccctc aagctcctag tcaatatgat      660
ccttaccttc atcctgaagc tgctcaaaat cgccgtaacg tcgtgttgca acagatgtac      720
atggaaaaac atctgacgaa agcagaatat gaaactgcc a tcgcaactcc cgtcgctgaa      780
ggtctacaat cactccaaca gcgctcaact tatccaaaat atatggataa ttatctaaaa      840
caagttattg aagaagtcaa aaaagaaacg aataaagata tttttaccgc tggtttaaaa      900
gtttatacca atattatccc cgatgcgcag cagactcttt ataatattta tcattctggt      960
gattatgttt actatccaga ccaagatttc caagttgctt caacgattgt tgatgtgaca     1020
aatggtcatt ttattgctca gcttggcgga cgtaatcaag atgaaaatgt ttcatttggg     1080
actaaccaag ctgttttaac tgatcgtgac tgggggttcta ccatgaagcc aatcacagcc     1140
tatgctcctg ctattgaatc tgggtgtttat acttctactg ctcagtcgac taatgactca     1200
gtctattatt ggcttggaa cactacccaa ttgtttaact gggaccttag atataacgga     1260
tggatgacaa tccaagctgc tattatgcta tcgcgaaatg tcccagcagt ccgagcactg     1320
gaagccgcag gacttgacta tgctcgatct ttcttaagca gtttaggtat taactatccc     1380
gaaatgcact actcaaacgc tatctcaagt aataacagta gctcagataa aaaatatggt     1440
gcaagtagtg aaaaaatggc cgctgcatac gctgcttttg caaatggtgg tatttatcat     1500
aaaccaaggt atgtcaataa agtggaaatt agtgatggta caagtaaaac ttttgatgaa     1560
aaagggaaaac gtgccatgaa agaaaccacg gcctatatga tgacagatat gttaaaaaac     1620
gttctcactt atggtacagg tactgctgct gccattcctg gtgttgcgca agctggtaaa     1680
acaggggactt ctaactacac tgatgaggaa ctagtataaa ttggtgaaaa atacggcctt     1740
tatccagatt atgttgggtac attagcgcca gacgaaaaat ttggtggcct tactaagcgc     1800
tacgccatgg ctgtttggac aggttacaaa aaccgcttga cccaggtata cggatcaagt     1860
ctagagattg catctgacgt ttatcgtagc atgatgactt acttaacaaa tggttacagt     1920
gaagattgga cgatgcaaaa tggctctttat cgcagtgggt gattcctcta cttaagcgga     1980
acctatgcga gcaacaccga ctatactaata tcggtttaca acaatcttta cagcaataac     2040
acgacaacag cttctagcca aacgacttca gatgatacta gtagtagcaa tgatacaagt     2100
aattcaacca atacagacaa caatggcagt catccatcta ccatgataa aaagacaact     2160
cattaa
2166

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<210> SEQ ID NO 8
<211> LENGTH: 721
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 8
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1          5          10          15
Leu Ser Ala Ile Leu Ser Leu Ile Ile Leu Val Ile Ile Ile Gly Gly
20          25          30
Leu Leu Phe Thr Phe Tyr Ile Ser Ser Ala Pro Lys Leu Ser Glu Ala
35          40          45
Gln Leu Lys Ser Thr Asn Ser Ser Leu Val Tyr Asp Gly Asn Asn Asn
50          55          60
Leu Ile Ala Asp Leu Gly Ser Glu Lys Arg Glu Asn Val Thr Ala Asp

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65					70					75				80	
Ser	Ile	Pro	Ile	Asn	Leu	Val	Asn	Ala	Ile	Thr	Ser	Ile	Glu	Asp	Lys
				85					90					95	
Arg	Phe	Phe	Asn	His	Arg	Gly	Val	Asp	Leu	Tyr	Arg	Ile	Phe	Gly	Ala
			100					105					110		
Ala	Phe	His	Asn	Leu	Thr	Ser	Gln	Thr	Thr	Gln	Gly	Gly	Ser	Thr	Leu
		115					120					125			
Asp	Gln	Gln	Leu	Ile	Lys	Leu	Ala	Tyr	Phe	Ser	Thr	Asn	Glu	Ser	Asp
	130					135					140				
Gln	Thr	Leu	Lys	Arg	Lys	Ala	Gln	Glu	Val	Trp	Leu	Ala	Leu	Gln	Met
145					150					155					160
Glu	Arg	Lys	Tyr	Thr	Lys	Gln	Glu	Ile	Leu	Thr	Phe	Tyr	Ile	Asn	Lys
			165						170					175	
Val	Tyr	Met	Gly	Asn	Gly	Asn	Tyr	Gly	Met	Leu	Thr	Ala	Ala	Lys	Ser
			180					185					190		
Tyr	Tyr	Gly	Lys	Asp	Leu	Lys	Asp	Leu	Ser	Tyr	Ala	Gln	Leu	Ala	Leu
	195						200					205			
Leu	Ala	Gly	Ile	Pro	Gln	Ala	Pro	Ser	Gln	Tyr	Asp	Pro	Tyr	Leu	His
	210					215					220				
Pro	Glu	Ala	Ala	Gln	Asn	Arg	Arg	Asn	Val	Val	Leu	Gln	Gln	Met	Tyr
225					230					235					240
Met	Glu	Lys	His	Leu	Thr	Lys	Ala	Glu	Tyr	Glu	Thr	Ala	Ile	Ala	Thr
			245						250					255	
Pro	Val	Ala	Glu	Gly	Leu	Gln	Ser	Leu	Gln	Gln	Arg	Ser	Thr	Tyr	Pro
			260					265					270		
Lys	Tyr	Met	Asp	Asn	Tyr	Leu	Lys	Gln	Val	Ile	Glu	Glu	Val	Lys	Lys
	275						280					285			
Glu	Thr	Asn	Lys	Asp	Ile	Phe	Thr	Ala	Gly	Leu	Lys	Val	Tyr	Thr	Asn
	290					295					300				
Ile	Ile	Pro	Asp	Ala	Gln	Gln	Thr	Leu	Tyr	Asn	Ile	Tyr	His	Ser	Gly
305					310					315					320
Asp	Tyr	Val	Tyr	Tyr	Pro	Asp	Gln	Asp	Phe	Gln	Val	Ala	Ser	Thr	Ile
			325						330					335	
Val	Asp	Val	Thr	Asn	Gly	His	Val	Ile	Ala	Gln	Leu	Gly	Gly	Arg	Asn
			340					345					350		
Gln	Asp	Glu	Asn	Val	Ser	Phe	Gly	Thr	Asn	Gln	Ala	Val	Leu	Thr	Asp
	355						360					365			
Arg	Asp	Trp	Gly	Ser	Thr	Met	Lys	Pro	Ile	Thr	Ala	Tyr	Ala	Pro	Ala
	370					375					380				
Ile	Glu	Ser	Gly	Val	Tyr	Thr	Ser	Thr	Ala	Gln	Ser	Thr	Asn	Asp	Ser
385					390					395					400
Val	Tyr	Tyr	Trp	Pro	Gly	Thr	Thr	Thr	Gln	Leu	Phe	Asn	Trp	Asp	Leu
			405						410					415	
Arg	Tyr	Asn	Gly	Trp	Met	Thr	Ile	Gln	Ala	Ala	Ile	Met	Leu	Ser	Arg
			420					425					430		
Asn	Val	Pro	Ala	Val	Arg	Ala	Leu	Glu	Ala	Ala	Gly	Leu	Asp	Tyr	Ala
	435						440					445			
Arg	Ser	Phe	Leu	Ser	Ser	Leu	Gly	Ile	Asn	Tyr	Pro	Glu	Met	His	Tyr
	450					455					460				
Ser	Asn	Ala	Ile	Ser	Ser	Asn	Asn	Ser	Ser	Ser	Asp	Lys	Lys	Tyr	Gly
465					470					475					480
Ala	Ser	Ser	Glu	Lys	Met	Ala	Ala	Ala	Tyr	Ala	Ala	Phe	Ala	Asn	Gly
			485						490					495	
Gly	Ile	Tyr	His	Lys	Pro	Arg	Tyr	Val	Asn	Lys	Val	Glu	Phe	Ser	Asp
			500					505					510		
Gly	Thr	Ser	Lys	Thr	Phe	Asp	Glu	Lys	Gly	Lys	Arg	Ala	Met	Lys	Glu
			515				520								

Thr	Thr	Ala	Tyr	Met	Met	Thr	Asp	Met	Leu	Lys	Thr	Val	Leu	Thr	Tyr
530						535					540				
Gly	Thr	Gly	Thr	Ala	Ala	Ala	Ile	Pro	Gly	Val	Ala	Gln	Ala	Gly	Lys
545					550					555					560
Thr	Gly	Thr	Ser	Asn	Tyr	Thr	Asp	Glu	Glu	Leu	Ala	Lys	Ile	Gly	Glu
			565					570						575	
Lys	Tyr	Gly	Leu	Tyr	Pro	Asp	Tyr	Val	Gly	Thr	Leu	Ala	Pro	Asp	Glu
		580						585					590		
Asn	Phe	Val	Gly	Phe	Thr	Lys	Arg	Tyr	Ala	Met	Ala	Val	Trp	Thr	Gly
595							600					605			
Tyr	Lys	Asn	Arg	Leu	Thr	Pro	Val	Tyr	Gly	Ser	Ser	Leu	Glu	Ile	Ala
610						615					620				
Ser	Asp	Val	Tyr	Arg	Ser	Met	Met	Thr	Tyr	Leu	Thr	Asn	Gly	Tyr	Ser
625					630					635					640
Glu	Asp	Trp	Thr	Met	Pro	Asn	Gly	Leu	Tyr	Arg	Ser	Gly	Gly	Phe	Leu
			645					650						655	
Tyr	Leu	Ser	Gly	Thr	Tyr	Ala	Ser	Asn	Thr	Asp	Tyr	Thr	Asn	Ser	Val
		660						665					670		
Tyr	Asn	Asn	Leu	Tyr	Ser	Asn	Asn	Thr	Thr	Thr	Ala	Ser	Ser	Gln	Thr
	675					680					685				
Thr	Ser	Asp	Asp	Thr	Ser	Ser	Ser	Asn	Asp	Thr	Ser	Asn	Ser	Thr	Asn
690					695					700					
Thr	Asp	Asn	Asn	Gly	Ser	His	Pro	Ser	Thr	Asp	Asp	Lys	Lys	Thr	Thr
705					710					715					720
His															

<210> SEQ ID NO 9

<211> LENGTH: 1470

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 9

gtgtcagaag	aaagcaaaga	agtcgaagta	acaaaagaat	cgcaaacatt	ggggcttaat	60
gaagccaagt	caatgacaat	tggtgaagct	gtacgcaaac	agtcagagat	aaaagcaggt	120
gttactaagg	atgatagtat	tttagataag	tacattaagc	aacaccgtga	cgaagtttct	180
tctcaaaaag	ttgatgctaa	gtatacacag	cttgatacac	ctagttttaga	taactttatc	240
aaaaaacaaa	gagaagcatt	gagtaaagcc	ggtcttggtg	atgacgaacc	tgtgtctgcg	300
gagtctgctg	agcaagatag	cactttgggt	gaagaagtag	ctgaagactt	agctccaatg	360
gagactactg	cgggtggtaac	tgggattccg	gtggaagcga	cagtcacctgt	gtagatcta	420
gatccatcag	agaggggtcat	tccagaacca	cagatgacca	aggaagaacc	aaaaagagat	480
cagtttcttt	ctgaagatag	ccaccatcca	gccaaacaaa	acacgaaaaa	aggttgggta	540
atagctttat	ttctgctatt	attggccatt	cttgagcttg	tatttggttg	gaaccatttc	600
ttgagacaag	acagtggtaa	aacaactcaa	acagcaagta	aacagacaaa	gacctctttg	660
cagaccgaca	gtgctaataa	agcaacgcgc	ttgaaggctg	ctgctaagac	tttcgaaaaa	720
ctatatggta	ctttttatac	agatgccaca	aagagcaaat	taaaaaatag	tgcctttgct	780
actttgcccag	atttagaagc	tgccttgaaa	gctttggaag	gctctgctta	ctatgataag	840
gcgaaagcaa	aagtcgattc	ccttaagaaa	gctattgctg	ctattacagc	ggttaacggg	900
aaatttggtt	ccgatgttgt	tgtagatggg	gaaaagggtt	cggctgaagt	caaggctgat	960
gctaattttg	atgatattat	aagtgcacc	ttgacaatag	gaaatgcaa	tcttgatgct	1020
gtcttgccag	caagcatcac	agaaggctcg	cagcaactag	ccagcaaggc	tgaggccgct	1080
aaagcagcta	atgagcaagc	agtccaggat	caagcagctc	aaggacaaag	tacatcagta	1140
gcaccatctg	gctatggctt	gacaagtatt	gatcctgcaa	gcttacaacg	gcatttatca	1200
cgtgtacctt	acaatcaaga	tgttattgct	gacagagcta	acccatcttg	ggcatttaac	1260
ccaggagttc	ttgaaaaaat	tgtagcaacc	tcacaagcta	gaggttatat	ttcaggcaac	1320
caatatattt	tagagccggg	taatattatt	aattggcaatg	gttactataa	tatgtttaag	1380
cctgatggca	cttatctgtt	ctctattaat	tgtaaagacg	gttattttgt	aggaaatggc	1440
aaagggttatg	ctgatgcttt	agattactga				1470

<210> SEQ ID NO 10
 <211> LENGTH: 489
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 10

Met	Ser	Glu	Glu	Ser	Lys	Glu	Val	Glu	Val	Thr	Lys	Glu	Ser	Gln	Thr	1	5	10	15
Leu	Gly	Leu	Asn	Glu	Ala	Lys	Ser	Met	Thr	Ile	Gly	Glu	Ala	Val	Arg	20	25	30	
Lys	Gln	Ser	Glu	Ile	Lys	Ala	Gly	Val	Thr	Lys	Asp	Asp	Ser	Ile	Leu	35	40	45	
Asp	Lys	Tyr	Ile	Lys	Gln	His	Arg	Asp	Glu	Val	Ser	Ser	Gln	Lys	Phe	50	55	60	
Asp	Ala	Lys	Tyr	Thr	Glu	Leu	Asp	Thr	Ala	Ser	Leu	Asp	Asn	Phe	Ile	65	70	75	80
Lys	Lys	Gln	Arg	Glu	Ala	Leu	Ser	Lys	Ala	Gly	Leu	Val	Asp	Asp	Glu	85	90	95	
Pro	Val	Ser	Ala	Glu	Ser	Ala	Glu	Gln	Asp	Ser	Thr	Leu	Val	Glu	Glu	100	105	110	
Val	Ala	Glu	Asp	Leu	Ala	Pro	Met	Glu	Thr	Thr	Ala	Val	Val	Thr	Gly	115	120	125	
Ile	Pro	Val	Glu	Ala	Thr	Val	Pro	Val	Leu	Asp	Leu	Asp	Pro	Ser	Glu	130	135	140	
Arg	Val	Ile	Pro	Glu	Pro	Gln	Met	Thr	Lys	Glu	Glu	Pro	Lys	Arg	Asp	145	150	155	160
Gln	Phe	Leu	Ser	Glu	Asp	Ser	His	His	Pro	Ala	Lys	Gln	Asn	Thr	Lys	165	170	175	
Lys	Gly	Trp	Leu	Ile	Ala	Leu	Phe	Leu	Leu	Leu	Leu	Ala	Ile	Leu	Ala	180	185	190	
Val	Val	Phe	Gly	Trp	Asn	His	Phe	Leu	Arg	Gln	Asp	Ser	Gly	Lys	Thr	195	200	205	
Thr	Gln	Thr	Ala	Ser	Lys	Gln	Thr	Lys	Thr	Ser	Leu	Gln	Thr	Asp	Ser	210	215	220	
Ala	Lys	Lys	Ala	Thr	Arg	Leu	Lys	Ala	Ala	Ala	Lys	Ala	Phe	Glu	Lys	225	230	235	240
Leu	Tyr	Gly	Thr	Phe	Tyr	Thr	Asp	Ala	Thr	Lys	Ser	Lys	Leu	Lys	Asn	245	250	255	
Ser	Ala	Phe	Ala	Thr	Leu	Pro	Asp	Leu	Glu	Ala	Ala	Leu	Lys	Ala	Leu	260	265	270	
Glu	Gly	Ser	Ala	Tyr	Tyr	Asp	Lys	Ala	Lys	Ala	Lys	Val	Asp	Ser	Leu	275	280	285	
Lys	Lys	Ala	Ile	Ala	Ala	Ile	Thr	Ala	Val	Asn	Gly	Lys	Phe	Val	Ser	290	295	300	
Asp	Val	Val	Val	Asp	Gly	Glu	Lys	Val	Ser	Ala	Glu	Val	Lys	Ala	Asp	305	310	315	320
Ala	Asn	Phe	Asp	Asp	Leu	Ser	Ser	Ala	Thr	Leu	Thr	Ile	Gly	Asn	Ala	325	330	335	
Asn	Leu	Asp	Ala	Val	Leu	Gln	Ala	Ser	Ile	Thr	Glu	Gly	Arg	Gln	Gln	340	345	350	
Leu	Ala	Ser	Lys	Ala	Glu	Ala	Ala	Lys	Ala	Ala	Asn	Glu	Gln	Ala	Val	355	360	365	
Gln	Asp	Gln	Ala	Ala	Gln	Gly	Gln	Ser	Thr	Ser	Val	Ala	Pro	Ser	Gly	370	375	380	
Tyr	Gly	Leu	Thr	Ser	Tyr	Asp	Pro	Ala	Ser	Leu	Gln	Arg	His	Leu	Ser	385	390	395	400
Arg	Val	Pro	Tyr	Asn	Gln	Asp	Val	Ile	Ala	Asp	Arg	Ala	Asn	Pro	Ser	405	410	415	

Trp	Ala	Phe	Asn	Pro	Gly	Val	Leu	Glu	Lys	Ile	Val	Ala	Thr	Ser	Gln
			420					425					430		
Ala	Arg	Gly	Tyr	Ile	Ser	Gly	Asn	Gln	Tyr	Ile	Leu	Glu	Pro	Val	Asn
		435					440					445			
Ile	Ile	Asn	Gly	Asn	Gly	Tyr	Tyr	Asn	Met	Phe	Lys	Pro	Asp	Gly	Thr
	450					455					460				
Tyr	Leu	Phe	Ser	Ile	Asn	Cys	Lys	Thr	Gly	Tyr	Phe	Val	Gly	Asn	Gly
465					470					475					480
Lys	Gly	Tyr	Ala	Asp	Ala	Leu	Asp	Tyr							
				485											

<210> SEQ ID NO 11

<211> LENGTH: 861

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 11

ttgcggttat	ggttcgttat	gaataatcgt	catttattta	gtgggatatt	tttctttggt	60
attagtttat	gtctggcctt	tttattgcta	aatattatta	tccctaagtc	aaattcacgt	120
ttgaaaaaga	gtgattttct	gaaaaaagaa	caagtagcta	tccaatatgt	tgctatagga	180
gattcattga	cagaaggagt	aggtgatcta	actcatcaag	gtggttttgt	tcctttgtta	240
acgaatgata	tcagtgaata	ttttaaggct	aatgttaatc	atcaaaatta	cggcgtatct	300
ggtgatacca	gtcaacaaat	tcttgatagg	atgataaaac	aaaagcagat	acagttatct	360
ttaaaaaaag	cagatataat	gacgttaacc	gttggtggta	atgatgttat	ggcagttatt	420
cgaagaatt	tagcggattt	gcaagtttct	agttttagaa	agccagctcg	tcagtatcaa	480
aaacgattaa	gacagattat	cgagttagcc	agaaaagata	ataaagatct	tcctatTTTT	540
attttaggca	tctataatcc	gttttatttg	aattttccag	aactaactga	tatgcaaaaa	600
gtgattgatg	actggaatac	caaaaactaag	gagggttggtg	gagaatacga	tcgtgtgtac	660
tttgtgccaa	taaatgacct	cttgataaaa	gggataaatg	gacaagaagg	aattgttcat	720
tcttcaggag	atcaaaactac	aattgtcaat	gatgccttgt	ttactgggga	ccattttcac	780
ccaaataata	ctggctatca	aatcatgtca	aatgcagtaa	tggagaaaat	taaaaagcat	840
gaaaaaaaaa	tcaaacctta	a				861

<210> SEQ ID NO 12

<211> LENGTH: 286

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 12

Met	Arg	Leu	Trp	Phe	Val	Met	Asn	Asn	Arg	His	Leu	Phe	Ser	Gly	Ile
1				5					10					15	
Phe	Phe	Phe	Val	Ile	Ser	Leu	Cys	Leu	Ala	Phe	Leu	Leu	Leu	Asn	Ile
			20					25					30		
Ile	Ile	Pro	Lys	Ser	Asn	Ser	Arg	Leu	Lys	Lys	Ser	Asp	Phe	Leu	Lys
		35				40					45				
Lys	Glu	Gln	Val	Ala	Ile	Gln	Tyr	Val	Ala	Ile	Gly	Asp	Ser	Leu	Thr
	50				55					60					
Glu	Gly	Val	Gly	Asp	Leu	Thr	His	Gln	Gly	Gly	Phe	Val	Pro	Leu	Leu
65				70					75					80	
Thr	Asn	Asp	Leu	Ser	Glu	Tyr	Phe	Lys	Ala	Asn	Val	Asn	His	Gln	Asn
			85				90						95		
Tyr	Gly	Val	Ser	Gly	Asp	Thr	Ser	Gln	Gln	Ile	Leu	Asp	Arg	Met	Ile
		100					105						110		
Lys	Gln	Lys	Gln	Ile	Gln	Leu	Ser	Leu	Lys	Lys	Ala	Asp	Ile	Met	Thr
	115					120					125				
Leu	Thr	Val	Gly	Gly	Asn	Asp	Val	Met	Ala	Val	Ile	Arg	Lys	Asn	Leu
	130				135						140				
Ala	Asp	Leu	Gln	Val	Ser	Ser	Phe	Arg	Lys	Pro	Ala	Arg	Gln	Tyr	Gln
145				150						155					160

Lys	Arg	Leu	Arg	Gln	Ile	Ile	Glu	Leu	Ala	Arg	Lys	Asp	Asn	Lys	Asp
				165					170					175	
Leu	Pro	Ile	Phe	Ile	Leu	Gly	Ile	Tyr	Asn	Pro	Phe	Tyr	Leu	Asn	Phe
			180					185					190		
Pro	Glu	Leu	Thr	Asp	Met	Gln	Lys	Val	Ile	Asp	Asp	Trp	Asn	Thr	Lys
		195					200					205			
Thr	Lys	Glu	Val	Val	Gly	Glu	Tyr	Asp	Arg	Val	Tyr	Phe	Val	Pro	Ile
	210					215					220				
Asn	Asp	Leu	Leu	Tyr	Lys	Gly	Ile	Asn	Gly	Gln	Glu	Gly	Ile	Val	His
225					230				235					240	
Ser	Ser	Gly	Asp	Gln	Thr	Thr	Ile	Val	Asn	Asp	Ala	Leu	Phe	Thr	Gly
			245					250						255	
Asp	His	Phe	His	Pro	Asn	Asn	Thr	Gly	Tyr	Gln	Ile	Met	Ser	Asn	Ala
		260					265						270		
Val	Met	Glu	Lys	Ile	Lys	Lys	His	Glu	Lys	Lys	Ile	Lys	Pro		
		275					280					285			

<210> SEQ ID NO 13

<211> LENGTH: 696

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 13

atggtataaat	tgggttttcgc	tcgccacggt	gagtcagaat	ggaacaaagc	taacctcttc	60
actgggtggg	cagatgttga	tctttcagaa	aaagggacac	aacaagcgat	tgatgcaggt	120
aaattgatca	aagaagcagg	tattgaattt	gaccttgctt	tcacttcagt	attgacacgt	180
gctatcaaaa	caactaacct	tgcccttgaa	aatgcaggct	aattgtgggt	tccaactgaa	240
aaatcatggc	gcttgaacga	gcgtcactat	ggtgctttga	ctggcaaaaa	caaagctgaa	300
gctgcagaac	aattttgtga	tgaacaagtt	catatctggc	gtcgttcata	cgacgtgttg	360
ccgccagcta	tggctaaaaga	tgatgagtat	tcagcacaca	aagaccgtcg	ttatgctgat	420
cttgacccag	cccttattcc	agatgctgaa	aacttaaaag	tcactcttga	acgcgcaatg	480
ccttactggg	aagaaaaaat	tgctccagct	cttcttgacg	gtaaaaacgt	ctttgttggc	540
gcacatggta	actcaatccg	cgctcttggt	aaacacatta	aaggtctttc	agatgacgaa	600
atcatggatg	tggaaattcc	aaacttccca	ccacttggtt	ttgaattaga	tgaaaaactt	660
aacattgtta	aagaatacta	ccttggtggt	gaataa			696

<210> SEQ ID NO 14

<211> LENGTH: 231

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 14

Met	Val	Lys	Leu	Val	Phe	Ala	Arg	His	Gly	Glu	Ser	Glu	Trp	Asn	Lys
1				5					10					15	
Ala	Asn	Leu	Phe	Thr	Gly	Trp	Ala	Asp	Val	Asp	Leu	Ser	Glu	Lys	Gly
			20				25					30			
Thr	Gln	Gln	Ala	Ile	Asp	Ala	Gly	Lys	Leu	Ile	Lys	Glu	Ala	Gly	Ile
		35				40					45				
Glu	Phe	Asp	Leu	Ala	Phe	Thr	Ser	Val	Leu	Thr	Arg	Ala	Ile	Lys	Thr
	50				55					60					
Thr	Asn	Leu	Ala	Leu	Glu	Asn	Ala	Gly	Gln	Leu	Trp	Val	Pro	Thr	Glu
65				70					75					80	
Lys	Ser	Trp	Arg	Leu	Asn	Glu	Arg	His	Tyr	Gly	Ala	Leu	Thr	Gly	Lys
			85				90						95		
Asn	Lys	Ala	Glu	Ala	Ala	Glu	Gln	Phe	Cys	Asp	Glu	Gln	Val	His	Ile
		100					105					110			
Trp	Arg	Arg	Ser	Tyr	Asp	Val	Leu	Pro	Pro	Ala	Met	Ala	Lys	Asp	Asp
		115				120					125				
Glu	Tyr	Ser	Ala	His	Lys	Asp	Arg	Arg	Tyr	Ala	Asp	Leu	Asp	Pro	Ala

130	135	140
Leu Ile Pro Asp Ala	Glu Asn Leu Lys Val Thr	Leu Glu Arg Ala Met
145	150	155
Pro Tyr Trp Glu Glu Lys Ile Ala	Pro Ala Leu Leu Asp Gly Lys Asn	160
	165	170
Val Phe Val Gly Ala His Gly Asn Ser Ile Arg Ala Leu Val Lys His		175
	180	185
Ile Lys Gly Leu Ser Asp Asp Glu Ile Met Asp Val Glu Ile Pro Asn		190
	195	200
Phe Pro Pro Leu Val Phe Glu Leu Asp Glu Lys Leu Asn Ile Val Lys		205
	210	215
Glu Tyr Tyr Leu Gly Gly Glu		220
225	230	

<210> SEQ ID NO 15

<211> LENGTH: 1056

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 15

atgaaaaact	caaataaact	cattgctagt	gttgtgacat	tggcctcagt	gatggcttta	60
gcagcttgct	aatcaactaa	tgacaatact	aagggttattt	cgatgaaagg	tgatacaatt	120
agcggttagtg	attttttacaa	tgaaacaaaa	aacacagaag	tatcgcaaaa	agcgatgcta	180
aatctggtaa	ttagtcgtgt	ttttgaagct	caatatgggtg	ataaggtttc	aaaaaaagaa	240
gttgaaaagg	cgtatcataa	aacagctgaa	cagtatggcg	cttcattctc	tgctgctttg	300
gcacaatcaa	gcttgacacc	tgagactttt	aagcgtcaga	tccgctcttc	aaaattagta	360
gaatatgcgg	ttaaagaagc	agctaaaaaa	gaattgacaa	cacaagaata	taagaaagca	420
tatgaatctt	atactccaac	aatggcagtc	gaaatgatta	ctttagataa	tgaagagaca	480
gctaaatcag	tcttagagga	actaaaagcc	gaaggcgag	actttacagc	tattgctaaa	540
gaaaaacaa	caacacctga	gaaaaaagt	acctataaat	ttgattcagg	tgcgacaaat	600
gtaccgactg	atgtcgtaaa	agcggcttca	agtttgaatg	agggtggcat	atcagacgtt	660
atctcggttt	tagatccaac	ttcttatcaa	aagaagtttt	acattgttaa	gggtactaaa	720
aaagcagaaa	aaaaatcaga	ttggcaagaa	tataagaaac	gtttgaaagc	tatcattata	780
gctgaaaaat	caaaaagatat	gaatttccaa	aacaagggtta	ttgcaaatgc	attggataaa	840
gctaattgtaa	aaattaaaga	caaagctttt	gctaataattt	tggcgcaata	tgcaaatctt	900
gggtcaaaaaa	ctaaagctgc	aagtgaaagt	tcaacaacca	gcgaatcatc	aaaagctgca	960
gaagagaacc	catcagaatc	agagcaaaac	cagacatcat	cagctgaaga	accaactgag	1020
actgaggctc	agacgcaaga	gccagctgca	caataa			1056

<210> SEQ ID NO 16

<211> LENGTH: 351

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 16

Met Lys Asn Ser Asn Lys Leu Ile Ala Ser Val Val Thr Leu Ala Ser	
1	15
Val Met Ala Leu Ala Ala Cys Gln Ser Thr Asn Asp Asn Thr Lys Val	
20	30
Ile Ser Met Lys Gly Asp Thr Ile Ser Val Ser Asp Phe Tyr Asn Glu	
35	45
Thr Lys Asn Thr Glu Val Ser Gln Lys Ala Met Leu Asn Leu Val Ile	
50	60
Ser Arg Val Phe Glu Ala Gln Tyr Gly Asp Lys Val Ser Lys Lys Glu	
65	80
Val Glu Lys Ala Tyr His Lys Thr Ala Glu Gln Tyr Gly Ala Ser Phe	
85	95
Ser Ala Ala Leu Ala Gln Ser Ser Leu Thr Pro Glu Thr Phe Lys Arg	
100	110

Gln	Ile	Arg	Ser	Ser	Lys	Leu	Val	Glu	Tyr	Ala	Val	Lys	Glu	Ala	Ala	
		115					120					125				
Lys	Lys	Glu	Leu	Thr	Thr	Gln	Glu	Tyr	Lys	Lys	Ala	Tyr	Glu	Ser	Tyr	
		130				135					140					
Thr	Pro	Thr	Met	Ala	Val	Glu	Met	Ile	Thr	Leu	Asp	Asn	Glu	Glu	Thr	
					150					155					160	
Ala	Lys	Ser	Val	Leu	Glu	Glu	Leu	Lys	Ala	Glu	Gly	Ala	Asp	Phe	Thr	
				165					170					175		
Ala	Ile	Ala	Lys	Glu	Lys	Thr	Thr	Thr	Pro	Glu	Lys	Lys	Val	Thr	Tyr	
			180					185					190			
Lys	Phe	Asp	Ser	Gly	Ala	Thr	Asn	Val	Pro	Thr	Asp	Val	Val	Lys	Ala	
		195					200					205				
Ala	Ser	Ser	Leu	Asn	Glu	Gly	Gly	Ile	Ser	Asp	Val	Ile	Ser	Val	Leu	
		210				215					220					
Asp	Pro	Thr	Ser	Tyr	Gln	Lys	Lys	Phe	Tyr	Ile	Val	Lys	Val	Thr	Lys	
					230					235					240	
Lys	Ala	Glu	Lys	Lys	Ser	Asp	Trp	Gln	Glu	Tyr	Lys	Lys	Arg	Leu	Lys	
				245				250						255		
Ala	Ile	Ile	Ile	Ala	Glu	Lys	Ser	Lys	Asp	Met	Asn	Phe	Gln	Asn	Lys	
			260					265					270			
Val	Ile	Ala	Asn	Ala	Leu	Asp	Lys	Ala	Asn	Val	Lys	Ile	Lys	Asp	Lys	
		275					280				285					
Ala	Phe	Ala	Asn	Ile	Leu	Ala	Gln	Tyr	Ala	Asn	Leu	Gly	Gln	Lys	Thr	
		290				295					300					
Lys	Ala	Ala	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Glu	Ser	Ser	Lys	Ala	Ala	
					310				315					320		
Glu	Glu	Asn	Pro	Ser	Glu	Ser	Glu	Gln	Thr	Gln	Thr	Ser	Ser	Ala	Glu	
				325				330						335		
Glu	Pro	Thr	Glu	Thr	Glu	Ala	Gln	Thr	Gln	Glu	Pro	Ala	Ala	Gln		
			340					345					350			

<210> SEQ ID NO 17

<211> LENGTH: 1275

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 17

ttgaaaaaat	taaatgttat	tcttggttgg	ttattaagca	ttctgatgtt	gagtttagct	60
attgtgttta	ttaatcgttg	gaaactaaac	gaagatagtc	agcgtatagt	tttggctgaa	120
aagaaaaaaa	acacgtcaga	tttagtgatc	aaagctgtaa	aacatattaa	aaaagatcaa	180
aaagactatt	attatttttc	cccgataaaa	caagcagatg	atTTTTTTgt	agataattta	240
cctgtttcat	tatacaaaaa	aaagaattca	gataaagaat	tgatttttagt	aaggcctaaa	300
ctgcaatctt	ctcacctaag	atcagttaac	actttgacta	tttctaaaat	agtttatcag	360
aaaaaatttt	ttcatTTTggc	taaaaaatca	gaaaaagtta	taagtacata	tcacgttaca	420
gacgacttga	aaccgTTTca	ggtaaaggat	ctagtatcag	gacatttaga	aagaatacaa	480
gaagaagtTg	aaaaaaaaata	tccagatgct	ggTTTtaata	gcgataagta	taatggctta	540
aaagaatcta	attctTTtatt	aagcgatggc	tttgaggtaa	aatcgggaaa	ccttattttt	600
gataaaaaagc	taacgatacc	tttgacgaca	ttatttgatg	ttattaatcc	agatttttta	660
gcaaatagcg	atagagctgc	gtatgataat	tataggacct	acaaagaaca	gcatcccaaa	720
aaactagttg	cattaacgTt	tgatgatggT	ccagatccga	cgacgactcc	tcaagtttta	780
gatatttttg	caaaatacca	ggctaaggga	actttcttta	tgataggTtc	aaaggTtgtg	840
aataatgaaa	accttactaa	acgtgttagc	gacgctggcc	atgaaattgc	taatcatact	900
tgggatcatc	ctaactctgac	taatctttca	gtcagcgaga	ttcaacatca	agttaatatg	960
acgaaccagg	ctattgaaaa	agcttgTggc	aagaaacctc	gctattttacg	ccctccatac	1020
ggagctacaa	atgcaactgt	tcagcaatcc	tcaggattaa	cacaaatgct	ttggacggtt	1080
gatacaagag	attgggaaaa	tcatagcact	gatggcatta	tgactaatgt	caaaaaccaa	1140
ttgcaaccgg	gaggagTtgt	tttaatgcat	gatattcatc	aaacaactat	caatgctttg	1200
ccgacagtta	tggaaatatct	aaaagcagaa	ggatacgaat	gtgtgactgt	atcagaactc	1260

tatgcgcatc agtaa

1275

<210> SEQ ID NO 18

<211> LENGTH: 424

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 18

Met	Lys	Lys	Leu	Asn	Val	Ile	Leu	Val	Gly	Leu	Leu	Ser	Ile	Leu	Met
1			5						10					15	
Leu	Ser	Leu	Ala	Ile	Val	Phe	Ile	Asn	Arg	Trp	Lys	Leu	Asn	Glu	Asp
		20						25					30		
Ser	Gln	Arg	Ile	Val	Leu	Ala	Glu	Lys	Lys	Lys	Asn	Thr	Ser	Asp	Leu
	35						40					45			
Val	Ile	Lys	Ala	Val	Lys	His	Ile	Lys	Lys	Asp	Gln	Lys	Asp	Tyr	Tyr
	50					55					60				
Tyr	Phe	Ser	Pro	Ile	Lys	Gln	Ala	Asp	Asp	Phe	Phe	Val	Asp	Asn	Leu
65					70					75					80
Pro	Val	Ser	Leu	Tyr	Lys	Lys	Lys	Asn	Ser	Asp	Lys	Glu	Leu	Ile	Leu
			85						90					95	
Val	Arg	Pro	Lys	Leu	Gln	Ser	Ser	His	Leu	Arg	Ser	Val	Asn	Thr	Leu
		100						105					110		
Thr	Ile	Ser	Lys	Ile	Val	Tyr	Gln	Lys	Lys	Phe	Phe	His	Leu	Ala	Lys
	115						120					125			
Lys	Ser	Glu	Lys	Val	Ile	Ser	Thr	Tyr	His	Val	Thr	Asp	Asp	Leu	Lys
	130					135					140				
Pro	Phe	Gln	Val	Lys	Asp	Leu	Val	Ser	Gly	His	Leu	Glu	Arg	Ile	Gln
145					150					155					160
Glu	Glu	Val	Glu	Lys	Lys	Tyr	Pro	Asp	Ala	Gly	Phe	Asn	Ser	Asp	Lys
			165						170					175	
Tyr	Asn	Gly	Leu	Lys	Glu	Ser	Asn	Ser	Leu	Leu	Ser	Asp	Gly	Phe	Glu
		180						185					190		
Val	Lys	Ser	Gly	Asn	Leu	Ile	Phe	Asp	Lys	Lys	Leu	Thr	Ile	Pro	Leu
	195						200						205		
Thr	Thr	Leu	Phe	Asp	Val	Ile	Asn	Pro	Asp	Phe	Leu	Ala	Asn	Ser	Asp
	210					215					220				
Arg	Ala	Ala	Tyr	Asp	Asn	Tyr	Arg	Thr	Tyr	Lys	Glu	Gln	His	Pro	Lys
225					230					235					240
Lys	Leu	Val	Ala	Leu	Thr	Phe	Asp	Asp	Gly	Pro	Asp	Pro	Thr	Thr	Thr
			245						250					255	
Pro	Gln	Val	Leu	Asp	Ile	Leu	Ala	Lys	Tyr	Gln	Ala	Lys	Gly	Thr	Phe
		260						265					270		
Phe	Met	Ile	Gly	Ser	Lys	Val	Val	Asn	Asn	Glu	Asn	Leu	Thr	Lys	Arg
	275						280					285			
Val	Ser	Asp	Ala	Gly	His	Glu	Ile	Ala	Asn	His	Thr	Trp	Asp	His	Pro
	290					295					300				
Asn	Leu	Thr	Asn	Leu	Ser	Val	Ser	Glu	Ile	Gln	His	Gln	Val	Asn	Met
305					310					315					320
Thr	Asn	Gln	Ala	Ile	Glu	Lys	Ala	Cys	Gly	Lys	Lys	Pro	Arg	Tyr	Leu
			325						330					335	
Arg	Pro	Pro	Tyr	Gly	Ala	Thr	Asn	Ala	Thr	Val	Gln	Gln	Ser	Ser	Gly
		340						345					350		
Leu	Thr	Gln	Met	Leu	Trp	Thr	Val	Asp	Thr	Arg	Asp	Trp	Glu	Asn	His
	355						360					365			
Ser	Thr	Asp	Gly	Ile	Met	Thr	Asn	Val	Lys	Asn	Gln	Leu	Gln	Pro	Gly
	370					375					380				
Gly	Val	Val	Leu	Met	His	Asp	Ile	His	Gln	Thr	Thr	Ile	Asn	Ala	Leu
385					390					395					400

Pro Thr Val Met Glu Tyr Leu Lys Ala Glu Gly Tyr Glu Cys Val Thr
405 410 415
Val Ser Glu Leu Tyr Ala His Gln
420

<210> SEQ ID NO 19
<211> LENGTH: 1251
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 19

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atgcttaaga gactctggtt aattctaggt cctcttctta ttgcctttgt tttagtagtg      60
attactatitt ttagttttcc tacacaactt gatcattcca tagctcagga aaaagcaaatt      120
gccgttgcca tcacagatag ttcttttaaa aatgggttga ttaaaagaca agctttatca      180
gatgagactt gtcgttttgc gccttttttt gggtctagcg aatggagtcg aatggatagt      240
atgcaccctt cgggtgcttg agagcgctac aagcggagct atagaccatt ttttaattggt      300
aagagaggat cagcatcttt gtcgcattat tatgggtata aacaaattac caatgaaatg      360
caaaagaaaa aagccatctt tgtagtatct cctcaatggt ttactgctca agggattaat      420
cctagtgcgg ttcagatgta cttgtctaac actcaagtga ttgaattttt actaaaagct      480
agaactgata aagaatcaca gtttgcagca aagcgtttgc ttgagcttaa ccctgggtgtg      540
tctaaatcaa acttattgaa aaaagtaagt aagggttaagt ctcttagtcg gttagacaga      600
gctattttga aatgtcaaca tcaagtagca ttgagagaag agtccctttt tagtttttta      660
ggcaaactta ctaactatga aaaaagaatt ttgcctcgcg ttaagggatt acctaaagta      720
ttttcgtata aacaattgaa tgcattagca actaagagag gccaattagc aacaaccaac      780
aaccgttttg ggattaaaaa tacattttat cgtaaacgaa tagcacctaa atacaatctt      840
tataagaatt tccaagttaa ttatagttac ctggcgtcac cagaatacaa tgattttcag      900
cttttattat cagaatttgc taaacgaaaa acagatgtac tctttgttat aactcctggt      960
aataaagctt gggcggatta taccggctta aatcaagata agtatcaagc ggcagttcgt     1020
aaaataaaat tccagttaaa gtcacaagga tttcatcgca ttgctgactt ctcaaaagat     1080
gggtggtgagt cctactttat gcaagatacc atccatctcg gttggaatgg ctgggttagct     1140
tttgataaga aagtgcaacc atttctagaa acgaagcagc cagtgcccaa ctataaaatg     1200
aacccttatt tttatagtaa aatttgggca aataggaaag acttgcaata g               1251

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<210> SEQ ID NO 20
<211> LENGTH: 416
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 20

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Met Leu Lys Arg Leu Trp Leu Ile Leu Gly Pro Leu Leu Ile Ala Phe
1           5           10           15
Val Leu Val Val Ile Thr Ile Phe Ser Phe Pro Thr Gln Leu Asp His
20           25           30
Ser Ile Ala Gln Glu Lys Ala Asn Ala Val Ala Ile Thr Asp Ser Ser
35           40           45
Phe Lys Asn Gly Leu Ile Lys Arg Gln Ala Leu Ser Asp Glu Thr Cys
50           55           60
Arg Phe Val Pro Phe Phe Gly Ser Ser Glu Trp Ser Arg Met Asp Ser
65           70           75           80
Met His Pro Ser Val Leu Ala Glu Arg Tyr Lys Arg Ser Tyr Arg Pro
85           90           95
Phe Leu Ile Gly Lys Arg Gly Ser Ala Ser Leu Ser His Tyr Tyr Gly
100          105          110
Ile Gln Gln Ile Thr Asn Glu Met Gln Lys Lys Lys Ala Ile Phe Val
115          120          125
Val Ser Pro Gln Trp Phe Thr Ala Gln Gly Ile Asn Pro Ser Ala Val
130          135          140
Gln Met Tyr Leu Ser Asn Thr Gln Val Ile Glu Phe Leu Leu Lys Ala
145          150          155          160

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Arg	Thr	Asp	Lys	Glu	Ser	Gln	Phe	Ala	Ala	Lys	Arg	Leu	Leu	Glu	Leu		
				165					170					175			
Asn	Pro	Gly	Val	Ser	Lys	Ser	Asn	Leu	Leu	Lys	Lys	Val	Ser	Lys	Gly		
			180					185					190				
Lys	Ser	Leu	Ser	Arg	Leu	Asp	Arg	Ala	Ile	Leu	Lys	Cys	Gln	His	Gln		
		195				200						205					
Val	Ala	Leu	Arg	Glu	Glu	Ser	Leu	Phe	Ser	Phe	Leu	Gly	Lys	Ser	Thr		
	210				215						220						
Asn	Tyr	Glu	Lys	Arg	Ile	Leu	Pro	Arg	Val	Lys	Gly	Leu	Pro	Lys	Val		
225					230					235					240		
Phe	Ser	Tyr	Lys	Gln	Leu	Asn	Ala	Leu	Ala	Thr	Lys	Arg	Gly	Gln	Leu		
			245					250						255			
Ala	Thr	Thr	Asn	Asn	Arg	Phe	Gly	Ile	Lys	Asn	Thr	Phe	Tyr	Arg	Lys		
		260					265						270				
Arg	Ile	Ala	Pro	Lys	Tyr	Asn	Leu	Tyr	Lys	Asn	Phe	Gln	Val	Asn	Tyr		
	275					280						285					
Ser	Tyr	Leu	Ala	Ser	Pro	Glu	Tyr	Asn	Asp	Phe	Gln	Leu	Leu	Leu	Ser		
	290					295					300						
Glu	Phe	Ala	Lys	Arg	Lys	Thr	Asp	Val	Leu	Phe	Val	Ile	Thr	Pro	Val		
305					310					315					320		
Asn	Lys	Ala	Trp	Ala	Asp	Tyr	Thr	Gly	Leu	Asn	Gln	Asp	Lys	Tyr	Gln		
			325					330						335			
Ala	Ala	Val	Arg	Lys	Ile	Lys	Phe	Gln	Leu	Lys	Ser	Gln	Gly	Phe	His		
		340					345						350				
Arg	Ile	Ala	Asp	Phe	Ser	Lys	Asp	Gly	Gly	Glu	Ser	Tyr	Phe	Met	Gln		
	355					360						365					
Asp	Thr	Ile	His	Leu	Gly	Trp	Asn	Gly	Trp	Leu	Ala	Phe	Asp	Lys	Lys		
	370				375						380						
Val	Gln	Pro	Phe	Leu	Glu	Thr	Lys	Gln	Pro	Val	Pro	Asn	Tyr	Lys	Met		
385				390						395					400		
Asn	Pro	Tyr	Phe	Tyr	Ser	Lys	Ile	Trp	Ala	Asn	Arg	Lys	Asp	Leu	Gln		
			405					410						415			

<210> SEQ ID NO 21

<211> LENGTH: 2136

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 21

atgagagaat	tacatatcaa	aacttataag	ttattaacga	aaagtgctgt	tttacttggc	60
ttaattttcat	ttccactaac	tgttttctgct	gccgataatg	cttctgtcac	caacaaagca	120
gattttttcaa	cagatacgat	ttatcagatt	gtaacagatc	gtttttaacga	tggtaatacc	180
tctaataatg	gtaagactga	tgtttttgat	aaaaatgacc	ttaaaaaata	ccatggaggt	240
gattggcaag	gaatcatcgc	caagattaag	gatgggtacc	tgacagatat	ggggatttct	300
gccatttgga	tttcttctcc	tgttgaaaat	atcgacagta	ttgatccttc	taatggaagt	360
gctgcatatc	atgggtattg	ggctaaggac	ttctttaaaa	caaaccagca	ttttggcact	420
gaagcagact	ttcaacaact	agtcaaagta	gctcatcaac	accatattaa	ggtagttatt	480
gatttttgctc	ctaatacatc	gtctacagcc	gaaaaagaag	gcacaacttt	caaagaagat	540
ggcgcttttat	ataaaaaacg	taaattagtt	ggtaaatttt	cagatgataa	agacaagatt	600
tttaatcatg	aatcttggac	cgatttttagt	acttatgaaa	attctattta	tcattcaatg	660
tacggactag	ctgatttaaa	taacattaat	ccgaaagttg	accagtacat	gaaagaagct	720
attgataaat	ggtagacct	gggtgttgat	ggatccgag	ttgacgctgt	taaacatatg	780
tcacaagggt	ggcaaaaaaa	ttggttgagt	catatctatg	aaaaacataa	tgtctttgtt	840
ttcgggggaat	ggttctcggg	acataccgac	gatgattatg	atatgacgac	atttgctaac	900
aatagtggga	tggggctttt	agatttttaga	tttgccaatg	ctattagaca	gttgatataca	960
ggtttttcaa	cgtttaccat	gcgagatttt	tacaagggtc	ttgaaaatag	agatcagggtg	1020
actaatgaag	tgacagacca	ggtgaccttt	attgataatc	atgatatgga	acgcttcgca	1080
acaaaagtgg	ctaataatca	aactgctgtt	aatcaagcct	atgctttgct	tttaacatct	1140

agaggtgtgc	ctaataattta	ttatggtaca	gagcagtatg	caacaggtga	taaagatcct	1200
aataatcgtg	gtgatatgcc	aagttttaat	aaagagtcac	aagcctataa	agtgattagt	1260
aagctagctc	ctttaagaaa	acaaaatcaa	gcttttagctt	atggaacaac	tgaacaacgt	1320
tggattagtg	atcatgtttt	ggtatttgag	cgtaaatttg	gtaatcatgt	cgactagtg	1380
gctattaata	gagatcaaac	gaatggttat	acaattacta	atgctaaaac	agccttgccc	1440
caaaatagct	acaaggacaa	attagaaggt	cttcttgggc	gtcaagaatt	aatagttgga	1500
gcagatggca	ctattagtag	ctttgaactt	ggagcggggc	aagtcgctgt	atggacttat	1560
gaaggagagg	acaagacacc	acaacttgga	gatgtcgatg	cttcagtggg	tattgctgga	1620
aataagatta	ctatttcagg	tcaaggtttt	ggtaattcta	aaggtcaagt	gacttttgga	1680
gaaatctctg	ctgagatcct	ttcttggtca	gataccctta	tcaccttaaa	agtaccgacg	1740
gttccagcaa	attattataa	catttcagtg	acaactgccg	ataagcaaac	cagcaatagt	1800
taccaagcct	ttgaagtatt	gactgataaa	caaattcctg	ttcgtttact	catcaatgat	1860
tttaagacag	taccagggga	acaactatat	ctcatgggtg	atgtttttga	gatgggggga	1920
aatgacgcta	agaatgctgt	tggtcctcta	tttaataaca	ctcagaccat	tgccaagtac	1980
ccaaactggg	tctttgatac	tcattctacca	atcaataaag	aaatagcagt	caaacttggt	2040
aaaaaagata	gtattgggaa	tgttttatgg	acaagtcctg	agacttatag	tataaagaca	2100
gggcatgaag	cacaaacat	tactataaaa	aaataa			2136

<210> SEQ ID NO 22

<211> LENGTH: 711

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 22

Met	Arg	Glu	Leu	His	Ile	Lys	Thr	Tyr	Lys	Leu	Leu	Thr	Lys	Ser	Ala
1				5					10					15	
Val	Leu	Leu	Gly	Leu	Ile	Ser	Phe	Pro	Leu	Thr	Val	Ser	Ala	Ala	Asp
			20					25					30		
Asn	Ala	Ser	Val	Thr	Asn	Lys	Ala	Asp	Phe	Ser	Thr	Asp	Thr	Ile	Tyr
		35					40					45			
Gln	Ile	Val	Thr	Asp	Arg	Phe	Asn	Asp	Gly	Asn	Thr	Ser	Asn	Asn	Gly
	50					55				60					
Lys	Thr	Asp	Val	Phe	Asp	Lys	Asn	Asp	Leu	Lys	Lys	Tyr	His	Gly	Gly
65				70					75					80	
Asp	Trp	Gln	Gly	Ile	Ile	Ala	Lys	Ile	Lys	Asp	Gly	Tyr	Leu	Thr	Asp
			85					90					95		
Met	Gly	Ile	Ser	Ala	Ile	Trp	Ile	Ser	Ser	Pro	Val	Glu	Asn	Ile	Asp
			100					105					110		
Ser	Ile	Asp	Pro	Ser	Asn	Gly	Ser	Ala	Ala	Tyr	His	Gly	Tyr	Trp	Ala
		115				120						125			
Lys	Asp	Phe	Phe	Lys	Thr	Asn	Gln	His	Phe	Gly	Thr	Glu	Ala	Asp	Phe
	130					135					140				
Gln	Gln	Leu	Val	Lys	Val	Ala	His	Gln	His	His	Ile	Lys	Val	Val	Ile
145					150					155				160	
Asp	Phe	Ala	Pro	Asn	His	Thr	Ser	Thr	Ala	Glu	Lys	Glu	Gly	Thr	Thr
			165					170						175	
Phe	Lys	Glu	Asp	Gly	Ala	Leu	Tyr	Lys	Asn	Gly	Lys	Leu	Val	Gly	Lys
		180						185					190		
Phe	Ser	Asp	Asp	Lys	Asp	Lys	Ile	Phe	Asn	His	Glu	Ser	Trp	Thr	Asp
	195					200						205			
Phe	Ser	Thr	Tyr	Glu	Asn	Ser	Ile	Tyr	His	Ser	Met	Tyr	Gly	Leu	Ala
	210					215					220				
Asp	Leu	Asn	Asn	Ile	Asn	Pro	Lys	Val	Asp	Gln	Tyr	Met	Lys	Glu	Ala
225					230					235				240	
Ile	Asp	Lys	Trp	Leu	Asp	Leu	Gly	Val	Asp	Gly	Ile	Arg	Val	Asp	Ala
			245					250						255	
Val	Lys	His	Met	Ser	Gln	Gly	Trp	Gln	Lys	Asn	Trp	Leu	Ser	His	Ile
			260					265					270		

Tyr	Glu	Lys	His	Asn	Val	Phe	Val	Phe	Gly	Glu	Trp	Phe	Ser	Gly	His
		275					280					285			
Thr	Asp	Asp	Asp	Tyr	Asp	Met	Thr	Thr	Phe	Ala	Asn	Asn	Ser	Gly	Met
	290					295					300				
Gly	Leu	Leu	Asp	Phe	Arg	Phe	Ala	Asn	Ala	Ile	Arg	Gln	Leu	Tyr	Thr
305					310					315					320
Gly	Phe	Ser	Thr	Phe	Thr	Met	Arg	Asp	Phe	Tyr	Lys	Val	Leu	Glu	Asn
				325					330					335	
Arg	Asp	Gln	Val	Thr	Asn	Glu	Val	Thr	Asp	Gln	Val	Thr	Phe	Ile	Asp
			340					345					350		
Asn	His	Asp	Met	Glu	Arg	Phe	Ala	Thr	Lys	Val	Ala	Asn	Asn	Gln	Thr
		355					360					365			
Ala	Val	Asn	Gln	Ala	Tyr	Ala	Leu	Leu	Leu	Thr	Ser	Arg	Gly	Val	Pro
	370					375					380				
Asn	Ile	Tyr	Tyr	Gly	Thr	Glu	Gln	Tyr	Ala	Thr	Gly	Asp	Lys	Asp	Pro
385					390					395					400
Asn	Asn	Arg	Gly	Asp	Met	Pro	Ser	Phe	Asn	Lys	Glu	Ser	Gln	Ala	Tyr
				405					410					415	
Lys	Val	Ile	Ser	Lys	Leu	Ala	Pro	Leu	Arg	Lys	Gln	Asn	Gln	Ala	Leu
			420					425					430		
Ala	Tyr	Gly	Thr	Thr	Glu	Gln	Arg	Trp	Ile	Ser	Asp	His	Val	Leu	Val
		435					440					445			
Phe	Glu	Arg	Lys	Phe	Gly	Asn	His	Val	Ala	Leu	Val	Ala	Ile	Asn	Arg
	450					455					460				
Asp	Gln	Thr	Asn	Gly	Tyr	Thr	Ile	Thr	Asn	Ala	Lys	Thr	Ala	Leu	Pro
465					470					475					480
Gln	Asn	Ser	Tyr	Lys	Asp	Lys	Leu	Glu	Gly	Leu	Leu	Gly	Gly	Gln	Glu
				485					490					495	
Leu	Ile	Val	Gly	Ala	Asp	Gly	Thr	Ile	Ser	Ser	Phe	Glu	Leu	Gly	Ala
			500					505					510		
Gly	Gln	Val	Ala	Val	Trp	Thr	Tyr	Glu	Gly	Glu	Asp	Lys	Thr	Pro	Gln
		515					520					525			
Leu	Gly	Asp	Val	Asp	Ala	Ser	Val	Gly	Ile	Ala	Gly	Asn	Lys	Ile	Thr
	530					535					540				
Ile	Ser	Gly	Gln	Gly	Phe	Gly	Asn	Ser	Lys	Gly	Gln	Val	Thr	Phe	Gly
545					550					555					560
Glu	Ile	Ser	Ala	Glu	Ile	Leu	Ser	Trp	Ser	Asp	Thr	Leu	Ile	Thr	Leu
				565					570					575	
Lys	Val	Pro	Thr	Val	Pro	Ala	Asn	Tyr	Tyr	Asn	Ile	Ser	Val	Thr	Thr
			580					585					590		
Ala	Asp	Lys	Gln	Thr	Ser	Asn	Ser	Tyr	Gln	Ala	Phe	Glu	Val	Leu	Thr
		595					600					605			
Asp	Lys	Gln	Ile	Pro	Val	Arg	Leu	Leu	Ile	Asn	Asp	Phe	Lys	Thr	Val
	610					615					620				
Pro	Gly														

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<210> SEQ ID NO 23
<211> LENGTH: 1248
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 23
atgaaatcat ggcaaaaagt tatcgtcggc ggagcaagtt tgacacttgc aagtaccttg      60
ttagtgggat gtggatcagg ttcaaaagat aaaaaggaag ctggcgctga ctcaaagact    120
attaaacttt ggggtaccgac tggctctaaa aaatcatatg cagataccat tgcaaaattt    180
gaaaaagatt ctggttacac cgttaaagtg gttgaatcag aagatccaaa agcacaagaa    240
aaaatcaaaa aagatgcctc aactgctgcc gatgtctttt cacttcctca tgatcaactt    300
ggtcaacttg tagaatctgg tactattcaa gaagttccag aaaagtacaa taaagaaatt    360
gctgctactt ctactgatca ggcgctcgtc ggtgcacagt acaaagggaa aacatatgct    420
ttcccatttg gtattgaatc acaagttctt ttctacaata aatcaaaatt agctgctgaa    480
gacgttactt catatgatac aattactaca aaagcaactt ttggtggtac ctttaaacia    540
gctaacactt acgctactgg tccattattc atgtcagttg gtaacacttt atttggggaa    600
aacggtgaag atgtaaaaagg tactaaactgg ggcaatgaaa aaggcgctgc tgttcttaaa    660
tggatcgtag accaagcttc aaataaaggt tttgttagct tagatgctaa caacgttatg    720
tctaaatttg gtgacggttc agtagcttcc tttgaatcag gaccgtggga ctatgaagct    780
gctcaaaaag ctatcggtaa agaaaacctt ggtgttgcta tttatccaaa agtaactatt    840
ggaggcgaaa cggttcaaca aaaagcattc ttgggtgtaa aactttacgc agtcaaccaa    900
gcaccagcta aaggtgatac aaaacgtatc gcagctagct acaaattggc atcctacttg    960
actaatgctg aaagccaaga aaaccaattc aaaactcgta acattgtccc agccaacaaa   1020
gaagttcaat cttcagaagc tgttcaatca aacgaacttg ctaaaaccgt tatcactatg   1080
ggttcttctt cagactacac tgtcgtaatg ccaaaactta gccaaatggg cacattctgg   1140
actgaaagtg ctgctattct tagtgatgcc ttcaacggta aaatcaaaga aaacgactac   1200
cttactaagt tgcaacaatt cgacaaagat atcgctgcaa caaaataa                   1248

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<210> SEQ ID NO 24
<211> LENGTH: 415
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 24
Met Lys Ser Trp Gln Lys Val Ile Val Gly Gly Ala Ser Leu Thr Leu
1      5      10      15
Ala Ser Thr Leu Val Gly Cys Gly Ser Gly Ser Lys Asp Lys Lys
20     25     30
Glu Ala Gly Ala Asp Ser Lys Thr Ile Lys Leu Trp Val Pro Thr Gly
35     40     45
Ser Lys Lys Ser Tyr Ala Asp Thr Ile Ala Lys Phe Glu Lys Asp Ser
50     55     60
Gly Tyr Thr Val Lys Val Val Glu Ser Glu Asp Pro Lys Ala Gln Glu
65     70     75     80
Lys Ile Lys Lys Asp Ala Ser Thr Ala Ala Asp Val Phe Ser Leu Pro
85     90     95
His Asp Gln Leu Gly Gln Leu Val Glu Ser Gly Thr Ile Gln Glu Val
100    105    110
Pro Glu Lys Tyr Asn Lys Glu Ile Ala Ala Thr Ser Thr Asp Gln Ala
115    120    125
Leu Val Gly Ala Gln Tyr Lys Gly Lys Thr Tyr Ala Phe Pro Phe Gly
130    135    140
Ile Glu Ser Gln Val Leu Phe Tyr Asn Lys Ser Lys Leu Ala Ala Glu
145    150    155    160
Asp Val Thr Ser Tyr Asp Thr Ile Thr Thr Lys Ala Thr Phe Gly Gly
165    170    175
Thr Phe Lys Gln Ala Asn Thr Tyr Ala Thr Gly Pro Leu Phe Met Ser
180    185    190
Val Gly Asn Thr Leu Phe Gly Glu Asn Gly Glu Asp Val Lys Gly Thr

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Ile	His	Lys	Asn	Lys	Ala	Ser	Arg	Asp	Lys	Ala	Arg	Leu	Ala	Ala	Lys
65					70					75					80
Leu	Gly														

<210> SEQ ID NO 29

<211> LENGTH: 351

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 29

atgaaaagat	atgaagtgac	tgtcaatgga	caggtttatg	aagtgaagttt	acgtgaacta	60
gttgatggag	aaactgttga	agttagccag	ccagcagcac	ccgctactga	gaaagaaatg	120
aatgccaacg	ctgctggcgg	tggcattcag	gtaaaaggctc	caatgtcttg	aacagtcttg	180
tctatctttg	ctacagaagg	aaaagctgtt	aaaaaaggag	aagctgttct	ggctcttagag	240
gccatgaaaa	tggagaatga	aattctagca	cctgcagatg	gtctggtttc	aaaaattcat	300
gttggtggcta	accaaacggt	cgagtctgaa	caagttttga	tttcattcta	g	351

<210> SEQ ID NO 30

<211> LENGTH: 116

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 30

Met	Lys	Arg	Tyr	Glu	Val	Thr	Val	Asn	Gly	Gln	Val	Tyr	Glu	Val	Ser
1				5				10					15		
Leu	Arg	Glu	Leu	Val	Asp	Gly	Glu	Thr	Val	Glu	Val	Ser	Gln	Pro	Ala
			20					25					30		
Ala	Pro	Ala	Thr	Glu	Lys	Glu	Met	Asn	Ala	Asn	Ala	Ala	Gly	Gly	Gly
			35					40					45		
Ile	Gln	Val	Lys	Ala	Pro	Met	Ser	Gly	Thr	Val	Leu	Ser	Ile	Phe	Ala
	50					55					60				
Thr	Glu	Gly	Lys	Ala	Val	Lys	Lys	Gly	Glu	Ala	Val	Leu	Val	Leu	Glu
65					70					75					80
Ala	Met	Lys	Met	Glu	Asn	Glu	Ile	Leu	Ala	Pro	Ala	Asp	Gly	Leu	Val
				85					90					95	
Ser	Lys	Ile	His	Val	Val	Ala	Asn	Gln	Thr	Val	Glu	Ser	Glu	Gln	Val
			100					105					110		
Leu	Ile	Ser	Phe												
			115												

<210> SEQ ID NO 31

<211> LENGTH: 750

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 31

atggtaaaaa	aacaaaagcg	tcgaaaaata	aaatccatgt	cttgggcaag	aaaactacta	60
atagctgtac	ttttaattct	aggtttagca	ttgcttttta	acaaacctat	ccgaaataca	120
ttaattgctc	gaaactctaa	taaatatcaa	gtaacgaaag	tttcgaaaaa	acaaatcaaa	180
aagaataaag	aggctaagtc	aacatttgat	ttccaagccg	tagagccagt	tagtacagag	240
agtgtcttgc	aagcacaaat	ggcggctcag	caacttcctg	ttataggggg	cattgccata	300
ccagagcttg	gcattaatth	accaattttt	aaaggttttag	gaaataactga	gcttattttat	360
ggcgcaggaa	cgatgaaaga	agaacaagtt	atgggaggag	aaaataatta	ttctcttgcc	420
agtcatacata	tttttggaat	tacaggttca	tctcaaagtc	tcttttcgcc	gcttgaaaga	480
gcacaaaatg	ggatgtccat	ctatttaaca	gataaagaaa	aaatttacga	atacatcata	540
aaagatgttt	tcacggtagc	tcctgaacgc	gttgatgtta	tcgatgatac	agctggctctc	600
aaagaagtga	ctttagtgac	ttgtacagat	atcgaagcaa	cagaacgtat	tattgtcaaa	660
ggagaactaa	aaacagaata	cgattttgat	aaagcgcccg	ccgatgtatt	gaaagctttt	720
aatcattctt	ataaccaagt	atctacctag				750

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<210> SEQ ID NO 32
<211> LENGTH: 249
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 32
Met Val Lys Lys Gln Lys Arg Arg Lys Ile Lys Ser Met Ser Trp Ala
1          5          10          15
Arg Lys Leu Leu Ile Ala Val Leu Leu Ile Leu Gly Leu Ala Leu Leu
20          25          30
Phe Asn Lys Pro Ile Arg Asn Thr Leu Ile Ala Arg Asn Ser Asn Lys
35          40          45
Tyr Gln Val Thr Lys Val Ser Lys Lys Gln Ile Lys Lys Asn Lys Glu
50          55          60
Ala Lys Ser Thr Phe Asp Phe Gln Ala Val Glu Pro Val Ser Thr Glu
65          70          75          80
Ser Val Leu Gln Ala Gln Met Ala Ala Gln Gln Leu Pro Val Ile Gly
85          90          95
Gly Ile Ala Ile Pro Glu Leu Gly Ile Asn Leu Pro Ile Phe Lys Gly
100         105         110
Leu Gly Asn Thr Glu Leu Ile Tyr Gly Ala Gly Thr Met Lys Glu Glu
115         120         125
Gln Val Met Gly Gly Glu Asn Asn Tyr Ser Leu Ala Ser His His Ile
130         135         140
Phe Gly Ile Thr Gly Ser Ser Gln Met Leu Phe Ser Pro Leu Glu Arg
145         150         155         160
Ala Gln Asn Gly Met Ser Ile Tyr Leu Thr Asp Lys Glu Lys Ile Tyr
165         170         175
Glu Tyr Ile Ile Lys Asp Val Phe Thr Val Ala Pro Glu Arg Val Asp
180         185         190
Val Ile Asp Asp Thr Ala Gly Leu Lys Glu Val Thr Leu Val Thr Cys
195         200         205
Thr Asp Ile Glu Ala Thr Glu Arg Ile Ile Val Lys Gly Glu Leu Lys
210         215         220
Thr Glu Tyr Asp Phe Asp Lys Ala Pro Ala Asp Val Leu Lys Ala Phe
225         230         235         240
Asn His Ser Tyr Asn Gln Val Ser Thr
245

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<210> SEQ ID NO 33
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 33
ttggaggaaa tcacaatggc attgaacatt gaaaacatta ttgctgaaat taaagaagct      60
tcaatccttg agcttaacga tcttgtaaaa gctatcgaag aagaatttgg tgtaactgca      120
gctgctcctg tagctgctgc agctgctggg ggtgctgaag aagctgctaa agattcattc      180
gacgttgaat tgacatctgc tggcgacaaa aaagttggcg ttatcaaagc tgttcgtgaa      240
atcacagggtc ttggtcttaa agaagctaaa ggtccttggtg atggagcacc tgctaacgtt      300
aaagaaggcg ttgctgctgc agaagctgaa gaaatcaaag ctaaacttga agaagctgga      360
gcaacaatca ctcttaaata a                                     381

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<210> SEQ ID NO 34
<211> LENGTH: 126
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 34
Met Glu Glu Ile Thr Met Ala Leu Asn Ile Glu Asn Ile Ile Ala Glu

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1				5					10					15			
Ile	Lys	Glu	Ala	Ser	Ile	Leu	Glu	Leu	Asn	Asp	Leu	Val	Lys	Ala	Ile		
			20					25					30				
Glu	Glu	Glu	Phe	Gly	Val	Thr	Ala	Ala	Ala	Pro	Val	Ala	Ala	Ala	Ala		
		35					40					45					
Ala	Gly	Gly	Ala	Glu	Glu	Ala	Ala	Lys	Asp	Ser	Phe	Asp	Val	Glu	Leu		
	50					55					60						
Thr	Ser	Ala	Gly	Asp	Lys	Lys	Val	Gly	Val	Ile	Lys	Ala	Val	Arg	Glu		
65					70				75					80			
Ile	Thr	Gly	Leu	Gly	Leu	Lys	Glu	Ala	Lys	Gly	Leu	Val	Asp	Gly	Ala		
			85					90					95				
Pro	Ala	Asn	Val	Lys	Glu	Gly	Val	Ala	Ala	Ala	Glu	Ala	Glu	Glu	Ile		
		100						105					110				
Lys	Ala	Lys	Leu	Glu	Glu	Ala	Gly	Ala	Thr	Ile	Thr	Leu	Lys				
		115					120						125				

<210> SEQ ID NO 35

<211> LENGTH: 1764

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 35

atggctgttg	aaattattat	gccaaaactc	ggtgttgaca	tgcaagaagg	tgaaatcatc	60
gagtggaaaa	aacaagaagg	tgatactgtc	aatgaaggcg	atattcttct	tgaaatcatg	120
tcagataaaa	ccaatatgga	acttgaggca	gaagactcag	gtgttcttct	taaaattaca	180
cgtcaagcag	gtgaaacagt	acctgtaaca	gaagttatcg	gatataatcg	tgctgaaggt	240
gaatctgttg	aggtttctag	cccagctgct	tcagatgtga	atgttgctcg	tacaacagaa	300
gatttagaag	ctgctggact	tgaagtgcc	aaagcaccag	ctcaagctgc	ttcagctgca	360
ccaaaagctg	cacttgctga	tgatgagtat	gacatcatcg	ttgttggtgg	tgccctgca	420
ggttattatg	cagctattcg	tggtgctcaa	cttggtggta	aaattgccat	cgttgagaaa	480
tctgaatttg	gtggaacttg	cttgaacgta	gggtgatcc	caaccaaacc	ttaccttaaa	540
aatgctgaaa	tccttgatgg	tattaagatt	gcagcaggac	gtgggattaa	ccttgccctca	600
actaactata	ctattgacat	ggacaaaaca	gttgacttta	aaaacaccgt	tgtaaaaacc	660
ttaacaggcg	gcgttcaagg	tcttctaaaa	gctaataaag	tcactatctt	taatgggctt	720
ggtcaagtc	accctgacaa	gactgtaacc	attgggtcac	aaaccattaa	gggtcgcaac	780
gttatccttg	ctacagggtc	taaaagtatca	cgtatcaata	tcccagggtat	tgactctaaa	840
cttgtcttaa	cgtcagatga	tatccttgac	ctccgtgaaa	tgccaaaatc	actagcagtt	900
atgggcgggtg	gtgttggttg	tatcgagctt	ggacttggtt	gggcatctta	cgggtgtggat	960
gttaccgtta	ttgaaatggc	tgaccgtatt	atcccagcta	tggtataaaga	agtctctctt	1020
gaacttcaaa	aaatcctttc	taagaaaggc	atgaagatca	aaacatctgt	tggtgtctct	1080
gaaattgttg	aagcaaataa	ccaattgact	ttgaaactta	acaatgggtga	agaagttggt	1140
gctgaaaaag	ctcttctttc	tatcggacgt	gtatcacaaa	tgaacgggtct	ggaaaatctt	1200
aaccttgaaa	tggatcgtaa	ccgtatcaaa	gttaatgact	accaagagac	atcaattcca	1260
ggtatctatg	cgccagggtga	cgttaacgga	acgaaaatgc	ttgctcacgc	tgcttaccgt	1320
atgggtgaag	tggctgcaga	aaatgcgatg	catggcaaca	caactcgtaa	agctaaccct	1380
aaatacactc	cagcagctgt	ttacacacac	cctgaagtgg	caatggttgg	tttaactgaa	1440
gaacaagcgc	gtgaacaata	tggtgatgtg	cttattggta	aaaacagctt	tactggtaat	1500
ggacgcgcga	ttgcttcaaa	tgaagcacat	ggttttgtta	aagttattgc	tgatgccaaa	1560
taccacgaaa	tcttaggtgt	tcatattatt	ggccagctg	cagctgagat	gattaacgaa	1620
gcagctacta	ttatggaatc	tgaattaacc	gttgatgaat	tggtattatc	aattcatgga	1680
cacccaacct	tctctgaagt	gatgtacgaa	gcctttgcag	atgtgcttgg	cgaagctatc	1740
cataacccac	caaaacgtaa	gtaa				1764

<210> SEQ ID NO 36

<211> LENGTH: 587

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 36

Met	Ala	Val	Glu	Ile	Ile	Met	Pro	Lys	Leu	Gly	Val	Asp	Met	Gln	Glu	1	5	10	15
Gly	Glu	Ile	Ile	Glu	Trp	Lys	Lys	Gln	Glu	Gly	Asp	Thr	Val	Asn	Glu	20	25	30	
Gly	Asp	Ile	Leu	Leu	Glu	Ile	Met	Ser	Asp	Lys	Thr	Asn	Met	Glu	Leu	35	40	45	
Glu	Ala	Glu	Asp	Ser	Gly	Val	Leu	Leu	Lys	Ile	Thr	Arg	Gln	Ala	Gly	50	55	60	
Glu	Thr	Val	Pro	Val	Thr	Glu	Val	Ile	Gly	Tyr	Ile	Gly	Ala	Glu	Gly	65	70	75	80
Glu	Ser	Val	Glu	Val	Ser	Ser	Pro	Ala	Ala	Ser	Asp	Val	Asn	Val	Ala	85	90	95	
Arg	Thr	Thr	Glu	Asp	Leu	Glu	Ala	Ala	Gly	Leu	Glu	Val	Pro	Lys	Ala	100	105	110	
Pro	Ala	Gln	Ala	Ala	Ser	Ala	Ala	Pro	Lys	Ala	Ala	Leu	Ala	Asp	Asp	115	120	125	
Glu	Tyr	Asp	Ile	Ile	Val	Val	Gly	Gly	Gly	Pro	Ala	Gly	Tyr	Tyr	Ala	130	135	140	
Ala	Ile	Arg	Gly	Ala	Gln	Leu	Gly	Gly	Lys	Ile	Ala	Ile	Val	Glu	Lys	145	150	155	160
Ser	Glu	Phe	Gly	Gly	Thr	Cys	Leu	Asn	Val	Gly	Cys	Ile	Pro	Thr	Lys	165	170	175	
Thr	Tyr	Leu	Lys	Asn	Ala	Glu	Ile	Leu	Asp	Gly	Ile	Lys	Ile	Ala	Ala	180	185	190	
Gly	Arg	Gly	Ile	Asn	Leu	Ala	Ser	Thr	Asn	Tyr	Thr	Ile	Asp	Met	Asp	195	200	205	
Lys	Thr	Val	Asp	Phe	Lys	Asn	Thr	Val	Val	Lys	Thr	Leu	Thr	Gly	Gly	210	215	220	
Val	Gln	Gly	Leu	Leu	Lys	Ala	Asn	Lys	Val	Thr	Ile	Phe	Asn	Gly	Leu	225	230	235	240
Gly	Gln	Val	Asn	Pro	Asp	Lys	Thr	Val	Thr	Ile	Gly	Ser	Gln	Thr	Ile	245	250	255	
Lys	Gly	Arg	Asn	Val	Ile	Leu	Ala	Thr	Gly	Ser	Lys	Val	Ser	Arg	Ile	260	265	270	
Asn	Ile	Pro	Gly	Ile	Asp	Ser	Lys	Leu	Val	Leu	Thr	Ser	Asp	Asp	Ile	275	280	285	
Leu	Asp	Leu	Arg	Glu	Met	Pro	Lys	Ser	Leu	Ala	Val	Met	Gly	Gly	Gly	290	295	300	
Val	Val	Gly	Ile	Glu	Leu	Gly	Leu	Val	Trp	Ala	Ser	Tyr	Gly	Val	Asp	305	310	315	320
Val	Thr	Val	Ile	Glu	Met	Ala	Asp	Arg	Ile	Ile	Pro	Ala	Met	Asp	Lys	325	330	335	
Glu	Val	Ser	Leu	Glu	Leu	Gln	Lys	Ile	Leu	Ser	Lys	Lys	Gly	Met	Lys	340	345	350	
Ile	Lys	Thr	Ser	Val	Gly	Val	Ser	Glu	Ile	Val	Glu	Ala	Asn	Asn	Gln	355	360	365	
Leu	Thr	Leu	Lys	Leu	Asn	Asn	Gly	Glu	Glu	Val	Val	Ala	Glu	Lys	Ala	370	375	380	
Leu	Leu	Ser	Ile	Gly	Arg	Val	Ser	Gln	Met	Asn	Gly	Leu	Glu	Asn	Leu	385	390	395	400
Asn	Leu	Glu	Met	Asp	Arg	Asn	Arg	Ile	Lys	Val	Asn	Asp	Tyr	Gln	Glu	405	410	415	
Thr	Ser	Ile	Pro	Gly	Ile	Tyr	Ala	Pro	Gly	Asp	Val	Asn	Gly	Thr	Lys	420	425	430	
Met	Leu	Ala	His	Ala	Ala	Tyr	Arg	Met	Gly	Glu	Val	Ala	Ala	Glu	Asn	435	440	445	
Ala	Met	His	Gly	Asn	Thr	Thr	Arg	Lys	Ala	Asn	Leu	Lys	Tyr	Thr	Pro				

450	Ala Ala Val Tyr Thr His	455	Pro Glu Val Ala Met	460	Val Gly Leu Thr Glu
465	Glu Gln Ala Arg Glu Gln Tyr Gly Asp	470	Val Leu Ile Gly Lys Asn Ser	475	480
	485	490	495		
Phe Thr Gly Asn Gly Arg Ala Ile Ala Ser Asn Glu Ala His Gly Phe					
500	505	510			
Val Lys Val Ile Ala Asp Ala Lys Tyr His Glu Ile Leu Gly Val His					
515	520	525			
Ile Ile Gly Pro Ala Ala Ala Glu Met Ile Asn Glu Ala Ala Thr Ile					
530	535	540			
Met Glu Ser Glu Leu Thr Val Asp Glu Leu Leu Leu Ser Ile His Gly					
545	550	555			560
His Pro Thr Phe Ser Glu Val Met Tyr Glu Ala Phe Ala Asp Val Leu					
565	570	575			
Gly Glu Ala Ile His Asn Pro Pro Lys Arg Lys					
580	585				

<210> SEQ ID NO 37

<211> LENGTH: 3636

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 37

atgggagaat	cttattctgt	tgaagcgggt	ttgacagctg	ttgataaaac	ctttggcaaa	60
acattacaat	cggcaatccg	ttcaatcgat	ggcttggaaa	agcgttcaac	cggtttttca	120
tcggtgtctc	aaaaagctag	ttccatgttt	aaatccatgt	taggagcgaa	tttagccgga	180
caagctatct	cagcaatgac	aaggacagtg	tcatacaggcc	ttgggtctat	gcttggcgag	240
atgaatagtt	cagcgaaaagc	gtggaaaact	tttgacgccca	atttagcgga	cattgggttt	300
ggaaaaaac	aaattttggc	agctaaaacg	gcgatgcaag	actatgcaac	taaaacaatc	360
tactcggcat	cagatatggc	tagcacgtat	gcacagttag	cggcagttgg	tgtgaaagat	420
accggaaagc	tcgtaaaagc	ttttggcggg	ttagctgcat	ctgctgaaaa	cccgaagcag	480
gccatgaagt	ctatcagtca	acaaatgacg	caagcagtag	gaagaccaac	agttgcatgg	540
caagacttta	ggataatgct	ggaacaggcg	cctgcaggga	tggctaaagt	cgctaaatct	600
atgggtaaaa	atcttgatga	actcgtcgcc	gatatccagg	cgggtagggt	taaaaccagc	660
gatttttttg	aagcggtaaa	aaaagcaggc	aatgataaga	gtttccaaaa	gatggcaact	720
gagttcaaaa	ctgttgacca	agccatcgac	ggtatgcgag	aaggcttatc	caacaaattg	780
caaccagcgt	ttgaaaaagt	gaaccaattt	ggaattagag	cgatcgaagc	aatcggtaaa	840
caactcgata	aagttgattt	ttctaagttt	gctagtaatc	ttgggaaatt	ccttgaagga	900
attaatatcg	ataaaaattgt	atctaataat	tcatacggcga	tttcatctgt	cacttcaaag	960
gttaaagaat	tttggggcgg	tttcaaacaa	actggagcaa	ttagtgtctt	ttcaggagct	1020
ttaaaaagtg	tttggggagc	gttaaaaaat	gtagctagcg	ctatgagtgg	aggcagttgg	1080
aaaaactttg	gctctattgt	aggcggaatt	gtaaagcatg	tgtctaattt	tgcaaaagct	1140
attgctgatg	ttgtcggtaa	aatggaacct	ggcagattgc	aaagctggat	agccactttt	1200
gcagcagtcg	ggggagggtt	aaagtatttt	gaaaagctaa	caggacaaaag	cgttgttggc	1260
tcttttttag	ataaaatcag	tacaaaattt	ggattatttg	gcaaaaaagc	taaagaagga	1320
accgatcaag	cagcgaatgg	ctctcgtaaa	agtgttgtaa	tcatacagcca	aatctttaat	1380
ggcttgggta	atatcgttaa	gtctgctggg	acagccatat	caacagctgc	aaaaggatatc	1440
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gcaatatcaa	cagttgcgca	aggtataggc	actgggctag	caatcgcttt	tagaggttta	1560
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aactccatta	gcgctgttat	ccaatcgcta	actggtgtga	ttaccgcagt	attcaatggc	1980
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accgcttttg	aaggatttgg	gaatgggtgta	aaatcagctc	tagaaggtgt	tggggcagta	2100
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ccagctctag	cacaagctgg	cgctggcttt	gccgcgtttg	ttgctcaatc	atcaacattt	2640
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caagccgaga	gagcagcaag	agccaaggcg	atgattcatt	cgccgtcaag	gttggttgca	3300
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gcagatagac	tgactagcat	tgtagctaaa	ttccaagggtg	ttgtcaaata	agagagttcg	3480
caatcggttat	cgcagcaaca	agagtttgta	catacagctc	aaccagcgta	tataaacttt	3540
agtttagggc	gaaacgaata	cgaagcattt	gtaagtgcga	tcactaatca	acaagcaaaa	3600
attgaaaaaa	tcagactaaa	gagaagcagc	tggtag			3636

<210> SEQ ID NO 38

<211> LENGTH: 1211

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 38

Met	Gly	Glu	Ser	Tyr	Ser	Val	Glu	Ala	Val	Leu	Thr	Ala	Val	Asp	Lys
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Thr	Phe	Gly	Lys	Thr	Leu	Gln	Ser	Ala	Ile	Arg	Ser	Ile	Asp	Gly	Leu
			20					25					30		
Glu	Lys	Arg	Ser	Thr	Gly	Phe	Ser	Ser	Val	Ser	Gln	Lys	Ala	Ser	Ser
		35					40					45			
Met	Phe	Lys	Ser	Met	Leu	Gly	Ala	Asn	Leu	Ala	Gly	Gln	Ala	Ile	Ser
	50					55				60					
Ala	Met	Thr	Arg	Thr	Val	Ser	Ser	Gly	Leu	Gly	Ser	Met	Leu	Gly	Glu
65					70					75					80
Met	Asn	Ser	Ser	Ala	Lys	Ala	Trp	Lys	Thr	Phe	Asp	Ala	Asn	Leu	Ala
			85						90				95		
Asp	Ile	Gly	Phe	Gly	Lys	Lys	Gln	Ile	Leu	Ala	Ala	Lys	Thr	Ala	Met
		100						105					110		
Gln	Asp	Tyr	Ala	Thr	Lys	Thr	Ile	Tyr	Ser	Ala	Ser	Asp	Met	Ala	Ser
	115						120					125			
Thr	Tyr	Ala	Gln	Leu	Ala	Ala	Val	Gly	Val	Lys	Asp	Thr	Gly	Lys	Leu
	130					135					140				
Val	Lys	Ala	Phe	Gly	Gly	Leu	Ala	Ala	Ser	Ala	Glu	Asn	Pro	Lys	Gln
145				150						155					160
Ala	Met	Lys	Ser	Ile	Ser	Gln	Gln	Met	Thr	Gln	Ala	Val	Gly	Arg	Pro
			165						170					175	
Thr	Val	Ala	Trp	Gln	Asp	Phe	Arg	Ile	Met	Leu	Glu	Gln	Ala	Pro	Ala
			180						185					190	

Gly	Met	Ala	Lys	Val	Ala	Lys	Ser	Met	Gly	Lys	Asn	Leu	Asp	Glu	Leu		
		195					200					205					
Val	Ala	Asp	Ile	Gln	Ala	Gly	Arg	Val	Lys	Thr	Ser	Asp	Phe	Leu	Glu		
		210					215					220					
Ala	Val	Lys	Lys	Ala	Gly	Asn	Asp	Lys	Ser	Phe	Gln	Lys	Met	Ala	Thr		
225						230					235				240		
Glu	Phe	Lys	Thr	Val	Asp	Gln	Ala	Ile	Asp	Gly	Met	Arg	Glu	Gly	Leu		
				245						250					255		
Ser	Asn	Lys	Leu	Gln	Pro	Ala	Phe	Glu	Lys	Val	Asn	Gln	Phe	Gly	Ile		
			260						265					270			
Arg	Ala	Ile	Glu	Ala	Ile	Gly	Lys	Gln	Leu	Asp	Lys	Val	Asp	Phe	Ser		
		275					280						285				
Lys	Phe	Ala	Ser	Asn	Leu	Gly	Lys	Phe	Leu	Glu	Gly	Ile	Asn	Ile	Asp		
		290					295					300					
Lys	Ile	Val	Ser	Asn	Ile	Ser	Ser	Ala	Ile	Ser	Ser	Val	Thr	Ser	Lys		
305					310						315				320		
Val	Lys	Glu	Phe	Trp	Gly	Gly	Phe	Lys	Gln	Thr	Gly	Ala	Ile	Ser	Ala		
				325						330					335		
Phe	Ser	Gly	Ala	Leu	Lys	Ser	Val	Trp	Gly	Ala	Leu	Lys	Asn	Val	Ala		
			340					345						350			
Ser	Ala	Met	Ser	Gly	Gly	Ser	Trp	Lys	Asn	Phe	Gly	Ser	Ile	Val	Gly		
		355					360					365					
Gly	Ile	Val	Lys	His	Val	Ser	Asn	Phe	Ala	Lys	Ala	Ile	Ala	Asp	Val		
		370					375					380					
Val	Gly	Lys	Met	Glu	Pro	Gly	Arg	Leu	Gln	Ser	Trp	Ile	Ala	Thr	Phe		
385					390						395				400		
Ala	Ala	Val	Gly	Gly	Gly	Leu	Lys	Leu	Phe	Glu	Lys	Leu	Thr	Gly	Gln		
				405						410					415		
Ser	Val	Val	Gly	Ser	Phe	Leu	Asp	Lys	Ile	Ser	Thr	Lys	Phe	Gly	Leu		
			420					425					430				
Phe	Gly	Lys	Lys	Ala	Lys	Glu	Gly	Thr	Asp	Gln	Ala	Ala	Asn	Gly	Ser		
		435					440					445					
Arg	Lys	Ser	Gly	Gly	Ile	Ile	Ser	Gln	Ile	Phe	Asn	Gly	Leu	Gly	Asn		
		450					455					460					
Ile	Val	Lys	Ser	Ala	Gly	Thr	Ala	Ile	Ser	Thr	Ala	Ala	Lys	Gly	Ile		
465					470						475				480		
Gly	Thr	Gly	Ile	Lys	Thr	Ala	Leu	Ser	Gly	Ala	Pro	Pro	Ile	Ile	Ser		
				485						490					495		
Ser	Leu	Gly	Thr	Ala	Ile	Ser	Thr	Val	Ala	Gln	Gly	Ile	Gly	Thr	Gly		
			500					505					510				
Leu	Ala	Ile	Ala	Phe	Arg	Gly	Leu	Gly	Ala	Ala	Ile	Ala	Met	Val	Pro		
		515					520					525					
Pro	Thr	Thr	Trp	Leu	Ala	Leu	Gly	Thr	Ala	Ile	Leu	Met	Val	Gly	Ala		
		530					535					540					
Ala	Phe	Ala	Leu	Ala	Gly	Thr	Gln	Ala	Asp	Gly	Ile	Ser	Gln	Ile	Leu		
545					550					555					560		
Arg	Thr	Ile	Gly	Asp	Val	Val	Val	Gln	Val	Leu	Gln	Gln	Val	Thr	Asp		
				565						570					575		
Ser	Leu	Ala	Thr	Leu	Leu	Thr	Ile	Ile	Ala	Asn	Ala	Ile	Gly	Ser	Met		
			580					585					590				
Leu	Pro	Ile	Val	Ala	Gly	Ala	Ile	Ser	Gln	Ile	Val	Gly	Ala	Val	Ala		
		595					600					605					
Gly	Gly	Leu	Ser	Gln	Leu	Ile	Ile	Ala	Val	Ser	Thr	Gly	Val	Ser	Leu		
		610					615					620					
Val	Ile	Gly	Ala	Phe	Thr	Gly	Leu	Leu	Gly	Gly	Ile	Ser	Gly	Val	Ile		
625					630						635				640		
Asn	Ser	Ile	Ser	Ala	Val	Ile	Gln	Ser	Leu	Thr	Gly	Val	Ile	Thr	Ala		

				645					650				655				
Val	Phe	Asn	Gly	Ile	Ala	Thr	Val	Ile	Ser	Ser	Val	Gly	Ser	Thr	Ile		
			660					665					670				
Lys	Asp	Val	Leu	Thr	Gly	Leu	Gly	Thr	Ala	Phe	Glu	Gly	Phe	Gly	Asn		
		675					680					685					
Gly	Val	Lys	Ser	Ala	Leu	Glu	Gly	Val	Gly	Ala	Val	Ile	Glu	Ser	Phe		
	690					695					700						
Gly	Ser	Ala	Val	Arg	Asn	Val	Leu	Asp	Gly	Val	Ala	Asn	Ile	Leu	Asp		
705				710					715						720		
Ser	Met	Gly	Thr	Ala	Ala	Leu	Asn	Ala	Gly	Arg	Gly	Val	Lys	Glu	Met		
			725					730						735			
Ala	Lys	Gly	Ile	Lys	Met	Leu	Val	Asp	Leu	Ser	Leu	Gly	Asp	Leu	Val		
		740					745						750				
Ala	Thr	Leu	Ala	Ala	Val	Ala	Ser	Gly	Leu	Gly	Lys	Met	Ala	Ser	Ser		
	755					760						765					
Ala	Gly	Glu	Met	Thr	Thr	Leu	Gly	Ser	Ala	Met	Ser	Lys	Val	Ala	Asn		
	770					775					780						
Gly	Met	Thr	Arg	Leu	Ala	Thr	Ser	Ala	Thr	Ile	Ala	Ile	Thr	Gly	Leu		
785				790						795					800		
Thr	Val	Phe	Ala	Thr	Thr	Met	Ala	Thr	Ile	Lys	Thr	Ala	Val	Ala	Thr		
			805						810					815			
Leu	Pro	Pro	Val	Leu	Thr	Met	Ala	Ala	Ser	Gly	Phe	Thr	Thr	Phe	Thr		
		820					825						830				
Thr	Gln	Ala	Val	Ala	Ala	Val	Thr	Gly	Leu	Ala	Ala	Ile	Asn	Ala	Pro		
	835					840						845					
Ile	Thr	Met	Phe	Lys	Ala	Gln	Leu	Met	Thr	Ile	Thr	Pro	Ala	Leu	Ala		
	850					855					860						
Gln	Ala	Gly	Ala	Gly	Phe	Ala	Ala	Phe	Val	Ala	Gln	Ser	Ser	Thr	Phe		
865				870					875						880		
Ser	Thr	Gly	Leu	Ala	Ser	Ala	Gly	Pro	Thr	Ile	Ala	Ala	Phe	Asn	Ala		
			885					890						895			
Asn	Leu	Met	Ser	Leu	Ser	Ala	Thr	Thr	Gly	Val	Leu	Val	Ala	Ser	Ile		
		900						905					910				
Ala	Gly	Leu	Ser	Ala	Val	Leu	Ser	Val	Val	Ser	Ala	Gly	Phe	Ser	Gln		
	915						920					925					
Ile	Gly	Ala	Ser	Ala	Thr	Ala	Thr	Val	Gly	Gln	Ile	Gln	Ala	Phe	Ala		
	930					935					940						
Ser	Ser	Thr	Thr	Val	Val	Ser	Ser	Ala	Phe	Ala	Ser	Met	Gln	Ser	Met		
945				950						955					960		
Ile	Gln	Ser	Ala	Met	Ala	Ala	Ile	Val	Ser	Ser	Ile	Ile	Thr	Ser	Phe		
			965					970						975			
Asn	Gln	Ala	Ala	Ser	Gln	Met	Gln	Ser	Ile	Leu	Ser	Arg	Met	Leu	Ser		
		980					985						990				
Gln	Ala	Arg	Thr	Phe	Gly	Ser	Gln	Leu	Glu	Gln	Gln	Met	Arg	Gln	Ser		
	995						1000					1005					
Gly	Gln	Arg	Ser	Gly	Gln	Asn	Leu	Ala	Arg	Gly	Leu	Ser	Ser	Gln			
	1010					1015					1020						
Gln	Gly	Ala	Val	Ile	Asn	Ala	Ile	Ser	Ser	Met	Val	Asn	Ala	Ala			
	1025					1030					1035						
Val	Ser	Arg	Ala	Asn	Ala	Gly	Ala	Gly	Pro	Met	Arg	Gln	Ala	Gly			
	1040					1045					1050						
Ala	Tyr	Ile	Gly	Gln	Gly	Leu	Ala	Gln	Gly	Met	Tyr	Ser	Ala	Leu			
	1055					1060					1065						
Gly	Ala	Val	Thr	Ala	Ala	Ala	Asn	Ala	Leu	Val	Ala	Gln	Ala	Glu			
	1070					1075					1080						
Arg	Ala	Ala	Arg	Ala	Lys	Ala	Met	Ile	His	Ser	Pro	Ser	Arg	Leu			
	1085					1090					1095						

Phe	Ala	Lys	Arg	Val	Gly	Gln	Tyr	Ile	Pro	Gln	Gly	Val	Ala	Met
1100						1105					1110			
Gly	Ile	Asp	Lys	Asn	Ala	Asp	Val	Val	Asp	Asp	Ser	Val	Gly	Gly
1115						1120					1125			
Leu	Phe	Asp	Ser	Ile	Asn	Ser	Phe	Asp	Phe	Asn	Ile	Ala	Asp	Arg
1130						1135					1140			
Leu	Thr	Ser	Ile	Gly	Ala	Lys	Phe	Gln	Gly	Val	Val	Lys	Ser	Glu
1145						1150					1155			
Ser	Ser	Gln	Ser	Leu	Ser	Gln	Gln	Gln	Glu	Phe	Val	His	Thr	Ala
1160						1165					1170			
Gln	Pro	Ala	Tyr	Ile	Asn	Phe	Ser	Leu	Gly	Gly	Asn	Glu	Tyr	Glu
1175						1180					1185			
Ala	Phe	Val	Ser	Asp	Ile	Thr	Asn	Gln	Gln	Ala	Lys	Ile	Glu	Lys
1190						1195					1200			
Ile	Arg	Leu	Lys	Arg	Ser	Ser	Trp							
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<210> SEQ ID NO 39

<211> LENGTH: 1206

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 39

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actgcggaag	ttttaactgt	tgataacggt	caagcaaacg	ttgttatcga	aggaacaggt	120
gttgaagggtg	tcttgacact	tcgtgaattg	actaacgacc	gcgatgctga	tattaacgac	180
tttgttaaaag	ctggcgacac	agttgaagta	cttgttcttc	gtcaagtagt	aggtaaagat	240
actgatacag	ttactttcct	agtatctaaa	aaacgtttgg	aagctcgtaa	agcctgggac	300
aaacttggtg	gtcgtgaagg	cgaagttggt	actgttaaag	gtaccctgtc	tgtaaagggt	360
ggcctttcag	ttgaatttga	aggacttcgt	ggatttatcc	ctgcttcaat	gattgacact	420
cgttttggtc	gcaacactga	aaaatttggt	ggacaagagt	ttgatgctaa	aatcaaagaa	480
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cacgtgactg	aattgtctca	cgaacgtaac	gtgtcaccta	aatcagttgt	ttcagttggt	720
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cttaaagcaa	caacacctgg	accatgggac	ggcgttgaac	aaaaacttgc	tcaaggtgat	840
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gggtattgatg	gacttggtca	tatttcacaa	atttcacaca	aacgtggtga	aaatccaaaa	960
gatgtacttt	ctgtaggaca	agaagtaaca	gttaaagtgc	ttgaagtga	tgcagctgat	1020
gagcgcgtat	cattatcaat	caaagctctt	gaagaacgcc	cagcgcaagc	tgaaggagac	1080
aacaaagaag	aaaaacgtca	atcacgcca	cgctcgccaa	aacgtgaatc	aagacgtgac	1140
tacgaactcc	cagaaacaca	aactggattc	tcaatggctg	atcttttcgg	tgatattgaa	1200
ttgtaa						1206

<210> SEQ ID NO 40

<211> LENGTH: 401

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 40

Met	Asn	Glu	Phe	Glu	Asp	Leu	Leu	Asn	Ser	Val	Ser	Glu	Val	Asn	Pro
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Gly	Asp	Val	Val	Thr	Ala	Glu	Val	Leu	Thr	Val	Asp	Asn	Gly	Gln	Ala
			20					25					30		
Asn	Val	Val	Ile	Glu	Gly	Thr	Gly	Val	Glu	Gly	Val	Leu	Thr	Leu	Arg
		35				40					45				
Glu	Leu	Thr	Asn	Asp	Arg	Asp	Ala	Asp	Ile	Asn	Asp	Phe	Val	Lys	Ala
	50					55					60				

Gly	Asp	Thr	Val	Glu	Val	Leu	Val	Leu	Arg	Gln	Val	Val	Gly	Lys	Asp	65	70	75	80
Thr	Asp	Thr	Val	Thr	Phe	Leu	Val	Ser	Lys	Lys	Arg	Leu	Glu	Ala	Arg	85	90	95	
Lys	Ala	Trp	Asp	Lys	Leu	Val	Gly	Arg	Glu	Gly	Glu	Val	Val	Thr	Val	100	105	110	
Lys	Gly	Thr	Arg	Ala	Val	Lys	Gly	Gly	Leu	Ser	Val	Glu	Phe	Glu	Gly	115	120	125	
Leu	Arg	Gly	Phe	Ile	Pro	Ala	Ser	Met	Ile	Asp	Thr	Arg	Phe	Val	Arg	130	135	140	
Asn	Thr	Glu	Lys	Phe	Val	Gly	Gln	Glu	Phe	Asp	Ala	Lys	Ile	Lys	Glu	145	150	155	160
Val	Asp	Ala	Ala	Glu	Asn	Arg	Phe	Ile	Leu	Ser	Arg	Arg	Glu	Val	Ile	165	170	175	
Glu	Glu	Ala	Ala	Lys	Glu	Ala	Arg	Ala	Glu	Val	Phe	Ser	Lys	Ile	Ser	180	185	190	
Glu	Gly	Ala	Val	Val	Thr	Gly	Thr	Val	Ala	Arg	Leu	Thr	Ser	Phe	Gly	195	200	205	
Ala	Phe	Ile	Asp	Leu	Gly	Gly	Val	Asp	Gly	Leu	Val	His	Val	Thr	Glu	210	215	220	
Leu	Ser	His	Glu	Arg	Asn	Val	Ser	Pro	Lys	Ser	Val	Val	Ser	Val	Gly	225	230	235	240
Glu	Glu	Val	Glu	Val	Lys	Val	Leu	Ser	Ile	Asp	Glu	Glu	Ala	Gly	Arg	245	250	255	
Val	Ser	Leu	Ser	Leu	Lys	Ala	Thr	Thr	Pro	Gly	Pro	Trp	Asp	Gly	Val	260	265	270	
Glu	Gln	Lys	Leu	Ala	Gln	Gly	Asp	Val	Val	Glu	Gly	Lys	Val	Lys	Arg	275	280	285	
Leu	Thr	Asp	Phe	Gly	Ala	Phe	Val	Glu	Val	Leu	Pro	Gly	Ile	Asp	Gly	290	295	300	
Leu	Val	His	Ile	Ser	Gln	Ile	Ser	His	Lys	Arg	Val	Glu	Asn	Pro	Lys	305	310	315	320
Asp	Val	Leu	Ser	Val	Gly	Gln	Glu	Val	Thr	Val	Lys	Val	Leu	Glu	Val	325	330	335	
Asn	Ala	Ala	Asp	Glu	Arg	Val	Ser	Leu	Ser	Ile	Lys	Ala	Leu	Glu	Glu	340	345	350	
Arg	Pro	Ala	Gln	Ala	Glu	Gly	Asp	Asn	Lys	Glu	Glu	Lys	Arg	Gln	Ser	355	360	365	
Arg	Pro	Arg	Arg	Pro	Lys	Arg	Glu	Ser	Arg	Arg	Asp	Tyr	Glu	Leu	Pro	370	375	380	
Glu	Thr	Gln	Thr	Gly	Phe	Ser	Met	Ala	Asp	Leu	Phe	Gly	Asp	Ile	Glu	385	390	395	400
Leu																			

<210> SEQ ID NO 41

<211> LENGTH: 900

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 41

atgttatact	attcttatct	taataaagga	gttactatga	agaaatcagt	tacattactg	60
tctatcggac	ttgccagcct	tttattggca	gcatgtgcgc	cacatcaatc	tcaaaaatca	120
agttgggaca	ctatcaaaga	aaaaggggtg	ttaaaagtag	ctaccccagg	aacctatcag	180
ccaacttctt	tttacaacga	taataatgag	ttagtaggtt	acgaagtaga	tatggtcaaa	240
gaaatcggta	aacgacttaa	cattaaagtc	aagtttggtg	aaacaggatt	tgaccaagcc	300
tttacctcag	ttgatagtgg	tcgagtggat	atttctttga	acaactttga	cattacccca	360
aaacgtcaga	aaaaatacaa	tatctctacg	ccttataaat	acggggtagg	aggcatgatt	420
gtccgtgctg	atggcagctc	aaacatagct	aaaaaagatc	ttagcgactg	gaaaggaaaa	480

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aaagcagccg gcgcttctgg aacagaatac atgaaagtag cgcaaaaaca gggagctgaa 540
ctgggtgacct acgataatgt tacaggagat gtttatctaa acgatgtggc taacgggtcga 600
acagattttca tcccaaatga ttaccagct caaaaattat ttgtggatta catgttatct 660
caaaatccaa atctaaatgt caaaatgagc gatgttcagt acaaccaac cgaacaagga 720
attgttatga acaaaaaaga cgatagcctc aagaaaaaaa tagatgctgt tattaaagac 780
atgataaaaag atggtagctt gaagaaaatc tctgaaacct actatgctgg tcaagatctg 840
acaaaacctt ttggcaaaga caaaaaaatt cccgtcattg atacgaaaga cgtaaactaa 900

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<210> SEQ ID NO 42

<211> LENGTH: 299

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 42

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Met Leu Tyr Tyr Ser Tyr Leu Asn Lys Gly Val Thr Met Lys Lys Ser
1      5      10      15
Val Thr Leu Leu Ser Ile Gly Leu Ala Ser Leu Leu Leu Ala Ala Cys
20      25      30
Ala Pro His Gln Ser Gln Lys Ser Ser Trp Asp Thr Ile Lys Glu Lys
35      40      45
Gly Val Leu Lys Val Ala Thr Pro Gly Thr Tyr Gln Pro Thr Ser Phe
50      55      60
Tyr Asn Asp Asn Asn Glu Leu Val Gly Tyr Glu Val Asp Met Val Lys
65      70      75      80
Glu Ile Gly Lys Arg Leu Asn Ile Lys Val Lys Phe Val Glu Thr Gly
85      90      95
Phe Asp Gln Ala Phe Thr Ser Val Asp Ser Gly Arg Val Asp Ile Ser
100     105     110
Leu Asn Asn Phe Asp Ile Thr Pro Lys Arg Gln Lys Lys Tyr Asn Ile
115     120     125
Ser Thr Pro Tyr Lys Tyr Gly Val Gly Gly Met Ile Val Arg Ala Asp
130     135     140
Gly Ser Ser Asn Ile Ala Lys Lys Asp Leu Ser Asp Trp Lys Gly Lys
145     150     155     160
Lys Ala Ala Gly Ala Ser Gly Thr Glu Tyr Met Lys Val Ala Gln Lys
165     170     175
Gln Gly Ala Glu Leu Val Thr Tyr Asp Asn Val Thr Gly Asp Val Tyr
180     185     190
Leu Asn Asp Val Ala Asn Gly Arg Thr Asp Phe Ile Pro Asn Asp Tyr
195     200     205
Pro Ala Gln Lys Leu Phe Val Asp Tyr Met Leu Ser Gln Asn Pro Asn
210     215     220
Leu Asn Val Lys Met Ser Asp Val Gln Tyr Asn Pro Thr Glu Gln Gly
225     230     235     240
Ile Val Met Asn Lys Lys Asp Asp Ser Leu Lys Lys Lys Ile Asp Ala
245     250     255
Val Ile Lys Asp Met Ile Lys Asp Gly Ser Leu Lys Lys Ile Ser Glu
260     265     270
Thr Tyr Tyr Ala Gly Gln Asp Leu Thr Lys Pro Phe Gly Lys Asp Lys
275     280     285
Lys Ile Pro Val Ile Asp Thr Lys Asp Val Asn
290     295

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<210> SEQ ID NO 43

<211> LENGTH: 2052

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 43

ttgatctata	acgattacgt	taacttatta	ggagatttta	tgaaaaaata	ttttatttta	60
aaaagtagtg	tattgagtat	cctgactagt	tttactctat	tagttacaga	tgttcaagca	120
gatcaagttg	atgtgcaatt	ccttggcgctc	aatgattttc	acggcgctct	tgataatacc	180
ggaacagctt	acacaccaag	tggtaaaaata	ccaaatgctg	ggacggctgc	tcaattaggt	240
gcttatatgg	atgacgctga	gatagacttc	aagcaagcaa	atcaagacgg	aacaagtata	300
cgtgttcaag	ctggagatat	ggtcggagcc	agtcctgcta	actctgcact	tttacaagat	360
gagcctactg	tcaaagtctt	taacaaaatg	aaatttgaat	atggcactct	tggtaatcat	420
gaatttgacg	aaggactaga	tgaatttaac	cgtatcatga	caggtcaagc	gcctgatcct	480
gaatcaacaa	ttaatgatat	caccaaacia	tatgagcacg	aagcttcgca	tcaaaccatc	540
gtcattgcta	atgttattga	taaaaaaacc	aaggatatcc	cctatggttg	gaaaccttat	600
gctataaaag	acatagccat	taatgacaaa	atcgttaaga	ttggcttcat	tggtgttggtg	660
actacagaga	ttccaaatct	cgttttaaag	caaaactatg	aacactatca	atttttagat	720
gtagctgaaa	ccattgccaa	atatgctaaa	gaactacaag	aacaacatgt	tcatgctatt	780
gtggtttttag	ctcatgttcc	tgcaacaagt	aaagatgggtg	ttgttgatca	tgaaatggct	840
acggtttatgg	aaaaagtga	ccaaatctat	cccgaacata	gcattgatat	tatttttgca	900
ggacataatc	atcaatacac	taatggaact	atcggtaaaa	cacgtatcgt	tcaagccctc	960
tctcaaggaa	aagcttatgc	agatgtccgt	ggtacgctag	atactgatac	caatgatttt	1020
attaaaactc	catcagcaaa	tggtgttgct	gtagcaccag	gtatcaaaac	agaaaattca	1080
gatatcaaaag	ctataataaa	tcatgcta	gatattgtta	aaacagttac	tgaacgaaaa	1140
atcgggaactg	caactaattc	ttcaactatt	tctaaaacag	aaaatattga	taaagaatct	1200
cctgtcggta	acttagcaac	aacggctcag	cttactattg	ctaagaaaac	ttttccaact	1260
gttgactttg	ctatgaccaa	taatggtggg	attcgaagtg	acctagtgtg	caaaaatgac	1320
cggaccatca	cctggggagc	tgacacaggc	gtacaaccat	ttggtaatat	ccttcaagtc	1380
attcaaatga	ctgggtcaaca	catttacgat	gtcctaaatc	agcaatacga	tgaaaaccag	1440
acctattttc	ttcaaatgtc	aggtttaaca	tacacttata	cagataatga	tcctaagaac	1500
tctgataccc	ccttcaagat	agttaagggt	tataaagaca	atggtgaaga	aattaactta	1560
acaactactt	acaccgttgt	tgtcaacgac	tttctttatg	gtggtggtga	tggtttttca	1620
gcattttaaaa	aagctaaatt	aatcggagct	attaacacag	atactgaagc	tttcatcaca	1680
tatatcacaa	atttagaagc	atcaggtaaa	actgttaatg	ctactataaa	aggggttaaa	1740
aattatgtaa	cttcaaacct	tgaaagtctg	acaaaagtta	atagtgtctg	taaacacagt	1800
atcattagta	aggttttttag	aaatcgtgat	ggcaatacag	tgtctagtga	agtcatttca	1860
gaccttttga	cttctactga	aaacactaat	aacagccttg	gcaaaaaaga	aacaacaaca	1920
aacaaaaata	ctatctctag	ttccactctt	ccaataacag	gggacaatta	taaaatgtct	1980
cctattatga	caatccttgc	cttgataagc	ttaggtggac	taaacgcttt	tattaaaaaa	2040
aggaaatcct	ag					2052

<210> SEQ ID NO 44

<211> LENGTH: 683

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 44

Met	Ile	Tyr	Asn	Asp	Tyr	Val	Asn	Leu	Leu	Gly	Asp	Phe	Met	Lys	Lys
1			5					10						15	
Tyr	Phe	Ile	Leu	Lys	Ser	Ser	Val	Leu	Ser	Ile	Leu	Thr	Ser	Phe	Thr
		20						25					30		
Leu	Leu	Val	Thr	Asp	Val	Gln	Ala	Asp	Gln	Val	Asp	Val	Gln	Phe	Leu
		35					40				45				
Gly	Val	Asn	Asp	Phe	His	Gly	Ala	Leu	Asp	Asn	Thr	Gly	Thr	Ala	Tyr
	50					55				60					
Thr	Pro	Ser	Gly	Lys	Ile	Pro	Asn	Ala	Gly	Thr	Ala	Ala	Gln	Leu	Gly
65				70					75				80		
Ala	Tyr	Met	Asp	Asp	Ala	Glu	Ile	Asp	Phe	Lys	Gln	Ala	Asn	Gln	Asp
			85					90					95		
Gly	Thr	Ser	Ile	Arg	Val	Gln	Ala	Gly	Asp	Met	Val	Gly	Ala	Ser	Pro
		100						105				110			
Ala	Asn	Ser	Ala	Leu	Leu	Gln	Asp	Glu	Pro	Thr	Val	Lys	Val	Phe	Asn
	115						120					125			

Lys	Met	Lys	Phe	Glu	Tyr	Gly	Thr	Leu	Gly	Asn	His	Glu	Phe	Asp	Glu	130	135	140
Gly	Leu	Asp	Glu	Phe	Asn	Arg	Ile	Met	Thr	Gly	Gln	Ala	Pro	Asp	Pro	145	150	155
Glu	Ser	Thr	Ile	Asn	Asp	Ile	Thr	Lys	Gln	Tyr	Glu	His	Glu	Ala	Ser	165	170	175
His	Gln	Thr	Ile	Val	Ile	Ala	Asn	Val	Ile	Asp	Lys	Lys	Thr	Lys	Asp	180	185	190
Ile	Pro	Tyr	Gly	Trp	Lys	Pro	Tyr	Ala	Ile	Lys	Asp	Ile	Ala	Ile	Asn	195	200	205
Asp	Lys	Ile	Val	Lys	Ile	Gly	Phe	Ile	Gly	Val	Val	Thr	Thr	Glu	Ile	210	215	220
Pro	Asn	Leu	Val	Leu	Lys	Gln	Asn	Tyr	Glu	His	Tyr	Gln	Phe	Leu	Asp	225	230	235
Val	Ala	Glu	Thr	Ile	Ala	Lys	Tyr	Ala	Lys	Glu	Leu	Gln	Glu	Gln	His	245	250	255
Val	His	Ala	Ile	Val	Val	Leu	Ala	His	Val	Pro	Ala	Thr	Ser	Lys	Asp	260	265	270
Gly	Val	Val	Asp	His	Glu	Met	Ala	Thr	Val	Met	Glu	Lys	Val	Asn	Gln	275	280	285
Ile	Tyr	Pro	Glu	His	Ser	Ile	Asp	Ile	Ile	Phe	Ala	Gly	His	Asn	His	290	295	300
Gln	Tyr	Thr	Asn	Gly	Thr	Ile	Gly	Lys	Thr	Arg	Ile	Val	Gln	Ala	Leu	305	310	315
Ser	Gln	Gly	Lys	Ala	Tyr	Ala	Asp	Val	Arg	Gly	Thr	Leu	Asp	Thr	Asp	325	330	335
Thr	Asn	Asp	Phe	Ile	Lys	Thr	Pro	Ser	Ala	Asn	Val	Val	Ala	Val	Ala	340	345	350
Pro	Gly	Ile	Lys	Thr	Glu	Asn	Ser	Asp	Ile	Lys	Ala	Ile	Ile	Asn	His	355	360	365
Ala	Asn	Asp	Ile	Val	Lys	Thr	Val	Thr	Glu	Arg	Lys	Ile	Gly	Thr	Ala	370	375	380
Thr	Asn	Ser	Ser	Thr	Ile	Ser	Lys	Thr	Glu	Asn	Ile	Asp	Lys	Glu	Ser	385	390	395
Pro	Val	Gly	Asn	Leu	Ala	Thr	Thr	Ala	Gln	Leu	Thr	Ile	Ala	Lys	Lys	405	410	415
Thr	Phe	Pro	Thr	Val	Asp	Phe	Ala	Met	Thr	Asn	Asn	Gly	Gly	Ile	Arg	420	425	430
Ser	Asp	Leu	Val	Val	Lys	Asn	Asp	Arg	Thr	Ile	Thr	Trp	Gly	Ala	Ala	435	440	445
Gln	Ala	Val	Gln	Pro	Phe	Gly	Asn	Ile	Leu	Gln	Val	Ile	Gln	Met	Thr	450	455	460
Gly	Gln	His	Ile	Tyr	Asp	Val	Leu	Asn	Gln	Gln	Tyr	Asp	Glu	Asn	Gln	465	470	475
Thr	Tyr	Phe	Leu	Gln	Met	Ser	Gly	Leu	Thr	Tyr	Thr	Tyr	Thr	Asp	Asn	485	490	495
Asp	Pro	Lys	Asn	Ser	Asp	Thr	Pro	Phe	Lys	Ile	Val	Lys	Val	Tyr	Lys	500	505	510
Asp	Asn	Gly	Glu	Glu	Ile	Asn	Leu	Thr	Thr	Thr	Tyr	Thr	Val	Val	Val	515	520	525
Asn	Asp	Phe	Leu	Tyr	Gly	Gly	Gly	Asp	Gly	Phe	Ser	Ala	Phe	Lys	Lys	530	535	540
Ala	Lys	Leu	Ile	Gly	Ala	Ile	Asn	Thr	Asp	Thr	Glu	Ala	Phe	Ile	Thr	545	550	555
Tyr	Ile	Thr	Asn	Leu	Glu	Ala	Ser	Gly	Lys	Thr	Val	Asn	Ala	Thr	Ile	565	570	575
Lys	Gly	Val	Lys	Asn	Tyr	Val	Thr	Ser	Asn	Leu	Glu	Ser	Ser	Thr	Lys			

			580					585				590					
Val	Asn	Ser	Ala	Gly	Lys	His	Ser	Ile	Ile	Ser	Lys	Val	Phe	Arg	Asn		
	595						600					605					
Arg	Asp	Gly	Asn	Thr	Val	Ser	Ser	Glu	Val	Ile	Ser	Asp	Leu	Leu	Thr		
	610					615					620						
Ser	Thr	Glu	Asn	Thr	Asn	Asn	Ser	Leu	Gly	Lys	Lys	Glu	Thr	Thr	Thr		
625					630					635					640		
Asn	Lys	Asn	Thr	Ile	Ser	Ser	Ser	Thr	Leu	Pro	Ile	Thr	Gly	Asp	Asn		
			645					650					655				
Tyr	Lys	Met	Ser	Pro	Ile	Met	Thr	Ile	Leu	Ala	Leu	Ile	Ser	Leu	Gly		
	660							665				670					
Gly	Leu	Asn	Ala	Phe	Ile	Lys	Lys	Arg	Lys	Ser							
	675						680										

<210> SEQ ID NO 45

<211> LENGTH: 3027

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 45

atgaagaaac	atcttaaaac	agttgccttg	accctcacta	cagtatcggt	agtcacccac	60
aatcaggaag	tttttagttt	agtcaaagag	ccaattctta	aacaaactca	agcttcttca	120
tcgatttctg	gcgctgacta	cgcagaaagt	agcggtaaaa	gcaagttaaa	gattaatgaa	180
acttctggcc	ctgttgatga	tacagtcact	gacttatttt	cggataaacg	tactactcct	240
gaaaaataa	aagataatct	tgctaaaggt	ccgagagaac	aagagttaaa	ggcagtaaca	300
gagaatacag	aatcagaaaa	gcagatcact	tctggatctc	aactagaaca	atcaaaagag	360
tctctttctt	taaataaaaac	agtgccatca	acgtctaatt	gggagatttg	tgattttatt	420
actaagggga	atacccttgt	tggtccttca	aaatcagggt	ttgaaaagtt	atctcaaact	480
gatcatctcg	tattgcctag	tcaagcagca	gatggaactc	aattgataca	agtagctagt	540
tttgctttta	ctccagataa	aaagacggca	attgcagaat	ataccagtag	ggctggagaa	600
aatggggaaa	taagccaact	agatgtggat	ggaaaagaaa	ttattaacga	aggtgaggtt	660
tttaattctt	atctactaaa	gaaggtaaca	atcccaactg	gttataaaca	tattggtcaa	720
gatgcttttg	tggacaataa	gaatattgct	gaggtaatc	ttcctgaaag	cctcgagact	780
atttctgact	atgcttttgc	tcacctagct	ttgaaacaga	tcgatttgcc	agataattta	840
aaagcgattg	gagaattagc	tttttttgat	aatcaaatta	caggtaaaact	ttctttgcc	900
cgtcagttaa	tgcgattagc	agaacgtgct	tttaaatcaa	accatatcaa	aacaattgag	960
tttagaggaa	atagtctaaa	agtgataggg	gaagctagtt	ttcaagataa	tgactctgag	1020
caactaatgc	tacctgacgg	tcttgaaaaa	atagaatcag	aagctttttac	aggaaatcca	1080
ggagatgatc	actacaataa	ccgtgttggt	ttgtggacaa	aatctggaaa	aaatccttct	1140
ggtcttgcta	ctgaaaatac	ctatgttaat	cctgataagt	cactatggca	ggaaagtcct	1200
gagattgatt	atactaaatg	gttagaggaa	gattttacct	atcaaaaaaa	tagtggtaca	1260
ggtttttcaa	ataaaggcct	acaaaaagta	aaacgtaata	aaaacttaga	aattccaaaa	1320
cagcacaatg	gtgttactat	tactgaaatt	ggtgataatg	cttttcgcaa	tgttgatttt	1380
caaaataaaa	ctttacgtaa	atatgatttg	gaagaagtaa	agcttccttc	aactattcgg	1440
aaaatagggtg	cttttgcttt	tcaatcta	aacttgaaat	cttttgaaagc	aagtgacgat	1500
ttagaagaga	ttaaagaggg	agcctttatg	aataatcgta	ttgaaacctt	ggaattaaaa	1560
gataaattag	ttactattgg	tgatgcggct	ttccatatta	atcatattta	tgccattggt	1620
cttccagaat	ctgtacaaga	aatagggcgt	tcagcatttc	ggcaaaatgg	tgcaaatat	1680
cttatttttta	tgggaagtaa	ggttaagacc	ttagggtgaga	tggcattttt	atcaaataga	1740
cttgaacatc	tggatctttc	tgagcaaaaa	cagtttacag	agattcctgt	tcaagccttt	1800
tcagacaatg	ccttgaaaaga	agtattatta	ccagcatcac	tgaaaacgat	tcgagaagaa	1860
gccttcaaaa	agaatcattt	aaaacaactg	gaagtggcat	ctgccttgct	ccatattgct	1920
tttaatgctt	tagatgataa	tgatggtgat	gaacaatttg	ataataaagt	ggttggttaa	1980
acgcatacata	attcctacgc	actagcagat	ggtgagcatt	ttatcgttga	tccagataag	2040
ttatcttcta	caatagtaga	ccttgaaaag	attttaaaaa	taatcgaagg	tttagattat	2100
tctacattac	gtcagactac	tcaaaactcag	tttagagaca	tgactactgc	aggtaaagcg	2160
ttgttgtcaa	aatctaacct	ccgacaagga	gaaaaacaaa	aattccttca	agaagcacia	2220
tttttccttg	gccgcgttga	tttggataaa	gccatagcta	aagctgagaa	ggcttttagtg	2280

accaagaagg	caacaaagaa	tggtcagttg	cttgaaagaa	gtattaacaa	agcgggtatta	2340
gcttataata	atagcgctat	taaaaaagct	aatgttaagc	gcttggaata	agagtttagac	2400
ttgctaacag	gattagttga	gggaaaagga	ccattagcgc	aagctacaat	ggtacaagga	2460
gtttatttat	taaagacgcc	tttgccattg	ccagaatatt	atatcggatt	gaacgtttat	2520
tttgacaagt	ctggaaaatt	gatttatgca	cttgatatga	gtgatactat	tggtcgaggga	2580
caaaaagacg	cttatggtaa	tcctatatta	aatgttgacg	aggataatga	aggttatcat	2640
gccttggcag	ttgccacttt	agctgattat	gaggggctcg	acatcaaac	aattttaaat	2700
agtaagctta	gtcaattaac	atctattcgt	caggtaccga	ctgcagccta	tcatagagcc	2760
ggtattttcc	aagctatcca	aaatgcagcg	gcagaagcag	agcagttatt	gcctaaacca	2820
ggtacgcact	ctgagaagtc	aagctcaagt	gaatctgcta	actctaaaga	tagaggattg	2880
caatcaaacc	caaaaacgaa	tagaggacga	cactctgcaa	tattgcctag	gacagggtca	2940
aaaggcagct	ttgtctatgg	aatcttaggt	tacactagcg	ttgctttact	gtcactaata	3000
actgctataa	aaaagaaaaa	atattaa				3027

<210> SEQ ID NO 46

<211> LENGTH: 1008

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 46

Met	Lys	Lys	His	Leu	Lys	Thr	Val	Ala	Leu	Thr	Leu	Thr	Thr	Val	Ser
1				5					10					15	
Val	Val	Thr	His	Asn	Gln	Glu	Val	Phe	Ser	Leu	Val	Lys	Glu	Pro	Ile
			20					25					30		
Leu	Lys	Gln	Thr	Gln	Ala	Ser	Ser	Ser	Ile	Ser	Gly	Ala	Asp	Tyr	Ala
		35					40					45			
Glu	Ser	Ser	Gly	Lys	Ser	Lys	Leu	Lys	Ile	Asn	Glu	Thr	Ser	Gly	Pro
	50					55					60				
Val	Asp	Asp	Thr	Val	Thr	Asp	Leu	Phe	Ser	Asp	Lys	Arg	Thr	Thr	Pro
65					70					75					80
Glu	Lys	Ile	Lys	Asp	Asn	Leu	Ala	Lys	Gly	Pro	Arg	Glu	Gln	Glu	Leu
				85					90					95	
Lys	Ala	Val	Thr	Glu	Asn	Thr	Glu	Ser	Glu	Lys	Gln	Ile	Thr	Ser	Gly
			100					105					110		
Ser	Gln	Leu	Glu	Gln	Ser	Lys	Glu	Ser	Leu	Ser	Leu	Asn	Lys	Thr	Val
		115					120					125			
Pro	Ser	Thr	Ser	Asn	Trp	Glu	Ile	Cys	Asp	Phe	Ile	Thr	Lys	Gly	Asn
	130					135					140				
Thr	Leu	Val	Gly	Leu	Ser	Lys	Ser	Gly	Val	Glu	Lys	Leu	Ser	Gln	Thr
145					150					155					160
Asp	His	Leu	Val	Leu	Pro	Ser	Gln	Ala	Ala	Asp	Gly	Thr	Gln	Leu	Ile
				165					170					175	
Gln	Val	Ala	Ser	Phe	Ala	Phe	Thr	Pro	Asp	Lys	Lys	Thr	Ala	Ile	Ala
			180					185					190		
Glu	Tyr	Thr	Ser	Arg	Ala	Gly	Glu	Asn	Gly	Glu	Ile	Ser	Gln	Leu	Asp
	195						200					205			
Val	Asp	Gly	Lys	Glu	Ile	Ile	Asn	Glu	Gly	Glu	Val	Phe	Asn	Ser	Tyr
	210					215					220				
Leu	Leu	Lys	Lys	Val	Thr	Ile	Pro	Thr	Gly	Tyr	Lys	His	Ile	Gly	Gln
225					230					235					240
Asp	Ala	Phe	Val	Asp	Asn	Lys	Asn	Ile	Ala	Glu	Val	Asn	Leu	Pro	Glu
			245						250					255	
Ser	Leu	Glu	Thr	Ile	Ser	Asp	Tyr	Ala	Phe	Ala	His	Leu	Ala	Leu	Lys
			260					265					270		
Gln	Ile	Asp	Leu	Pro	Asp	Asn	Leu	Lys	Ala	Ile	Gly	Glu	Leu	Ala	Phe
	275						280					285			
Phe	Asp	Asn	Gln	Ile	Thr	Gly	Lys	Leu	Ser	Leu	Pro	Arg	Gln	Leu	Met
	290					295					300				

Arg	Leu	Ala	Glu	Arg	Ala	Phe	Lys	Ser	Asn	His	Ile	Lys	Thr	Ile	Glu	305	310	315	320
Phe	Arg	Gly	Asn	Ser	Leu	Lys	Val	Ile	Gly	Glu	Ala	Ser	Phe	Gln	Asp	325	330	335	
Asn	Asp	Leu	Ser	Gln	Leu	Met	Leu	Pro	Asp	Gly	Leu	Glu	Lys	Ile	Glu	340	345	350	
Ser	Glu	Ala	Phe	Thr	Gly	Asn	Pro	Gly	Asp	Asp	His	Tyr	Asn	Asn	Arg	355	360	365	
Val	Val	Leu	Trp	Thr	Lys	Ser	Gly	Lys	Asn	Pro	Ser	Gly	Leu	Ala	Thr	370	375	380	
Glu	Asn	Thr	Tyr	Val	Asn	Pro	Asp	Lys	Ser	Leu	Trp	Gln	Glu	Ser	Pro	385	390	395	400
Glu	Ile	Asp	Tyr	Thr	Lys	Trp	Leu	Glu	Glu	Asp	Phe	Thr	Tyr	Gln	Lys	405	410	415	
Asn	Ser	Val	Thr	Gly	Phe	Ser	Asn	Lys	Gly	Leu	Gln	Lys	Val	Lys	Arg	420	425	430	
Asn	Lys	Asn	Leu	Glu	Ile	Pro	Lys	Gln	His	Asn	Gly	Val	Thr	Ile	Thr	435	440	445	
Glu	Ile	Gly	Asp	Asn	Ala	Phe	Arg	Asn	Val	Asp	Phe	Gln	Asn	Lys	Thr	450	455	460	
Leu	Arg	Lys	Tyr	Asp	Leu	Glu	Glu	Val	Lys	Leu	Pro	Ser	Thr	Ile	Arg	465	470	475	480
Lys	Ile	Gly	Ala	Phe	Ala	Phe	Gln	Ser	Asn	Asn	Leu	Lys	Ser	Phe	Glu	485	490	495	
Ala	Ser	Asp	Asp	Leu	Glu	Glu	Ile	Lys	Glu	Gly	Ala	Phe	Met	Asn	Asn	500	505	510	
Arg	Ile	Glu	Thr	Leu	Glu	Leu	Lys	Asp	Lys	Leu	Val	Thr	Ile	Gly	Asp	515	520	525	
Ala	Ala	Phe	His	Ile	Asn	His	Ile	Tyr	Ala	Ile	Val	Leu	Pro	Glu	Ser	530	535	540	
Val	Gln	Glu	Ile	Gly	Arg	Ser	Ala	Phe	Arg	Gln	Asn	Gly	Ala	Asn	Asn	545	550	555	560
Leu	Ile	Phe	Met	Gly	Ser	Lys	Val	Lys	Thr	Leu	Gly	Glu	Met	Ala	Phe	565	570	575	
Leu	Ser	Asn	Arg	Leu	Glu	His	Leu	Asp	Leu	Ser	Glu	Gln	Lys	Gln	Phe	580	585	590	
Thr	Glu	Ile	Pro	Val	Gln	Ala	Phe	Ser	Asp	Asn	Ala	Leu	Lys	Glu	Val	595	600	605	
Leu	Leu	Pro	Ala	Ser	Leu	Lys	Thr	Ile	Arg	Glu	Glu	Ala	Phe	Lys	Lys	610	615	620	
Asn	His	Leu	Lys	Gln	Leu	Glu	Val	Ala	Ser	Ala	Leu	Ser	His	Ile	Ala	625	630	635	640
Phe	Asn	Ala	Leu	Asp	Asp	Asn	Asp	Gly	Asp	Glu	Gln	Phe	Asp	Asn	Lys	645	650	655	
Val	Val	Val	Lys	Thr	His	His	Asn	Ser	Tyr	Ala	Leu	Ala	Asp	Gly	Glu	660	665	670	
His	Phe	Ile	Val	Asp	Pro	Asp	Lys	Leu	Ser	Ser	Thr	Ile	Val	Asp	Leu	675	680	685	
Glu	Lys	Ile	Leu	Lys	Leu	Ile	Glu	Gly	Leu	Asp	Tyr	Ser	Thr	Leu	Arg	690	695	700	
Gln	Thr	Thr	Gln	Thr	Gln	Phe	Arg	Asp	Met	Thr	Thr	Ala	Gly	Lys	Ala	705	710	715	720
Leu	Leu	Ser	Lys	Ser	Asn	Leu	Arg	Gln	Gly	Glu	Lys	Gln	Lys	Phe	Leu	725	730	735	
Gln	Glu	Ala	Gln	Phe	Phe	Leu	Gly	Arg	Val	Asp	Leu	Asp	Lys	Ala	Ile	740	745	750	
Ala	Lys	Ala	Glu	Lys	Ala	Leu	Val	Thr	Lys	Lys	Ala	Thr	Lys	Asn	Gly				

tcaataggta ccaacacaaaa accggaaaaa gattctcaat caaagaataa aaaatcaggg 1260
gtggataaat ag 1272

<210> SEQ ID NO 48

<211> LENGTH: 423

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 48

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Met Ser Lys Arg Gly Lys Ile Lys Ile Thr Thr Lys Thr Lys Leu Ile
1      5      10      15
Thr Ala Ser Val Ile Thr Leu Val Leu Ile Ile Thr Gly Ile Val Leu
20     25     30
Trp Lys Gln Gln Arg Asn Thr Leu Thr Ala Asp Ile Ala Lys Glu Pro
35     40     45
Tyr Ser Thr Val Ser Val Thr Glu Gly Ser Ile Ala Ser Ser Thr Leu
50     55     60
Leu Ser Gly Thr Val Lys Ala Leu Ser Glu Glu Tyr Ile Tyr Phe Asp
65     70     75     80
Ala Asn Lys Gly Asn Asp Ala Thr Val Thr Val Lys Val Gly Asp Gln
85     90     95
Val Thr Gln Gly Gln Gln Leu Val Gln Tyr Asn Thr Thr Thr Ala Gln
100    105    110
Ser Ala Tyr Asp Thr Ala Val Arg Ser Leu Asn Lys Ile Gly Arg Gln
115    120    125
Ile Asn His Leu Lys Thr Tyr Gly Val Pro Ala Val Ser Thr Glu Thr
130    135    140
Asn Arg Asp Glu Ala Thr Gly Glu Glu Thr Thr Thr Thr Val Gln Pro
145    150    155    160
Ser Ala Gln Gln Asn Ala Asn Tyr Lys Gln Gln Leu Gln Asp Leu Asn
165    170    175
Asp Ala Tyr Ala Asp Ala Gln Ala Glu Val Asn Lys Ala Gln Ile Ala
180    185    190
Leu Asn Asp Thr Val Val Ile Ser Ser Val Ser Gly Thr Val Val Glu
195    200    205
Val Asn Asn Asp Ile Asp Pro Ser Ser Lys Asn Ser Gln Thr Leu Val
210    215    220
His Val Ala Thr Glu Gly Gln Leu Gln Val Lys Gly Thr Leu Thr Glu
225    230    235    240
Tyr Asp Leu Ala Asn Val Lys Val Gly Gln Ser Val Lys Ile Lys Ser
245    250    255
Lys Val Tyr Ser Asn Gln Glu Trp Thr Gly Lys Ile Ser Tyr Val Ser
260    265    270
Asn Tyr Pro Thr Glu Ser Asn Ala Gly Ser Thr Thr Pro Ala Gly Ser
275    280    285
Thr Gly Ala Gly Ser Ser Thr Gly Ala Thr Tyr Asp Tyr Lys Ile Asp
290    295    300
Ile Ile Ser Pro Leu Asn Gln Leu Lys Gln Gly Phe Thr Val Ser Val
305    310    315    320
Glu Val Val Asn Glu Ala Lys Gln Ala Leu Val Pro Leu Thr Ala Val
325    330    335
Ile Lys Lys Asp Lys Lys His Tyr Val Trp Thr Tyr Asp Asp Ala Thr
340    345    350
Gly Lys Ala Lys Lys Val Glu Val Thr Leu Gly Asn Ala Asp Ala Gln
355    360    365
Gln Gln Glu Ile His Lys Gly Val Ala Val Gly Asp Ile Val Ile Ala
370    375    380
Asn Pro Asp Lys Asn Ile Lys Pro Asp Lys Lys Leu Glu Gly Val Ile

```


Ala Glu Val Thr Phe Asn Glu Val Val Leu Val Gly Gly Asp Lys Thr
35 40 45
Val Val Gly Thr Pro Val Val Glu Gly Ala Thr Val Val Gly Thr Val
50 55 60
Glu Lys Gln Gly Lys Gln Lys Lys Val Val Thr Phe Lys Tyr Lys Pro
65 70 75 80
Lys Lys Gly Ser His Arg Lys Gln Gly His Arg Gln Pro Tyr Thr Lys
85 90 95
Val Val Ile Asn Ala Ile Asn Ala
100

<210> SEQ ID NO 53
<211> LENGTH: 1293
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 53

atgatactat tgaaaagcct ctataagggc ttttttgctg caatgaagga ggaaaat ttt 60
gaggcaagat gttataatag agaaaaagga ggggtgtgtct tgattaaaac tatgcaatac 120
aaaaaaacga tggcaacagt tgttgctctt atcgtcgcac ttttgctatt tggcttgatt 180
tatgat ttac ttgggggttca aaaaaatgag cttagcagctc aaaaatctgc tcagccaaag 240
gtcaaaacag cgcgtgttgt agctaattggc gacattttta ttcattgat tctctacatg 300
agtgctagaa aagctgacga tacctatgat ttcactcctt attttgaata tgtaaggac 360
tggtattagcg gtgctgactt agctattgga gattatgaag ggaccattag cccagattat 420
cccttagcag gctatccctt attcaatgct ccagaagaga ttgcagggtgc tctgaaaaat 480
actggctatg atgtagtcga ttttagcccat aatcatatct tagattccca attagacggt 540
gcccttaaca ctaaaaaggt ttttcatcaa ttaggtatag acagtattgg catctatgac 600
aaggatcggt caaaaagaatc cttcttaatt aaaaatgtca atggtatcaa aattgcaatt 660
ttaggttatt cttatgggtta taacggcatg gaggccacac ttagccaaga agactatgag 720
aaacacatgt ctgatttaga tgaagctaag ataaaaaaag aacttcagct agctgaaaaa 780
aaggctgacg tgaccattgt tatgccacaa atgggaacag aatatgcctt agaaccgaca 840
gcagaacaaa aagaacttta ccacaaaatg attgattggg gagctgacgt cgtccttagga 900
ggccatccgc atgttattga accttcagag acagttataa aaggtaggca aaagaaattc 960
attatttact ctatgggaaa ttttatttca aatcagcggc ttgaaaccgt agatgatatc 1020
tggtactgagc gtggcctatt gatggacctt acttttgaga aaaaagataa caaaacaaaa 1080
attaaaacag ttgaggccca tccaacctg gtttttagcca aaggtaaagg cattgtgggt 1140
aaagaagggt ttgaactata caattatcga acaatgggtt tagaagattt tatcaaagg 1200
ggaaaatacc acgacaagat tgatgaggaa accaaagcaa aagtagcact tgcctatcag 1260
gaaattaatg atttagttaa cctgaaatgg taa 1293

<210> SEQ ID NO 54
<211> LENGTH: 430
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 54

Met Ile Leu Leu Lys Ser Leu Tyr Lys Gly Phe Phe Ala Ala Met Lys
1 5 10 15
Glu Glu Asn Phe Glu Ala Arg Cys Tyr Asn Arg Glu Lys Gly Gly Cys
20 25 30
Val Leu Ile Lys Thr Met Gln Tyr Lys Lys Thr Met Ala Thr Val Val
35 40 45
Ala Leu Ile Val Ala Leu Leu Phe Gly Leu Ile Tyr Asp Leu Leu
50 55 60
Gly Val Gln Lys Asn Glu Leu Ala Ala Gln Lys Ser Ala Gln Pro Lys
65 70 75 80
Val Lys Thr Ala Arg Val Val Ala Asn Gly Asp Ile Leu Ile His Asp
85 90 95
Ile Leu Tyr Met Ser Ala Arg Lys Ala Asp Asp Thr Tyr Asp Phe Thr

			100					105				110					
Pro	Tyr	Phe	Glu	Tyr	Val	Lys	Asp	Trp	Ile	Ser	Gly	Ala	Asp	Leu	Ala		
		115					120					125					
Ile	Gly	Asp	Tyr	Glu	Gly	Thr	Ile	Ser	Pro	Asp	Tyr	Pro	Leu	Ala	Gly		
	130					135					140						
Tyr	Pro	Leu	Phe	Asn	Ala	Pro	Glu	Glu	Ile	Ala	Gly	Ala	Leu	Lys	Asn		
145				150						155					160		
Thr	Gly	Tyr	Asp	Val	Val	Asp	Leu	Ala	His	Asn	His	Ile	Leu	Asp	Ser		
			165						170					175			
Gln	Leu	Asp	Gly	Ala	Leu	Asn	Thr	Lys	Lys	Val	Phe	His	Gln	Leu	Gly		
		180						185					190				
Ile	Asp	Ser	Ile	Gly	Ile	Tyr	Asp	Lys	Asp	Arg	Ser	Lys	Glu	Ser	Phe		
	195						200					205					
Leu	Ile	Lys	Asn	Val	Asn	Gly	Ile	Lys	Ile	Ala	Ile	Leu	Gly	Tyr	Ser		
	210					215					220						
Tyr	Gly	Tyr	Asn	Gly	Met	Glu	Ala	Thr	Leu	Ser	Gln	Glu	Asp	Tyr	Glu		
225				230						235					240		
Lys	His	Met	Ser	Asp	Leu	Asp	Glu	Ala	Lys	Ile	Lys	Lys	Glu	Leu	Gln		
			245					250						255			
Leu	Ala	Glu	Lys	Lys	Ala	Asp	Val	Thr	Ile	Val	Met	Pro	Gln	Met	Gly		
		260						265					270				
Thr	Glu	Tyr	Ala	Leu	Glu	Pro	Thr	Ala	Glu	Gln	Lys	Glu	Leu	Tyr	His		
	275						280					285					
Lys	Met	Ile	Asp	Trp	Gly	Ala	Asp	Val	Val	Leu	Gly	Gly	His	Pro	His		
	290					295					300						
Val	Ile	Glu	Pro	Ser	Glu	Thr	Val	Ile	Lys	Gly	Arg	Gln	Lys	Lys	Phe		
305				310						315					320		
Ile	Ile	Tyr	Ser	Met	Gly	Asn	Phe	Ile	Ser	Asn	Gln	Arg	Leu	Glu	Thr		
			325					330					335				
Val	Asp	Asp	Ile	Trp	Thr	Glu	Arg	Gly	Leu	Leu	Met	Asp	Leu	Thr	Phe		
		340						345				350					
Glu	Lys	Lys	Asp	Asn	Lys	Thr	Lys	Ile	Lys	Thr	Val	Glu	Ala	His	Pro		
	355					360						365					
Thr	Met	Val	Leu	Ala	Lys	Gly	Lys	Gly	Ile	Val	Gly	Lys	Glu	Gly	Phe		
	370					375					380						
Glu	Leu	Tyr	Asn	Tyr	Arg	Thr	Met	Val	Leu	Glu	Asp	Phe	Ile	Lys	Gly		
385				390						395					400		
Gly	Lys	Tyr	His	Asp	Lys	Ile	Asp	Glu	Glu	Thr	Lys	Ala	Lys	Val	Ala		
			405					410					415				
Leu	Ala	Tyr	Gln	Glu	Ile	Asn	Asp	Leu	Val	Asn	Leu	Lys	Trp				
		420						425				430					

<210> SEQ ID NO 55

<211> LENGTH: 2217

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 55

ttggagatga	catctttagg	aaaaaacgat	aaggaagttg	ctactgtgaa	gaaatttaaa	60
acacttatca	caggttttat	caacacaaga	ttgggtttta	taattactct	actcttttgt	120
tactggataa	agaccctgtg	ggcatatcat	acagactttt	cactagattt	gggaaatata	180
taccaagtct	ttctaactat	tatcaatcca	atcccactag	cttttttact	tttggggggt	240
gctcttttacg	ttaagaatac	ccgagccttt	tatatctgtt	cttgggtggt	ttatattatc	300
cttaacattc	tcttgatatt	aaattctata	tattaccgag	aattttcaga	ctttattaca	360
gtgagtgcca	tgctagctag	tagtaaagtc	tccgctggat	taggggactc	tgctttaaac	420
ctttttacgca	tctgggatatt	tatctatatt	cttgattttta	ttattctaatt	tagtttatct	480
atcgctaaaa	aaatcaaaaa	tgatcaacgt	ccttttaaca	agcgcgcagc	atttgccatc	540
accgctttat	ctagtctatt	gctttctatt	aatctttttt	tagcagaaat	tgatcgctccg	600

gaactattaa	cacgtggcctt	ttcaaatact	tatattgtga	gagctttagg	actaccagcg	660
tttaccctct	atagcggcaa	tcaaacctat	caagctcaaa	aagaacgaaa	tgagagctact	720
gcagaagaat	taattgatgt	taaaacttat	gtcaaaggac	attatgcagc	acctgatcct	780
cagtattttg	gaattggaaa	aggcaaaaat	attattgttc	ttcatttaga	aagctttcaa	840
caattcttaa	tagattataa	actaaaagaa	ggagataaag	aatatgaggt	aacgcctttt	900
atcaactcac	tttatcactc	aaatgctacc	ttagcattcc	ctaacttttt	tcacaggtt	960
aaagcaggta	aaacttctga	tgctgaaacc	atgatggaga	attccttatt	tggtttaaat	1020
agtgggtcct	ttatggtgaa	ctacggtggt	gaaaatacac	aatttgctac	tccaagtatt	1080
ttagcccaaa	aagggtggcta	taccagcgct	gtctttcatg	gtaacgttgg	aactttctgg	1140
aatcgcaata	atgcttataa	acaatggggc	tataattatt	tttttgattc	tagctacttc	1200
tctaaacaaa	atagtaagaa	ctcttttcaa	tatgggttaa	atgataagta	catgtttaag	1260
gattccataa	aatatcttga	acagatgcaa	caaccttttt	ataccaagtt	tatcactgtg	1320
agtaatcact	atccttatac	tagtctaaaa	ggcgaagta	gtgaagaagg	ttttccttta	1380
gccaaaacag	acgatgaaac	gatcaatggt	tactttgcta	ctgccaatta	tttagacgct	1440
gcccttaaat	ctttttttga	ttacttgaaa	gccactgggt	tgtacgacaa	ttctattttt	1500
gttttatatg	gtgatcatta	tggtatttca	aattctcgta	attctagtct	tgctccactt	1560
cttggtaaaag	attctgaaac	ttggtctgaa	tatgataatg	ctatgctaca	acgagtccccg	1620
tatatgatcc	atattccagg	ttatacgaat	ggtagtatca	aagaaacctt	tgcggtgaa	1680
atcgatgctc	ttcctacttt	actccacata	cttggtattg	acactagtca	gtttgttcaa	1740
ttaggacaag	atttattatc	acctcaaaaat	agccagattg	tggcacaacg	aacatctggg	1800
acttatatga	ctcctgaata	cactaactat	agtggacgtc	tgtacaacac	gcaaacaggt	1860
ttagaaatca	ctaataccga	tgaaatgact	atagccaaaa	ctaaggaaat	tcgctctgct	1920
gttgctcaac	aactagcagc	tagcgacgct	attcaaacgg	gtgatctcct	gcgctttgat	1980
actcaaaatg	gtctaaaagc	tattgatcct	aaccagttta	tctacactaa	gcagttaaaa	2040
caactgaaaag	atatttcagc	aaaactcgga	tcagagtcaa	caagtttata	cagtaaaaat	2100
ggtcataaat	caactcagaa	acttttttaa	gcaccatcct	acttagaact	aaatcccgta	2160
gaagctgacg	cggcaacttc	tgaactaaaa	gaggataacc	ccaaaaataa	agaataa	2217

<210> SEQ ID NO 56

<211> LENGTH: 738

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 56

Met	Glu	Met	Thr	Ser	Leu	Gly	Lys	Asn	Asp	Lys	Glu	Val	Ala	Thr	Val
1				5					10					15	
Lys	Lys	Phe	Lys	Thr	Leu	Ile	Thr	Gly	Phe	Ile	Asn	Thr	Arg	Leu	Gly
			20					25					30		
Phe	Ile	Ile	Thr	Leu	Leu	Phe	Cys	Tyr	Trp	Ile	Lys	Thr	Leu	Trp	Ala
		35					40					45			
Tyr	His	Thr	Asp	Phe	Ser	Leu	Asp	Leu	Gly	Asn	Ile	Tyr	Gln	Val	Phe
	50					55					60				
Leu	Thr	Ile	Ile	Asn	Pro	Ile	Pro	Leu	Ala	Phe	Leu	Leu	Leu	Gly	Val
65					70					75				80	
Ala	Leu	Tyr	Val	Lys	Asn	Thr	Arg	Ala	Phe	Tyr	Ile	Cys	Ser	Trp	Val
				85					90					95	
Val	Tyr	Ile	Ile	Leu	Asn	Ile	Leu	Leu	Ile	Ser	Asn	Ser	Ile	Tyr	Tyr
			100					105					110		
Arg	Glu	Phe	Ser	Asp	Phe	Ile	Thr	Val	Ser	Ala	Met	Leu	Ala	Ser	Ser
		115					120					125			
Lys	Val	Ser	Ala	Gly	Leu	Gly	Asp	Ser	Ala	Leu	Asn	Leu	Leu	Arg	Ile
	130					135					140				
Trp	Asp	Ile	Ile	Tyr	Ile	Leu	Asp	Phe	Ile	Ile	Leu	Ile	Ser	Leu	Ser
145					150					155				160	
Ile	Ala	Lys	Lys	Ile	Lys	Asn	Asp	Gln	Arg	Pro	Phe	Asn	Lys	Arg	Ala
				165					170					175	
Ala	Phe	Ala	Ile	Thr	Ala	Leu	Ser	Ser	Leu	Leu	Leu	Ser	Ile	Asn	Leu
			180					185						190	

Phe	Leu	Ala	Glu	Ile	Asp	Arg	Pro	Glu	Leu	Leu	Thr	Arg	Gly	Phe	Ser	195	200	205
Asn	Thr	Tyr	Ile	Val	Arg	Ala	Leu	Gly	Leu	Pro	Ala	Phe	Thr	Leu	Tyr	210	215	220
Ser	Gly	Asn	Gln	Thr	Tyr	Gln	Ala	Gln	Lys	Glu	Arg	Asn	Gly	Ala	Thr	225	230	235
Ala	Glu	Glu	Leu	Ile	Asp	Val	Lys	Thr	Tyr	Val	Lys	Gly	His	Tyr	Ala	245	250	255
Ala	Pro	Asp	Pro	Gln	Tyr	Phe	Gly	Ile	Gly	Lys	Gly	Lys	Asn	Ile	Ile	260	265	270
Val	Leu	His	Leu	Glu	Ser	Phe	Gln	Gln	Phe	Leu	Ile	Asp	Tyr	Lys	Leu	275	280	285
Lys	Glu	Gly	Asp	Lys	Glu	Tyr	Glu	Val	Thr	Pro	Phe	Ile	Asn	Ser	Leu	290	295	300
Tyr	His	Ser	Asn	Ala	Thr	Leu	Ala	Phe	Pro	Asn	Phe	Phe	His	Gln	Val	305	310	315
Lys	Ala	Gly	Lys	Thr	Ser	Asp	Ala	Glu	Thr	Met	Met	Glu	Asn	Ser	Leu	325	330	335
Phe	Gly	Leu	Asn	Ser	Gly	Ser	Phe	Met	Val	Asn	Tyr	Gly	Gly	Glu	Asn	340	345	350
Thr	Gln	Phe	Ala	Thr	Pro	Ser	Ile	Leu	Ala	Gln	Lys	Gly	Gly	Tyr	Thr	355	360	365
Ser	Ala	Val	Phe	His	Gly	Asn	Val	Gly	Thr	Phe	Trp	Asn	Arg	Asn	Asn	370	375	380
Ala	Tyr	Lys	Gln	Trp	Gly	Tyr	Asn	Tyr	Phe	Phe	Asp	Ser	Ser	Tyr	Phe	385	390	395
Ser	Lys	Gln	Asn	Ser	Lys	Asn	Ser	Phe	Gln	Tyr	Gly	Leu	Asn	Asp	Lys	405	410	415
Tyr	Met	Phe	Lys	Asp	Ser	Ile	Lys	Tyr	Leu	Glu	Gln	Met	Gln	Gln	Pro	420	425	430
Phe	Tyr	Thr	Lys	Phe	Ile	Thr	Val	Ser	Asn	His	Tyr	Pro	Tyr	Thr	Ser	435	440	445
Leu	Lys	Gly	Glu	Ser	Ser	Glu	Glu	Gly	Phe	Pro	Leu	Ala	Lys	Thr	Asp	450	455	460
Asp	Glu	Thr	Ile	Asn	Gly	Tyr	Phe	Ala	Thr	Ala	Asn	Tyr	Leu	Asp	Ala	465	470	475
Ala	Leu	Lys	Ser	Phe	Phe	Asp	Tyr	Leu	Lys	Ala	Thr	Gly	Leu	Tyr	Asp	485	490	495
Asn	Ser	Ile	Phe	Val	Leu	Tyr	Gly	Asp	His	Tyr	Gly	Ile	Ser	Asn	Ser	500	505	510
Arg	Asn	Ser	Ser	Leu	Ala	Pro	Leu	Leu	Gly	Lys	Asp	Ser	Glu	Thr	Trp	515	520	525
Ser	Glu	Tyr	Asp	Asn	Ala	Met	Leu	Gln	Arg	Val	Pro	Tyr	Met	Ile	His	530	535	540
Ile	Pro	Gly	Tyr	Thr	Asn	Gly	Ser	Ile	Lys	Glu	Thr	Phe	Gly	Gly	Glu	545	550	555
Ile	Asp	Ala	Leu	Pro	Thr	Leu	Leu	His	Ile	Leu	Gly	Ile	Asp	Thr	Ser	565	570	575
Gln	Phe	Val	Gln	Leu	Gly	Gln	Asp	Leu	Leu	Ser	Pro	Gln	Asn	Ser	Gln	580	585	590
Ile	Val	Ala	Gln	Arg	Thr	Ser	Gly	Thr	Tyr	Met	Thr	Pro	Glu	Tyr	Thr	595	600	605
Asn	Tyr	Ser	Gly	Arg	Leu	Tyr	Asn	Thr	Gln	Thr	Gly	Leu	Glu	Ile	Thr	610	615	620
Asn	Pro	Asp	Glu	Met	Thr	Ile	Ala	Lys	Thr	Lys	Glu	Ile	Arg	Ser	Ala	625	630	635
Val	Ala	Gln	Gln	Leu	Ala	Ala	Ser	Asp	Ala	Ile	Gln	Thr	Gly	Asp	Leu			

				645					650					655			
Leu	Arg	Phe	Asp	Thr	Gln	Asn	Gly	Leu	Lys	Ala	Ile	Asp	Pro	Asn	Gln		
			660					665					670				
Phe	Ile	Tyr	Thr	Lys	Gln	Leu	Lys	Gln	Leu	Lys	Asp	Ile	Ser	Ala	Lys		
		675					680					685					
Leu	Gly	Ser	Glu	Ser	Thr	Ser	Leu	Tyr	Ser	Lys	Asn	Gly	His	Lys	Ser		
	690					695					700						
Thr	Gln	Lys	Leu	Phe	Lys	Ala	Pro	Ser	Tyr	Leu	Glu	Leu	Asn	Pro	Val		
705					710				715						720		
Glu	Ala	Asp	Ala	Ala	Thr	Ser	Glu	Leu	Lys	Glu	Asp	Asn	Pro	Lys	Asn		
				725				730						735			
Lys	Glu																

<210> SEQ ID NO 57

<211> LENGTH: 813

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 57

atgaatttta	aaaaaataag	atttgggtttt	ttgctttgcc	tcctacttta	tccttttagca	60
gcttgtaaca	agtctgaaca	acttaatcac	tacgaaagaa	ttaaaaaac	aagaaaatta	120
gtcgttgctg	taagccctga	ttatgctcct	tttgaattta	aagctttagt	taatggaaaa	180
gatactattg	ttggagcaga	tgttcaatta	gctcaggcta	ttgctgatga	attagacgtt	240
gatcttgagc	tttcaccaat	gagttttgat	aatgttttgt	ctagttttaca	gactggtaaa	300
gctgatcttg	ctatttcagg	aatctcacat	actaaagaaa	gagctaaagt	atatgatttt	360
tcaattcctt	actatcaggc	agaaaacgct	atagtgatga	gagcatctga	tgctaaagtg	420
acaaaaaata	ttagtgacct	aaacggtaag	aaagtagccg	ctcaaaaagg	tagtatcgag	480
gaagggtttag	ttaaaataca	attaccaaaag	gccaatctga	tttctttgac	tgctatggga	540
gaagccatta	atgaactaaa	agcaggacaa	gtctatgcag	ttaccttaga	agcacctgta	600
gctgctgggt	ttttagccca	acataaggat	ctggcttttag	cacccttttag	cttaaaaacc	660
agtgatggag	atgccaaagc	agtggccctt	cctaaaaata	gtggagactt	aaccaaagcc	720
gttaataagg	ttattgctaa	gtagatgag	caagaacggt	acaagtcatt	tattgcagag	780
acaatagcac	taacgaaaaa	tactatgaag	taa			813

<210> SEQ ID NO 58

<211> LENGTH: 270

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 58

Met	Asn	Phe	Lys	Lys	Ile	Arg	Phe	Gly	Phe	Leu	Leu	Cys	Leu	Leu	Leu
1			5					10					15		
Tyr	Pro	Leu	Ala	Ala	Cys	Asn	Lys	Ser	Glu	Gln	Leu	Asn	His	Tyr	Glu
		20					25					30			
Arg	Ile	Lys	Lys	Thr	Arg	Lys	Leu	Val	Val	Ala	Val	Ser	Pro	Asp	Tyr
		35				40					45				
Ala	Pro	Phe	Glu	Phe	Lys	Ala	Leu	Val	Asn	Gly	Lys	Asp	Thr	Ile	Val
	50				55				60						
Gly	Ala	Asp	Val	Gln	Leu	Ala	Gln	Ala	Ile	Ala	Asp	Glu	Leu	Asp	Val
65			70					75					80		
Asp	Leu	Glu	Leu	Ser	Pro	Met	Ser	Phe	Asp	Asn	Val	Leu	Ser	Ser	Leu
		85					90					95			
Gln	Thr	Gly	Lys	Ala	Asp	Leu	Ala	Ile	Ser	Gly	Ile	Ser	His	Thr	Lys
		100					105					110			
Glu	Arg	Ala	Lys	Val	Tyr	Asp	Phe	Ser	Ile	Pro	Tyr	Tyr	Gln	Ala	Glu
	115					120					125				
Asn	Ala	Ile	Val	Met	Arg	Ala	Ser	Asp	Ala	Lys	Val	Thr	Lys	Asn	Ile
	130				135				140						
Ser	Asp	Leu	Asn	Gly	Lys	Lys	Val	Ala	Ala	Gln	Lys	Gly	Ser	Ile	Glu

145		150		155		160
Glu Gly Leu Val Lys Ile Gln Leu Pro Lys Ala Asn Leu Ile Ser Leu						
		165		170		175
Thr Ala Met Gly Glu Ala Ile Asn Glu Leu Lys Ala Gly Gln Val Tyr						
		180		185		190
Ala Val Thr Leu Glu Ala Pro Val Ala Ala Gly Phe Leu Ala Gln His						
		195		200		205
Lys Asp Leu Ala Leu Ala Pro Phe Ser Leu Lys Thr Ser Asp Gly Asp						
		210		215		220
Ala Lys Ala Val Ala Leu Pro Lys Asn Ser Gly Asp Leu Thr Lys Ala						
		225		230		235
Val Asn Lys Val Ile Ala Lys Leu Asp Glu Gln Glu Arg Tyr Lys Ser						
		245		250		255
Phe Ile Ala Glu Thr Ile Ala Leu Thr Lys Asn Thr Met Lys						
		260		265		270

<210> SEQ ID NO 59

<211> LENGTH: 2733

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 59

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agtgttgaag	aagttacttc	acgccaaaat	ttgacttatg	ccaatgaaat	cgtaacacaa	120
aggccaaaga	gagaatctgt	tattagtgat	aaatcgaatt	ttcccgtcat	atcaccttac	180
ctagcaagtg	tggatttttg	tgagagaaaa	acacctttgc	caacacctga	taaaggagta	240
aaagtaacta	ctgaacagtc	tattgctcaa	gtaagaaaagg	ggcctgaaga	aagaccctat	300
actgttactg	gcaagattac	gagtgtgatc	aatggctggg	gaggctatgg	cttttatatt	360
caagatagtg	aaggatttgg	actttatggt	tatcctcaaa	aagatttagg	atacagtaag	420
ggagatattg	ttcaattaac	aggtacactt	actcgcttta	aagggtgattt	acaactccaa	480
cagggtgactg	cacacaaaaa	gttagagtta	tcttttccga	cttctgttaa	agaagcagta	540
atatcagaat	tagaaacaac	aacaccctca	acattagtta	agttatctca	cgtgacagtt	600
ggagaattat	caactgatca	atataacaac	acatctttcc	ttgtaaggga	tgatagtggg	660
aaaagttagt	ttgttcatat	agatcatcgt	acaggggtta	aaggggctga	tgttggtact	720
aaaataagtc	aggggtgattt	gattaacctc	acagccatat	tgtctattgt	tgatgggtcaa	780
ttacaattaa	gaccgttttc	tcttgaacaa	ttggaagtgg	ttaaaaaggt	cacaagctca	840
aatagtgatg	cttcatctcg	taatattgtg	aaaataggcg	agattcaagg	agctagtcac	900
acgtcgccac	ttctcaaaaa	agcggtcacc	gtagaacagg	ttgttggtcac	ttatttagac	960
gattccactc	atttttatgt	tcaagatctt	aatgggtgatg	gtgatttagc	gacttcagat	1020
ggatttcgtg	tttttgctaa	aaacgctaag	gttcaagtcg	gcatgtttt	gaccatttca	1080
gggtgaagtgg	aagaattctt	tggtcgtggg	tatgaggaac	gtaagcagac	tgaccttacc	1140
atcacccaaa	ttgtggctaa	agcagtgacc	aaaacagggg	cagctcaagt	tccatcacccg	1200
cttgtttttag	ggaaagatcg	tatcgcgcca	gccaatatta	ttgataatga	tggcttgctg	1260
gtgtttgatc	cagaagaaga	cgctattgat	tattgggaat	caatggaagg	catgttagtg	1320
gcggttgatg	atgctaaaaat	ccttgggtcca	atgaaaaata	aagaaattta	tgtcttacct	1380
ggctctagta	caagaccggt	aaataattca	gggtggagtat	tacttccagc	taattcttat	1440
aacacagatg	tgattcctgt	tcttttcaaa	aaaggcaaac	aaattattaa	agcaggagac	1500
tcttacaaaag	gaagatttagc	tgggcccagta	tcttatagct	atggtaatta	caagggtcttt	1560
gttgatgaca	gcaaaaaacat	gccaaagttta	atggatgggtc	atctaaaacc	tgaaaaaaca	1620
aacttgcaaaa	aagaccttag	caagttaagc	attgcttctt	acaatattga	aaacttctca	1680
gccaatcctt	cttcaactaa	agatgagaag	gtcaaacgga	ttgccgaatc	ctttattcat	1740
gatctgaatg	ctccagacat	tattggatta	attgaagtcc	aagataataa	tgggccgact	1800
gatgatggga	caacggatgc	gacacaaagc	gcgcaacgcc	tcattgatgc	tattaaaaaa	1860
ctagggtggcc	caacttatcg	ttatgttgat	attgctccag	aaaataatgt	tgacggaggt	1920
caaccagggtg	gtaatatctg	aacaggattc	ctttatcaac	cagagcgctg	cagcctttct	1980
gataagccaa	aaggcggtgc	tcgtgatgct	ctaacttggg	ttaatggaga	attaaacctt	2040
agtgttggtc	gaattgatcc	aactaacgcc	gcttggaag	atgttcgtaa	atcactagca	2100
gcagaattta	tcttccaagg	tcgtaaaagtc	gttggtgttg	caaatcattt	gaactctaag	2160

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cgtgggggata atgctcttta tggttgtgtg caaccagtca cttttaaatc tgagcaaaga 2220
cgtcacgtct tggctaatat gctagcaciaa tttgcgaaag aaggggcaaa acaccaagct 2280
aatattgtga tgctaggtga ctttaaatgat tttgaattca caaagacgat tcaattaatc 2340
gaagaagggtg acatgggttaa cttgggtgagc cgacatgata tttcagatcg gtattcttat 2400
tttcaccaag gcaataatca gacccttgat aatatattag tttcacgcca tttacttgat 2460
cactacgaat ttgacatggt tcatgtgaat tccccattta tggaagctca cggacgcgca 2520
tcagatcatg atccattggt acttcaatta tcattttcca aagaaaatga taaggcagag 2580
tcttctaaac aaagtgtaaa agctaaaaaaa acttcaaaag gaaaactggt gccaaaaaca 2640
ggagatagtc ttgtttatgt gataacgcta ctaggaacgg ctagttttatt agtgcctatt 2700
ttattattga ctaaaggcaa aaaggaatca tag 2733

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<210> SEQ ID NO 60

<211> LENGTH: 910

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 60

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Met Ile Asn Lys Lys Cys Ile Ile Pro Val Ser Leu Leu Thr Leu Ala
1           5           10           15
Ile Thr Leu Thr Ser Val Glu Glu Val Thr Ser Arg Gln Asn Leu Thr
20           25           30
Tyr Ala Asn Glu Ile Val Thr Gln Arg Pro Lys Arg Glu Ser Val Ile
35           40           45
Ser Asp Lys Ser Asn Phe Pro Val Ile Ser Pro Tyr Leu Ala Ser Val
50           55           60
Asp Phe Gly Glu Arg Lys Thr Pro Leu Pro Thr Pro Asp Lys Gly Val
65           70           75           80
Lys Val Thr Thr Glu Gln Ser Ile Ala Gln Val Arg Lys Gly Pro Glu
85           90           95
Glu Arg Pro Tyr Thr Val Thr Gly Lys Ile Thr Ser Val Ile Asn Gly
100          105          110
Trp Gly Gly Tyr Gly Phe Tyr Ile Gln Asp Ser Glu Gly Ile Gly Leu
115          120          125
Tyr Val Tyr Pro Gln Lys Asp Leu Gly Tyr Ser Lys Gly Asp Ile Val
130          135          140
Gln Leu Thr Gly Thr Leu Thr Arg Phe Lys Gly Asp Leu Gln Leu Gln
145          150          155          160
Gln Val Thr Ala His Lys Lys Leu Glu Leu Ser Phe Pro Thr Ser Val
165          170          175
Lys Glu Ala Val Ile Ser Glu Leu Glu Thr Thr Thr Pro Ser Thr Leu
180          185          190
Val Lys Leu Ser His Val Thr Val Gly Glu Leu Ser Thr Asp Gln Tyr
195          200          205
Asn Asn Thr Ser Phe Leu Val Arg Asp Asp Ser Gly Lys Ser Ile Val
210          215          220
Val His Ile Asp His Arg Thr Gly Val Lys Gly Ala Asp Val Val Thr
225          230          235          240
Lys Ile Ser Gln Gly Asp Leu Ile Asn Leu Thr Ala Ile Leu Ser Ile
245          250          255
Val Asp Gly Gln Leu Gln Leu Arg Pro Phe Ser Leu Glu Gln Leu Glu
260          265          270
Val Val Lys Lys Val Thr Ser Ser Asn Ser Asp Ala Ser Ser Arg Asn
275          280          285
Ile Val Lys Ile Gly Glu Ile Gln Gly Ala Ser His Thr Ser Pro Leu
290          295          300
Leu Lys Lys Ala Val Thr Val Glu Gln Val Val Val Thr Tyr Leu Asp
305          310          315          320
Asp Ser Thr His Phe Tyr Val Gln Asp Leu Asn Gly Asp Gly Asp Leu

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Ala	Thr	Ser	Asp	Gly	Ile	Arg	Val	Phe	Ala	Lys	Asn	Ala	Lys	Val	Gln	325	330	335
																340	345	350
Val	Gly	Asp	Val	Leu	Thr	Ile	Ser	Gly	Glu	Val	Glu	Glu	Phe	Phe	Gly			
																355	360	365
Arg	Gly	Tyr	Glu	Glu	Arg	Lys	Gln	Thr	Asp	Leu	Thr	Ile	Thr	Gln	Ile			
																370	375	380
Val	Ala	Lys	Ala	Val	Thr	Lys	Thr	Gly	Thr	Ala	Gln	Val	Pro	Ser	Pro			
																385	390	400
Leu	Val	Leu	Gly	Lys	Asp	Arg	Ile	Ala	Pro	Ala	Asn	Ile	Ile	Asp	Asn			
																405	410	415
Asp	Gly	Leu	Arg	Val	Phe	Asp	Pro	Glu	Glu	Asp	Ala	Ile	Asp	Tyr	Trp			
																420	425	430
Glu	Ser	Met	Glu	Gly	Met	Leu	Val	Ala	Val	Asp	Asp	Ala	Lys	Ile	Leu			
																435	440	445
Gly	Pro	Met	Lys	Asn	Lys	Glu	Ile	Tyr	Val	Leu	Pro	Gly	Ser	Ser	Thr			
																450	455	460
Arg	Pro	Leu	Asn	Asn	Ser	Gly	Gly	Val	Leu	Leu	Pro	Ala	Asn	Ser	Tyr			
																465	470	475
Asn	Thr	Asp	Val	Ile	Pro	Val	Leu	Phe	Lys	Lys	Gly	Lys	Gln	Ile	Ile			
																485	490	495
Lys	Ala	Gly	Asp	Ser	Tyr	Lys	Gly	Arg	Leu	Ala	Gly	Pro	Val	Ser	Tyr			
																500	505	510
Ser	Tyr	Gly	Asn	Tyr	Lys	Val	Phe	Val	Asp	Asp	Ser	Lys	Asn	Met	Pro			
																515	520	525
Ser	Leu	Met	Asp	Gly	His	Leu	Lys	Pro	Glu	Lys	Thr	Asn	Leu	Gln	Lys			
																530	535	540
Asp	Leu	Ser	Lys	Leu	Ser	Ile	Ala	Ser	Tyr	Asn	Ile	Glu	Asn	Phe	Ser			
																545	550	555
Ala	Asn	Pro	Ser	Ser	Thr	Lys	Asp	Glu	Lys	Val	Lys	Arg	Ile	Ala	Glu			
																565	570	575
Ser	Phe	Ile	His	Asp	Leu	Asn	Ala	Pro	Asp	Ile	Ile	Gly	Leu	Ile	Glu			
																580	585	590
Val	Gln	Asp	Asn	Asn	Gly	Pro	Thr	Asp	Asp	Gly	Thr	Thr	Asp	Ala	Thr			
																595	600	605
Gln	Ser	Ala	Gln	Arg	Leu	Ile	Asp	Ala	Ile	Lys	Lys	Leu	Gly	Gly	Pro			
																610	615	620
Thr	Tyr	Arg	Tyr	Val	Asp	Ile	Ala	Pro	Glu	Asn	Asn	Val	Asp	Gly	Gly			
																625	630	635
Gln	Pro	Gly	Gly	Asn	Ile	Arg	Thr	Gly	Phe	Leu	Tyr	Gln	Pro	Glu	Arg			
																645	650	655
Val	Ser	Leu	Ser	Asp	Lys	Pro	Lys	Gly	Gly	Ala	Arg	Asp	Ala	Leu	Thr			
																660	665	670
Trp	Val	Asn	Gly	Glu	Leu	Asn	Leu	Ser	Val	Gly	Arg	Ile	Asp	Pro	Thr			
																675	680	685
Asn	Ala	Ala	Trp	Lys	Asp	Val	Arg	Lys	Ser	Leu	Ala	Ala	Glu	Phe	Ile			
																690	695	700
Phe	Gln	Gly	Arg	Lys	Val	Val	Val	Val	Ala	Asn	His	Leu	Asn	Ser	Lys			
																705	710	715
Arg	Gly	Asp	Asn	Ala	Leu	Tyr	Gly	Cys	Val	Gln	Pro	Val	Thr	Phe	Lys			
																725	730	735
Ser	Glu	Gln	Arg	His	Val	Leu	Ala	Asn	Met	Leu	Ala	Gln	Phe	Ala				
																740	745	750
Lys	Glu	Gly	Ala	Lys	His	Gln	Ala	Asn	Ile	Val	Met	Leu	Gly	Asp	Phe			
																755	760	765
Asn	Asp	Phe	Glu	Phe	Thr	Lys	Thr	Ile	Gln	Leu	Ile	Glu	Glu	Gly	Asp			
																770	775	780

Met	Val	Asn	Leu	Val	Ser	Arg	His	Asp	Ile	Ser	Asp	Arg	Tyr	Ser	Tyr
785					790					795					800
Phe	His	Gln	Gly	Asn	Asn	Gln	Thr	Leu	Asp	Asn	Ile	Leu	Val	Ser	Arg
			805						810					815	
His	Leu	Leu	Asp	His	Tyr	Glu	Phe	Asp	Met	Val	His	Val	Asn	Ser	Pro
			820					825					830		
Phe	Met	Glu	Ala	His	Gly	Arg	Ala	Ser	Asp	His	Asp	Pro	Leu	Leu	Leu
		835					840					845			
Gln	Leu	Ser	Phe	Ser	Lys	Glu	Asn	Asp	Lys	Ala	Glu	Ser	Ser	Lys	Gln
	850					855					860				
Ser	Val	Lys	Ala	Lys	Lys	Thr	Ser	Lys	Gly	Lys	Leu	Leu	Pro	Lys	Thr
865					870					875					880
Gly	Asp	Ser	Leu	Val	Tyr	Val	Ile	Thr	Leu	Leu	Gly	Thr	Ala	Ser	Leu
			885						890					895	
Leu	Val	Pro	Ile	Leu	Leu	Leu	Thr	Lys	Gly	Lys	Lys	Glu	Ser		
			900					905					910		

<210> SEQ ID NO 61

<211> LENGTH: 6180

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 61

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gtcttttgtaa	gttcatgtat	gcttttaaca	gtgggcctcg	gagttgccgt	acctactgga	120
ttcagccaat	ctaattggcgt	gatggttgta	aaggctgcgg	aagtgccggc	gacagattta	180
tcacgtcagg	cgtctgattc	ggagagggtg	gatgaatcgt	ctttattgca	gaaagaaaac	240
ttatcagtag	attcatttaa	attagaaaat	ttaaattggat	gggaagctga	aaatgataca	300
gcaggtaatt	tggggaaaatt	taaagatcca	gatagttcgg	gctatcaaaa	tattttgaca	360
tcatctggaa	agaatatcag	tgtagctgtt	gctcccaaag	gttcaggtaa	aatgaacatt	420
aaagtaacta	aaagatcaaa	ttttcagggt	ggatattatg	taggtggtct	tagaactcaa	480
actccggtat	tgaagttaaa	tgatgtttat	cgatattcct	ttacaactaa	aaaattatca	540
ggaaattcct	cagagttcaa	aacgagagtt	aagcccgttg	aatctaataa	taaactaggg	600
aaagagcttg	ttattagggt	ggataataaa	aatgtatcta	ctaagcatga	ttggcttcca	660
gacatctctg	atggaactca	tactgtggac	ttcactggtc	ttgataaaaa	attatctgtt	720
gcttttcagat	tttctccaag	acaaaacttcg	aatgttgttt	acgaattttc	taacataaat	780
ataaaaaaca	ttagtcctgc	atcagtgccg	gctattcctt	cgaaagtfff	agaggggaacc	840
agcgtcttgt	cgggtactgc	aatatcttct	ggagatacat	tagaaaaaag	aaaatcgfff	900
gatggcgata	tcctaagagt	ttataaagat	agcaaaatca	ttgctagaac	agtaataaaa	960
ggcaataagt	gggatgttaa	actttcaaag	cctcttattg	caggtgaaaa	attagatttt	1020
gagattttgc	atccgagatc	tcaaaacgtt	agtaaaaaaa	tttcaaaaca	agtcgaagct	1080
aaaccatttg	atccagcttc	ctataaagaa	aaagttatag	ccaaattaaa	gccggtttat	1140
gaagctacta	gtgaaaaaat	cacaaatgat	gcttggttgg	atgaaaatgc	gaaggatttg	1200
caaaaaacaaa	aattagaaga	acaatatatt	tctggaaaag	tagcgatatc	agaggctgga	1260
actaaacaag	aagctataga	tgcagcatat	aataaatatt	caagtcaaac	agatccagac	1320
tctcttccta	gtcagtataa	acaaggtaat	aaagaaaatg	aacaagaaaa	agggcgtaaa	1380
gatttaaatcc	agactcgtga	tctgacgttg	aaagccattc	aagaagacaa	atggctaaca	1440
gagcaggaga	aaacaattca	aaaagaagaa	gcattaaaag	cttttgaaac	tggtatagaa	1500
agtgttaatc	aaacagtatc	attagaacag	ttgaagcaac	ggttaatagt	gtataaagct	1560
tctgaaaaag	attcagagaa	aaaagaatat	cctgagtcaa	ttcctaatac	gcatattcca	1620
gggaaagaaa	aagaagttaa	agctgctaaa	caagaagaac	ttaaaaaatt	acatgacaca	1680
actcttgaaa	aatcaatca	agataaatgg	ttgacgccag	accaacaagc	tgaacagtta	1740
aaacaagcgg	aagttacttt	taaaaaaggc	caagaagcaa	ttaaaagtgc	tcagacttta	1800
actcagcttg	agacagactt	agctgattat	gtttctgaga	atgaaggtaa	gggaaattct	1860
attcccgata	aatacaaatc	tggcaataaa	gatgatttgg	taaataaggc	tgaagttaaa	1920
cttaagggaag	ctcacgaagc	tactaaacaa	gcaattgaaa	aagatccatg	gttgagtccg	1980
gaacagaaaa	aagctcaaaa	agaaaaagcc	aaagcaagac	tagatgaggg	cttgaaagct	2040
cttaaagctg	cagatagttt	agagattcct	aaagtgcag	aagaagcttt	cgttgataaa	2100

gaaaaaaatc	cagattcaat	tccaaatcaa	cataaagctg	gaactgctga	tcaagctaga	2160
aaacaagctt	tagatagttt	agataaggag	gttcaaaaag	agttagagtc	aattgataac	2220
gataatactc	taacaactga	tgagaaaagca	gctgctaaga	aaaaagtcaa	tgacgcttat	2280
gatgtagcta	agcaaacagc	tatggaagcc	aattcttatg	aagatttgac	tactattaaa	2340
gatgagttct	tatctaattt	acctcataaa	caaggaacgc	cgcttaaaga	tcaacaatct	2400
gatgctattg	cagaattaga	gaagaagcag	caagaaattg	aaaaagctat	tgaggggtgat	2460
aaaacattac	caagagacga	aaaagagaaa	caaattgctg	actctaagga	acgcttaaaa	2520
tctgacacgc	aaaaagttaa	agatgctaaa	aatgctgatg	ctattaaaaa	agcatttgaa	2580
gaagggaaaag	tgaatattcc	tcaagcacat	atcccagggtg	atttgaacaa	ggataaagaa	2640
aaacttcttg	cagaattgaa	gcaaaaagca	gatgatactg	aaaaagctat	tgatgttgat	2700
aaaactctga	cagaagatga	gaaaaaagag	caaaaagtca	aaacaaaagc	tgaacttgaa	2760
aaagctaaaa	ctgatgttaa	aaatactcag	acacgtgaag	aactagataa	aaaagttcca	2820
gaacttaaga	aagctattga	agacactcac	gttaaaggta	atcttgaagg	tgtaagaat	2880
aaggctattg	aagatcttaa	aaaagctcat	actgaaacag	ttgctaaaaa	aaatgggtgat	2940
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<210> SEQ ID NO 62

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<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 62

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Leu Gly Val Ala Val Pro Thr Gly Phe Ser Gln Ser Asn Gly Val Met
35           40           45
Val Val Lys Ala Ala Glu Val Pro Ala Thr Asp Leu Ser Arg Gln Ala
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Ser Asp Ser Glu Arg Val Asp Glu Ser Ser Leu Leu Gln Lys Glu Asn
65           70           75           80
Leu Ser Val Asp Ser Phe Lys Leu Glu Asn Leu Asn Gly Trp Glu Ala
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Glu Asn Asp Thr Ala Gly Asn Leu Gly Lys Phe Lys Asp Pro Asp Ser
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Ser Gly Tyr Gln Asn Ile Leu Thr Ser Ser Gly Lys Asn Ile Ser Val
115          120          125
Ala Val Ala Pro Lys Gly Ser Gly Lys Met Asn Ile Lys Val Thr Lys
130          135          140
Arg Ser Asn Phe Gln Gly Gly Tyr Tyr Val Gly Gly Leu Arg Thr Gln
145          150          155          160
Thr Pro Val Leu Lys Leu Asn Asp Val Tyr Arg Tyr Ser Phe Thr Thr
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Lys Lys Leu Ser Gly Asn Ser Ser Glu Phe Lys Thr Arg Val Lys Pro
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Val Glu Ser Asn Asn Lys Leu Gly Lys Glu Leu Val Ile Arg Val Asp
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Asn Lys Asn Val Ser Thr Lys His Asp Trp Leu Pro Asp Ile Ser Asp
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Gly Thr His Thr Val Asp Phe Thr Gly Leu Asp Lys Lys Leu Ser Val
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Ser Asn Ile Asn Ile Lys Asn Ile Ser Pro Ala Ser Val Pro Ala Ile
260          265          270
Pro Ser Lys Val Leu Glu Gly Thr Ser Val Leu Ser Gly Thr Ala Ile
275          280          285
Ser Ser Gly Asp Thr Leu Glu Lys Arg Lys Ser Phe Asp Gly Asp Ile
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Leu Arg Val Tyr Lys Asp Ser Lys Ile Ile Ala Arg Thr Val Ile Lys
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Gln	Lys	Gln	Lys	Leu	Glu	Glu	Gln	Tyr	Ile	Ser	Gly	Lys	Val	Ala	Ile	
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Ser	Glu	Ala	Gly	Thr	Lys	Gln	Glu	Ala	Ile	Asp	Ala	Ala	Tyr	Asn	Lys	
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Thr	Arg	Asp	Leu	Thr	Leu	Lys	Ala	Ile	Gln	Glu	Asp	Lys	Trp	Leu	Thr	
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Glu	Gln	Glu	Lys	Thr	Ile	Gln	Lys	Glu	Glu	Ala	Leu	Lys	Ala	Phe	Glu	
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Thr	Gly	Ile	Glu	Ser	Val	Asn	Gln	Thr	Val	Ser	Leu	Glu	Gln	Leu	Lys	
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Gln	Arg	Leu	Ile	Val	Tyr	Lys	Ala	Ser	Glu	Lys	Asp	Ser	Glu	Lys	Lys	
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Glu	Tyr	Pro	Glu	Ser	Ile	Pro	Asn	Gln	His	Ile	Pro	Gly	Lys	Glu	Lys	
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Glu	Val	Lys	Ala	Ala	Lys	Gln	Glu	Glu	Leu	Lys	Lys	Leu	His	Asp	Thr	
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Thr	Leu	Glu	Lys	Ile	Asn	Gln	Asp	Lys	Trp	Leu	Thr	Pro	Asp	Gln	Gln	
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Ala	Glu	Gln	Leu	Lys	Gln	Ala	Glu	Val	Thr	Phe	Lys	Lys	Gly	Gln	Glu	
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Tyr	Lys	Ser	Gly	Asn	Lys	Asp	Asp	Leu	Val	Asn	Lys	Ala	Glu	Val	Lys	
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Leu	Lys	Glu	Ala	His	Glu	Ala	Thr	Lys	Gln	Ala	Ile	Glu	Lys	Asp	Pro	
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Trp	Leu	Ser	Pro	Glu	Gln	Lys	Lys	Ala	Gln	Lys	Glu	Lys	Ala	Lys	Ala	
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Ile	Leu	Lys	Val	Thr	Glu	Glu	Ala	Phe	Val	Asp	Lys	Glu	Lys	Asn	Pro	
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Asp	Ser	Ile	Pro	Asn	Gln	His	Lys	Ala	Gly	Thr	Ala	Asp	Gln	Ala	Arg	
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Glu	Ala	Asn	Ser	Tyr	Glu	Asp	Leu	Thr	Thr	Ile	Lys	Asp	Glu	Phe	Leu	

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Ser Asn Leu Pro His Lys	Gln Gly Thr Pro Leu Lys Asp	Gln Gln Ser		
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Asp Ala Ile Ala Glu Leu	Glu Lys Lys Gln Gln Glu Ile Glu Lys Ala			
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Ile Glu Gly Asp Lys Thr	Leu Pro Arg Asp Glu Lys Glu Lys Gln Ile			
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Asn Ile Pro Gln Ala His	Ile Pro Gly Asp Leu Asn Lys Asp Lys Glu			
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Lys Leu Leu Ala Glu Leu	Lys Gln Lys Ala Asp Asp Thr Glu Lys Ala			
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Ile Asp Val Asp Lys Thr	Leu Thr Glu Asp Glu Lys Lys Glu Gln Lys			
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Val Lys Thr Lys Ala Glu	Leu Glu Lys Ala Lys Thr Asp Val Lys Asn			
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Thr Gln Thr Arg Glu Glu	Leu Asp Lys Lys Val Pro Glu Leu Lys Lys			
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Ala Ile Glu Asp Thr His	Val Lys Gly Asn Leu Glu Gly Val Lys Asn			
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Lys Ala Ile Glu Asp Leu	Lys Lys Ala His Thr Glu Thr Val Ala Lys			
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Lys Glu Ala Asp Lys Ala	Leu Ala Ala Gly Lys Asp Ala Ile Thr Lys			
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Ala Asp Asp Ala Asp Lys	Val Ser Thr Ala Val Thr Glu His Thr			
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Pro Lys Ile Lys Ala Ala	His Lys Thr Gly Asp Leu Lys Lys Ala			
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Gln Val Asp Ala Asn Thr	Ala Leu Asp Lys Ala Ala Glu Lys Glu			
1040	1045	1050		
Arg Gly Glu Ile Asn Lys	Asp Ala Thr Leu Thr Thr Glu Asp Lys			
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Ala Lys Gln Leu Lys Glu	Val Glu Thr Ala Leu Thr Lys Ala Lys			
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Asp Asn Val Lys Ala Ala	Lys Thr Ala Asp Ala Ile Asn Asp Ala			
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Arg Asp Lys Gly Val Ala	Thr Ile Asp Ala Val His Lys Ala Gly			
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Gln Asp Leu Gly Ala Arg	Lys Ser Gly Gln Val Ala Lys Leu Glu			
1115	1120	1125		
Glu Ala Ala Lys Ala Thr	Lys Asp Lys Ile Ser Ala Asp Pro Thr			
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Leu Thr Ser Lys Glu Lys	Glu Glu Gln Ser Lys Ala Val Asp Ala			
1145	1150	1155		
Glu Leu Lys Lys Ala Ile	Glu Ala Val Asn Ala Ala Asp Thr Ala			
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1175	1180	1185		
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Lys Ala Arg Lys Glu Ala	Ala Lys Ala Asp Leu	Glu Lys Glu Ala
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Glu Asn Leu Gly Thr Val	Ala Ile Arg Ser Ala	Tyr Val Ala Gly
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Lys Gln Ala Ala Ile Glu	Ala Leu Lys Gln Ala	Ala Ala Glu Thr
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Leu Ala Lys Ile Thr Thr	Asp Ala Lys Leu Thr	Glu Ala Gln Lys
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Ala Thr Val Arg Ser Ala	Gln Ser Ile Ala Ser	Val Lys Glu Ala
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Lys Asp Lys Gly Ile Thr	Ala Ile Arg Ala Ala	Tyr Val Pro Asn
2000	2005	2010
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gaaccatcag caaaacgtat tgctactttg tcaaaatacg ttaaaaaata tggcatcaaa      780
tacatttatt ttgaggaaaa tgcgtcaagt aaagtcgcaa aaaccctagc taaagaagca      840
ggagttaaag cggtgtgtct tagtccgctt gaaggtttga ctgaaaaaga gatgaaagct      900
ggccaagatt actttacggt catgcgtaaa aaccttgaaa ccttacgctt aaccactgat      960
gtggctggta aagaaattct tccagaaaaa gacacgacta agacagttta caatggttat     1020
ttcaaagaca aagaagtcaa agatcgtaaa ttatctgact ggtcaggtag ctggcaatct     1080
gtttacccct atctacaaga tggtaactta gaccaagttt gggactacaa ggctaaaaaa     1140
tctaaaggta aaatgacagc agccgagtac aaagattact acactactgg ttataaaaact     1200
gacgtggaac aaatcaaaat caatggtaag aaaaagacca tgacctttgt tcgtaatggg     1260
gaaaagaaaa ccttcactta cacatacgcc ggcaaagaaa tcttgacctt tccaaaagga     1320
aatcgcgggg ttcgtttcat gtttgaagct aaagaagcag atgctggcga attcaaatac     1380
gttcaattca gtgaccatgc cattgctcct gaaaaagcaa agcatttcca cctgtactgg     1440
ggtggtgaca gccaagaaaa attacataaa gagttagaac attggccaac ttactacggt     1500
tcagacttat ctggtcgtga aatcgcccaa gaaatcaatg ctcattaa      1548
  
```

<210> SEQ ID NO 64
 <211> LENGTH: 515
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 64

```

Met Lys Lys Lys Ile Leu Leu Met Met Ser Leu Ile Ser Val Phe Phe
 1             5             10            15
Ala Trp Gln Leu Thr Gln Ala Lys Gln Val Leu Ala Glu Gly Lys Val
      20             25            30
Lys Val Val Thr Thr Phe Tyr Pro Val Tyr Glu Phe Thr Lys Gly Val
      35             40            45
Ile Gly Asn Asp Gly Asp Val Phe Met Leu Met Lys Ala Gly Thr Asp
      50             55            60
Pro His Asp Phe Glu Pro Ser Thr Lys Ala Ile Lys Lys Ile Gln Asp
      65             70            75            80
Ala Asp Ala Phe Val Tyr Met Asp Asp Asn Met Glu Thr Trp Val Ser
      85             90            95
Asp Val Lys Lys Ser Leu Thr Ser Lys Lys Val Thr Ile Val Lys Gly
      100            105            110
Thr Gly Asn Met Leu Leu Val Ala Gly Ala Gly His Asp His Pro His
      115            120            125
Glu Asp Ala Asp Lys Lys His Glu His Asn Lys His Ser Glu Glu Gly
      130            135            140
His Asn His Ala Phe Asp Pro His Val Trp Leu Ser Pro Tyr Arg Ser
      145            150            155            160
  
```


Ile	Thr	Val	Val	Glu	Asn	Ile	Arg	Asp	Ser	Leu	Ser	Lys	Ala	Tyr	Pro		
				165					170					175			
Glu	Lys	Ala	Glu	Asn	Phe	Lys	Ala	Asn	Ala	Ala	Thr	Tyr	Ile	Glu	Lys		
			180					185					190				
Leu	Lys	Glu	Leu	Asp	Lys	Asp	Tyr	Thr	Ala	Ala	Leu	Ser	Asp	Ala	Lys		
		195				200						205					
Gln	Lys	Ser	Phe	Val	Thr	Gln	His	Ala	Ala	Phe	Gly	Tyr	Met	Ala	Leu		
	210				215						220						
Asp	Tyr	Gly	Leu	Asn	Gln	Ile	Ser	Ile	Asn	Gly	Val	Thr	Pro	Asp	Ala		
225				230					235					240			
Glu	Pro	Ser	Ala	Lys	Arg	Ile	Ala	Thr	Leu	Ser	Lys	Tyr	Val	Lys	Lys		
			245						250					255			
Tyr	Gly	Ile	Lys	Tyr	Ile	Tyr	Phe	Glu	Glu	Asn	Ala	Ser	Ser	Lys	Val		
		260						265					270				
Ala	Lys	Thr	Leu	Ala	Lys	Glu	Ala	Gly	Val	Lys	Ala	Ala	Val	Leu	Ser		
	275					280						285					
Pro	Leu	Glu	Gly	Leu	Thr	Glu	Lys	Glu	Met	Lys	Ala	Gly	Gln	Asp	Tyr		
	290				295					300							
Phe	Thr	Val	Met	Arg	Lys	Asn	Leu	Glu	Thr	Leu	Arg	Leu	Thr	Thr	Asp		
305				310						315					320		
Val	Ala	Gly	Lys	Glu	Ile	Leu	Pro	Glu	Lys	Asp	Thr	Thr	Lys	Thr	Val		
			325					330						335			
Tyr	Asn	Gly	Tyr	Phe	Lys	Asp	Lys	Glu	Val	Lys	Asp	Arg	Gln	Leu	Ser		
		340						345					350				
Asp	Trp	Ser	Gly	Ser	Trp	Gln	Ser	Val	Tyr	Pro	Tyr	Leu	Gln	Asp	Gly		
	355					360						365					
Thr	Leu	Asp	Gln	Val	Trp	Asp	Tyr	Lys	Ala	Lys	Lys	Ser	Lys	Gly	Lys		
	370				375						380						
Met	Thr	Ala	Ala	Glu	Tyr	Lys	Asp	Tyr	Tyr	Thr	Thr	Gly	Tyr	Lys	Thr		
385				390						395				400			
Asp	Val	Glu	Gln	Ile	Lys	Ile	Asn	Gly	Lys	Lys	Lys	Thr	Met	Thr	Phe		
			405					410						415			
Val	Arg	Asn	Gly	Glu	Lys	Lys	Thr	Phe	Thr	Tyr	Thr	Tyr	Ala	Gly	Lys		
		420						425					430				
Glu	Ile	Leu	Thr	Tyr	Pro	Lys	Gly	Asn	Arg	Gly	Val	Arg	Phe	Met	Phe		
	435						440					445					
Glu	Ala	Lys	Glu	Ala	Asp	Ala	Gly	Glu	Phe	Lys	Tyr	Val	Gln	Phe	Ser		
	450				455						460						
Asp	His	Ala	Ile	Ala	Pro	Glu	Lys	Ala	Lys	His	Phe	His	Leu	Tyr	Trp		
465				470						475				480			
Gly	Gly	Asp	Ser	Gln	Glu	Lys	Leu	His	Lys	Glu	Leu	Glu	His	Trp	Pro		
			485					490						495			
Thr	Tyr	Tyr	Gly	Ser	Asp	Leu	Ser	Gly	Arg	Glu	Ile	Ala	Gln	Glu	Ile		
			500					505					510				
Asn	Ala	His															
		515															

<210> SEQ ID NO 65

<211> LENGTH: 1248

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 65

atggcctacc	gtctatctat	aaaatatatt	ttattggagg	cttttcctaa	aatggcaaaa	60
gaaaaatacg	atcgtagtaa	acccacggtt	aacattggta	caatcggaca	cgttgaccat	120
ggtaaaaacta	ctttaacagc	tgcaatcaca	actgtattgg	cacgtcgctt	gccttcacat	180
gttaaccaac	caaaaagatta	cgcttctatc	gatgctgctc	cagaagaacg	cgaacgcgga	240
atcactatca	acactgcaca	cgttgagtac	gaaactgcaa	ctcgtcacta	tgcgcacatc	300

gacgctccag	gacacgcgga	ctacgttaaa	aacatgatca	ctggtgccgc	tcaaattggac	360
ggagctatcc	ttgtagttgc	ttcaactgat	ggaccaatgc	cacaaactcg	tgagcacatc	420
cttctttcac	gtcaggttgg	tgtaaacaac	cttatcgtgt	tcatgaacaa	agttgacctt	480
ggtgatgacg	aagagttgct	tgaattagtt	gagatggaaa	ttcgtgacct	tctttcagaa	540
tacgatttcc	caggtgatga	ccttccagtt	atccaaggtt	cagctcttaa	agctcttgaa	600
ggcgacacta	aatttgaaga	catcatcatg	gaattgatgg	atactgttga	ttcatacatt	660
ccagaaccag	aacgcgacac	tgacaaacca	ttgcttcttc	cagtcgaaga	cgtattctca	720
attacaggtc	gtggtacagt	tgcttcagga	cgtatcgacc	gtggtactgt	tcgtgtcaac	780
gacgaaatcg	aaatcgttgg	tatcaaagaa	gaaactaaaa	aagctgttgt	tactggtgtt	840
gaaatgttcc	gtaaacaact	tgacgaaggt	cttgcaggag	acaacgtagg	tatccttctt	900
cgtggtgttc	aacgtgacga	aatcgaacgt	ggtcaagtta	ttgctaaacc	aagttcaatc	960
aacccacaca	ctaaattcaa	aggtgaagta	tatatccttt	ctaaagacga	aggtggacgt	1020
cacactccat	tcttcaacaa	ctaccgtcca	caattctact	tccgtacaac	tgacgtaaca	1080
ggttcaatcg	aacttccagc	aggtacagaa	atgggttatgc	ctggtgataa	cgtgacaatc	1140
aacggttgagt	tgatccaccc	aatcgccgta	gaacaaggta	ctactttctc	aatccgtgaa	1200
ggtggacgta	ctggttggttc	aggtatcgtt	tcagaaatcg	aagcttaa		1248

<210> SEQ ID NO 66

<211> LENGTH: 415

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 66

Met	Ala	Tyr	Arg	Leu	Ser	Ile	Lys	Tyr	Ile	Leu	Leu	Glu	Ala	Phe	Pro
1			5						10					15	
Lys	Met	Ala	Lys	Glu	Lys	Tyr	Asp	Arg	Ser	Lys	Pro	His	Val	Asn	Ile
			20					25					30		
Gly	Thr	Ile	Gly	His	Val	Asp	His	Gly	Lys	Thr	Thr	Leu	Thr	Ala	Ala
		35					40					45			
Ile	Thr	Thr	Val	Leu	Ala	Arg	Arg	Leu	Pro	Ser	Ser	Val	Asn	Gln	Pro
	50					55					60				
Lys	Asp	Tyr	Ala	Ser	Ile	Asp	Ala	Ala	Pro	Glu	Glu	Arg	Glu	Arg	Gly
65				70						75				80	
Ile	Thr	Ile	Asn	Thr	Ala	His	Val	Glu	Tyr	Glu	Thr	Ala	Thr	Arg	His
			85					90					95		
Tyr	Ala	His	Ile	Asp	Ala	Pro	Gly	His	Ala	Asp	Tyr	Val	Lys	Asn	Met
			100					105					110		
Ile	Thr	Gly	Ala	Ala	Gln	Met	Asp	Gly	Ala	Ile	Leu	Val	Val	Ala	Ser
	115						120					125			
Thr	Asp	Gly	Pro	Met	Pro	Gln	Thr	Arg	Glu	His	Ile	Leu	Leu	Ser	Arg
	130					135					140				
Gln	Val	Gly	Val	Lys	His	Leu	Ile	Val	Phe	Met	Asn	Lys	Val	Asp	Leu
145				150					155					160	
Val	Asp	Asp	Glu	Glu	Leu	Leu	Glu	Leu	Val	Glu	Met	Glu	Ile	Arg	Asp
			165					170					175		
Leu	Leu	Ser	Glu	Tyr	Asp	Phe	Pro	Gly	Asp	Asp	Leu	Pro	Val	Ile	Gln
		180						185					190		
Gly	Ser	Ala	Leu	Lys	Ala	Leu	Glu	Gly	Asp	Thr	Lys	Phe	Glu	Asp	Ile
	195						200					205			
Ile	Met	Glu	Leu	Met	Asp	Thr	Val	Asp	Ser	Tyr	Ile	Pro	Glu	Pro	Glu
	210					215					220				
Arg	Asp	Thr	Asp	Lys	Pro	Leu	Leu	Leu	Pro	Val	Glu	Asp	Val	Phe	Ser
225				230						235				240	
Ile	Thr	Gly	Arg	Gly	Thr	Val	Ala	Ser	Gly	Arg	Ile	Asp	Arg	Gly	Thr
			245					250					255		
Val	Arg	Val	Asn	Asp	Glu	Ile	Glu	Ile	Val	Gly	Ile	Lys	Glu	Glu	Thr
		260					265					270			
Lys	Lys	Ala	Val	Val	Thr	Gly	Val	Glu	Met	Phe	Arg	Lys	Gln	Leu	Asp

<400> SEQUENCE: 69

```
atgaaaatta cagttgtagg cattggatac gttggattat cgatagggct cctacttgca      60
aaggaacacg acgtcacctt ttttgatatt gataataaaa aaattgattt aataaataaa      120
aggcaatccc ctcttaaaga agcagctata aacaaacttt tatgtaaggc aaaaaatatt      180
aatgcaactt cttctgaaga attagcatat aaggatgcga ctttcataat cttgtctttg      240
ccaaccaacc taaaatttaa taagcttgat acttccatta tcgaaatttc tgtaagtaat      300
attttaaaga taaacaaaaa ggctacaatt gtaataaagt cgacagttcc aattggtttt      360
acagaatatt taaggaatcg atttcactac aacgatatca ttttttcacc tgagttcctt      420
agggaaggat caactattca tgatcaattg tacccttcga gaactatagt tggaaatgaa      480
tctagaaatt ctcaattatt cttagacata ctaacagata tatcggttga aaaagactcg      540
ccatctttat tagttggctc ttctgaagca gaagcgataa agttattttc gaatgcatac      600
ttggcacaaa aaattgcttt ttttaatgag ttggatacgt ttgctgaaat gcaaaatttg      660
gactcaaaaa aaattattga ggctatggga tatgaccaga gaataggaaa ttcgcacaat      720
aatccttctt tcggttttgg tgggtactgt cttcctaagg atattaagca attagagtat      780
catttttaaag aaattccagc accaattatt accagtataa gtgaatctaa tttattaaga      840
aaaattcata tagcaaaaaa gattttgaac agctcagcta aaacaatagg aatttataga      900
attaattcca aaaaagattc ggataattgt agggaatctt ctacaattga tgttgctaaa      960
cttctaaaaa gcagtggtaa ggatgtttatc atctttgagc ccttaattaa caaaaaaaag    1020
tttttggggg gccctttaag taatgatttt aatgaattta ttaaattatt ggatattata    1080
gttgccaata gaatagatga tgctctgaga aaatgtaatt caaaagtttt tacacgtgat    1140
atttttcagt atgattaa                                     1158
```

<210> SEQ ID NO 70

<211> LENGTH: 385

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 70

```
Met Lys Ile Thr Val Val Gly Ile Gly Tyr Val Gly Leu Ser Ile Gly
1          5          10          15
Leu Leu Leu Ala Lys Glu His Asp Val Thr Phe Phe Asp Ile Asp Asn
20          25          30
Lys Lys Ile Asp Leu Ile Asn Lys Arg Gln Ser Pro Leu Lys Glu Ala
35          40          45
Ala Ile Asn Lys Leu Leu Cys Lys Ala Lys Asn Ile Asn Ala Thr Ser
50          55          60
Ser Glu Glu Leu Ala Tyr Lys Asp Ala Thr Phe Ile Ile Leu Ser Leu
65          70          75          80
Pro Thr Asn Leu Lys Phe Asn Lys Leu Asp Thr Ser Ile Ile Glu Ile
85          90          95
Ser Val Ser Asn Ile Leu Lys Ile Asn Lys Lys Ala Thr Ile Val Ile
100         105         110
Lys Ser Thr Val Pro Ile Gly Phe Thr Glu Tyr Leu Arg Asn Arg Phe
115         120         125
His Tyr Asn Asp Ile Ile Phe Ser Pro Glu Phe Leu Arg Glu Gly Ser
130         135         140
Thr Ile His Asp Gln Leu Tyr Pro Ser Arg Thr Ile Val Gly Asn Glu
145         150         155         160
Ser Arg Asn Ser Gln Leu Phe Leu Asp Ile Leu Thr Asp Ile Ser Val
165         170         175
Glu Lys Asp Ser Pro Ser Leu Leu Val Gly Ser Ser Glu Ala Glu Ala
180         185         190
Ile Lys Leu Phe Ser Asn Ala Tyr Leu Ala Gln Lys Ile Ala Phe Phe
195         200         205
Asn Glu Leu Asp Thr Phe Ala Glu Met Gln Asn Leu Asp Ser Lys Lys
210         215         220
Ile Ile Glu Ala Met Gly Tyr Asp Gln Arg Ile Gly Asn Ser His Asn
225         230         235         240
```

Asn	Pro	Ser	Phe	Gly	Phe	Gly	Gly	Tyr	Cys	Leu	Pro	Lys	Asp	Ile	Lys	
				245					250					255		
Gln	Leu	Glu	Tyr	His	Phe	Lys	Glu	Ile	Pro	Ala	Pro	Ile	Ile	Thr	Ser	
			260					265					270			
Ile	Ser	Glu	Ser	Asn	Leu	Leu	Arg	Lys	Ile	His	Ile	Ala	Lys	Met	Ile	
		275					280					285				
Leu	Asn	Ser	Ser	Ala	Lys	Thr	Ile	Gly	Ile	Tyr	Arg	Ile	Asn	Ser	Lys	
	290					295					300					
Lys	Asp	Ser	Asp	Asn	Cys	Arg	Glu	Ser	Ser	Thr	Ile	Asp	Val	Ala	Lys	
305					310					315					320	
Leu	Leu	Lys	Ser	Ser	Gly	Lys	Asp	Val	Ile	Ile	Phe	Glu	Pro	Leu	Ile	
				325				330						335		
Asn	Gln	Lys	Lys	Phe	Leu	Gly	Cys	Pro	Leu	Ser	Asn	Asp	Phe	Asn	Glu	
			340					345					350			
Phe	Ile	Lys	Tyr	Ser	Asp	Ile	Ile	Val	Ala	Asn	Arg	Ile	Asp	Asp	Ala	
	355					360						365				
Leu	Arg	Lys	Cys	Asn	Ser	Lys	Val	Phe	Thr	Arg	Asp	Ile	Phe	Gln	Tyr	
	370					375					380					
Asp																
385																

<210> SEQ ID NO 71

<211> LENGTH: 1170

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 71

atgattatta	ctaaaaagag	cttattttgtg	acaagtgtcg	ctttgtcggt	agtacctttg	60
gcgacagcgc	aggcacaaga	gtggacacca	cgatcgggta	cagaaatcaa	gtctgaactc	120
gtcctagttg	ataatgtttt	tacttatact	gtaaaatacg	gtgacacttt	aagcacaatt	180
gctgaagcaa	tggggattga	tgtgcatgtc	ttaggagata	ttaatcatat	tgctaattatt	240
gacctaattt	ttccagacac	gatcctaaca	gcaaactaca	atcaacacgg	tcaggcaacg	300
aatttgacgg	ttcaagcacc	tgcttctagt	ccagctagcg	ttagtcatgt	acctagcagt	360
gagccattac	cccaagcatc	tgccacctct	caaccgactg	ttcctatggc	accacctgcg	420
acaccatctg	atgtccaac	gacaccattc	gcattctgcaa	agccagatag	ttctgtgaca	480
gcgtcatctg	agctcacatc	gtcaacgaat	gatgtttcga	ctgagttgtc	tagcgaatca	540
caaaagcagc	cagaagtacc	acaagaagca	gttccaactc	ctaaagcagc	tgaacgact	600
gaagtcgaac	ctaagacaga	catctcagaa	gccccaaactt	cagctaatag	gcctgtacct	660
aacgagagtg	cttcagaaga	agtttcttct	gcggccccag	cacaagcccc	agcagaaaaa	720
gaagaaacct	ctgcgccagc	agcacaaaaa	gctgtagctg	acaccacaag	tggtgcaacc	780
tcaaatggcc	tttcttacgc	tccaaaccat	gcctacaatc	caatgaatgc	agggcttcaa	840
ccacaaacag	cagccttcaa	agaagaagtg	gcttctgcct	ttggtattac	gtcatttagt	900
ggttaccgtc	caggtgatcc	aggagatcat	ggtaaagggt	tggccattga	ttttatgggtg	960
cctgaaaatt	ctgctcttgg	tgatcaagtt	gctcaatatg	ccattgacca	tatggcagag	1020
cgtgggtatt	catacgttat	ttggaaacag	cgattctatg	cgccatttgc	aagtattttac	1080
ggaccagcct	acacatggaa	cccatgcca	gatcgcgga	gtattacaga	aaaccattat	1140
gatcatgttc	atgtctcctt	taatgcttaa				1170

<210> SEQ ID NO 72

<211> LENGTH: 389

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 72

Met	Ile	Ile	Thr	Lys	Lys	Ser	Leu	Phe	Val	Thr	Ser	Val	Ala	Leu	Ser	
1				5					10					15		
Leu	Val	Pro	Leu	Ala	Thr	Ala	Gln	Ala	Gln	Glu	Trp	Thr	Pro	Arg	Ser	
			20				25					30				
Val	Thr	Glu	Ile	Lys	Ser	Glu	Leu	Val	Leu	Val	Asp	Asn	Val	Phe	Thr	

atggctatcg	taggtcgtct	tggacgtgtc	cttggacctc	gtaacttgat	gccaaaccct	420
aaaactggta	cagtaacgat	ggatgttgct	aaagccgttg	aagagtctaa	aggtggtaaa	480
atcacttacc	gtgctgacaa	agcaggtaat	gttcaagctc	ttattggtaa	agtttcattt	540
gatgctgaca	aattggttga	aaacttcaaa	gccttccacg	atgtaatggc	taaagctaaa	600
cctgcaacag	ctaaaggaac	ttacatggca	aacgtctcaa	tcacatcaac	acaaggtgtt	660
ggatatcaagg	ttgatcctaa	ctcacttttaa				690

<210> SEQ ID NO 74

<211> LENGTH: 228

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 74

Met	Ala	Lys	Lys	Ser	Lys	Gln	Met	Arg	Ala	Ala	Leu	Glu	Lys	Val	Asp
1				5					10					15	
Ser	Thr	Lys	Ala	Tyr	Ser	Val	Glu	Glu	Ala	Val	Ala	Leu	Val	Lys	Glu
			20					25					30		
Thr	Asn	Phe	Ala	Lys	Phe	Asp	Ala	Ser	Val	Glu	Val	Ala	Tyr	Asn	Leu
		35					40					45			
Asn	Ile	Asp	Val	Arg	Lys	Ala	Asp	Gln	Gln	Ile	Arg	Gly	Ala	Met	Val
	50					55					60				
Leu	Pro	Asn	Gly	Thr	Gly	Lys	Thr	Gln	Arg	Val	Leu	Val	Phe	Ala	Arg
65					70					75				80	
Gly	Ala	Lys	Ala	Glu	Glu	Ala	Lys	Ala	Ala	Gly	Ala	Asp	Phe	Val	Gly
				85					90					95	
Glu	Asp	Asp	Leu	Val	Ala	Lys	Ile	Asn	Gly	Gly	Trp	Leu	Asp	Phe	Asp
			100					105					110		
Val	Val	Ile	Ala	Thr	Pro	Asp	Met	Met	Ala	Ile	Val	Gly	Arg	Leu	Gly
		115					120					125			
Arg	Val	Leu	Gly	Pro	Arg	Asn	Leu	Met	Pro	Asn	Pro	Lys	Thr	Gly	Thr
	130					135					140				
Val	Thr	Met	Asp	Val	Ala	Lys	Ala	Val	Glu	Glu	Ser	Lys	Gly	Gly	Lys
145					150					155					160
Ile	Thr	Tyr	Arg	Ala	Asp	Lys	Ala	Gly	Asn	Val	Gln	Ala	Leu	Ile	Gly
			165					170						175	
Lys	Val	Ser	Phe	Asp	Ala	Asp	Lys	Leu	Val	Glu	Asn	Phe	Lys	Ala	Phe
			180					185					190		
His	Asp	Val	Met	Ala	Lys	Ala	Lys	Pro	Ala	Thr	Ala	Lys	Gly	Thr	Tyr
		195					200					205			
Met	Ala	Asn	Val	Ser	Ile	Thr	Ser	Thr	Gln	Gly	Val	Gly	Ile	Lys	Val
	210					215					220				
Asp	Pro	Asn	Ser												
225															

<210> SEQ ID NO 75

<211> LENGTH: 498

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 75

atgcaatatt	gcatatctgt	gggaggtaaa	aatctcaatt	accgccaaaa	ccacaacagg	60
aggattttta	aaatggctaa	aaaagtcgaa	aaacttgtaa	aacttcaa	ccctgctggt	120
aaagctacac	cagctccacc	agttggacca	gctcttggtc	aagcagggtat	caacatcatg	180
ggcttcacta	aagaatttaa	cgctcgtaca	gctgatcaag	ctggtatgat	catcccagtt	240
ggtatctcag	tttatgaaga	caaatcattt	gatttcatca	ctaaaacacc	accagctgct	300
gttcttttga	aaaaagctgc	aggtgttgaa	aaaggatcag	gtacacctaa	cactactaag	360
gattgcgacag	ttactcgtgc	acaagtacaa	gaaattgctg	aaactaagat	gccagatttg	420
aacgctgcaa	acattgaagc	tgcaatgcgt	atgatcgaag	gtactgctcg	ttctatggga	480
ttcactgtta	ctgactag					498

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<210> SEQ ID NO 76
<211> LENGTH: 165
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 76
Met Gln Tyr Cys Ile Ser Val Gly Gly Lys Asn Leu Asn Tyr Arg Gln
1           5           10           15
Asn His Asn Arg Arg Ile Phe Lys Met Ala Lys Lys Val Glu Lys Leu
20           25           30
Val Lys Leu Gln Ile Pro Ala Gly Lys Ala Thr Pro Ala Pro Pro Val
35           40           45
Gly Pro Ala Leu Gly Gln Ala Gly Ile Asn Ile Met Gly Phe Thr Lys
50           55           60
Glu Phe Asn Ala Arg Thr Ala Asp Gln Ala Gly Met Ile Ile Pro Val
65           70           75           80
Val Ile Ser Val Tyr Glu Asp Lys Ser Phe Asp Phe Ile Thr Lys Thr
85           90           95
Pro Pro Ala Ala Val Leu Leu Lys Lys Ala Ala Gly Val Glu Lys Gly
100          105          110
Ser Gly Thr Pro Asn Thr Thr Lys Val Ala Thr Val Thr Arg Ala Gln
115          120          125
Val Gln Glu Ile Ala Glu Thr Lys Met Pro Asp Leu Asn Ala Ala Asn
130          135          140
Ile Glu Ala Ala Met Arg Met Ile Glu Gly Thr Ala Arg Ser Met Gly
145          150          155          160
Phe Thr Val Thr Asp
165

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<210> SEQ ID NO 77
<211> LENGTH: 807
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 77
atgaaaaaat tattatctct cagtttagta gccattagtt tacttaattt gagtgcttgt      60
gaatctgttg accgcgctat aaaaggcgat aaatacattg atgaaaaaac tgccaaagaa      120
gaaagcgaag cagcttctaa agcctatgaa gaaagcattc aaaaagctct caaagctgat      180
gctagccaat ttccacaact aaccaaagaa gtcggcgaag aagaagctaa ggtagctaatg      240
aggacaagtc aaggggacat tacccttaag ttattcccaa aatatgctcc ctagctgtt      300
gagaacttcc tcacccatgc taaaaaaggc tactatgata accttacctt ccategtgtg      360
atcaacgact ttatgattca atcaggtgac cccaaaggag atggcacagg tggatgaatcg      420
atttgaaaag gcaaggatcc taaaaaagat gctggcaatg gctttgtcaa cgaaatctct      480
ccatttttat atcatattcg cggtgctctt gccatggcaa atgctggtgc taatactaac      540
ggtagccaat tttatatcaa ccaaaacaag aaaaatcaaa gcaagggatt atcaagtacc      600
aactacccaa aacctatcat ctctgcctat gagcatggcg gcaatccaag ctagatggc      660
ggttatactg tatttggtca agtcattgat ggtatggatg ttgtcgataa aattgccgct      720
acttctatca accaaaatga taaaccagaa caagacatta cgattacctc aattgacatt      780
gtcaaaagatt atcgctttaa aaactaa
807

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<210> SEQ ID NO 78
<211> LENGTH: 268
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 78
Met Lys Lys Leu Leu Ser Leu Ser Leu Val Ala Ile Ser Leu Leu Asn
1           5           10           15
Leu Ser Ala Cys Glu Ser Val Asp Arg Ala Ile Lys Gly Asp Lys Tyr

```


ttggtcgggt	ctccctcaac	aggtcgaaca	ccaacatcag	tggcagctat	aaacagtaag	1260
tgggtgattc	aacgtctaat	gacggtcaaa	gaattagaaa	accgtgccga	tttaaaccat	1320
ggtaaagcca	tctattcaga	gtctgtcgac	tttaaagaca	taaaagatag	cctaggttat	1380
gataaatcgc	atcaatttgc	ttatgtcaaa	gagtcaactg	atgcgggtta	taacgcacaa	1440
gacgttaaag	gtaaaattgc	tttaattgaa	cgtgatccca	ataaaaccta	tgacgaaatg	1500
attgctttgg	ctaagaaaaca	tggagctctg	ggagtactta	tttttaataa	caagcctggg	1560
caatcaaacc	gctcaatgcy	tctaacagct	aatgggatgg	ggataccatc	tgctttcata	1620
tcgcacgaat	ttggtaaggc	catgtcccaa	ttaaatggca	atggtacagg	aagtttagag	1680
tttgacagtg	tgggtctcaa	agcaccgagt	caaaaaggca	atgaaatgaa	tcatttttca	1740
aattggggcc	taacttctga	tggctattta	aaacctgaca	ttactgcacc	aggtggcgat	1800
atctattcta	cctataacga	taaccactat	ggtagccaaa	caggaacaag	tatggcctct	1860
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ttgccaaaag	aaaaaattgc	tgatatcggt	aagaacctat	tgatgagcaa	tgctcaaatt	1980
catgttaatc	cagagacaaa	aacgaccacc	tcaccgcgtc	agcaaggggc	aggattactt	2040
aatattgacg	gagctgtcac	tagcggcctt	tatgtgacag	gaaaagacaa	ctatggcagt	2100
atatcattag	gcaacatcac	agatacagtg	acgtttgatg	tgactgttca	caacctaaag	2160
aataaagaca	aaacattacg	ttatgacaca	gaattgctaa	cagatcatgt	agaccacaaa	2220
aagggccgct	tcactttgac	ttctcactcc	ttaaaaacgt	accaaggagg	agaagttaca	2280
gtcccagcca	atggaaaagt	gactgtgaag	gttaccatgg	atgtctcaca	gttcacaaaa	2340
gagctaacaa	aacagatgcc	aaatgggttac	tatctagaag	gttttgctcg	ctttagagat	2400
agtcaagatg	accaactaaa	tagagtaaac	attccttttg	ttggttttta	agggcaattt	2460
gaaaacttag	cagttgcaga	agagtccatt	tacagattaa	aatctcaagg	caaaactggg	2520
ttttactttg	atgaatcagg	tccaaaagac	gatatctatg	tcggtaaaca	ctttacagga	2580
cttgctactc	ttggttcaga	gaccaatgtg	tcaacccaaa	cgatttctga	caatgggtcta	2640
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aaggaacaca	aaaatccact	gtgggtcagc	ccagaaagct	ttaaaggaga	taaaaacttt	2880
aatagtgcga	ttagatttgc	aaaatcaacg	accctgttag	gcacagcatt	ttctggaaaa	2940
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gatgtgggtc	gtgccaaaac	tcaagaaatg	acatttgaca	tgattttaga	ccgacaaaaa	3060
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ggagatcact	taccacaaaac	attaggtaaa	acaccaatta	aacttaagct	tacagacggg	3420
aattatcaga	ccaaagaaaac	gcttaaaagt	aatcttgaaa	tgacacagtc	tgacacaggg	3480
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gccttttaaag	gcttgaaaaa	taacgtgtat	aatgacttaa	cggttaacgt	atacgctaaa	3660
gatgaccacc	aaaaacaaaac	ccctatctgg	tctagtcaag	caggcgctag	tgtatccgct	3720
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gttgaccact	ttactcctga	caagacaaaa	gcccttgact	catcaggcat	tgtccgcgaa	3960
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cttgtgcggg	atgcagatgg	taaaccgatt	gaaaacctag	agtattataa	taactcaggt	4320
aacagtctta	tcttgccata	cggcaaatat	acggtcgaat	tgttgaccta	tgacaccaat	4380
gcagccaaac	tagagtcaga	taaaatcggt	tcctttacct	tgtagctga	taacaacttc	4440
caacaagtta	cctttaagat	aacgatgtta	gcaacttctc	aaataactgc	ccactttgat	4500
catcttttgc	cagaaggcag	tcgctgttag	cttaaaacag	ctcaagatca	gctaattccc	4560
cttgaacagt	ccttgtatgt	gcctaaaagc	tatggcaaaa	ccgttcaaga	aggcacttac	4620

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gaagttgttg tcagcctgcc taaaggctac cgtatcgaag gcaacacaaa ggtgaatacc 4680
ctaccaaagt aagtgcacga actatcatta cgccttgtca aagtaggaga tgcctcagat 4740
tcaactgggtg atcataaggt tatgtcaaaa aataattcac aggctttgac agcctctgcc 4800
acaccaacca agtcaacgac ctcagcaaca gcaaaagccc taccatcaac gggtgaaaaa 4860
atgggtctca agttgcgcat agtaggtctt gtgttactcg gacttacttg cgtctttagc 4920
cgaaaaaaat caaccaaaga ttga 4944

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<210> SEQ ID NO 80

<211> LENGTH: 1647

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 80

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Met Glu Lys Lys Gln Arg Phe Ser Leu Arg Lys Tyr Lys Ser Gly Thr
1      5      10      15
Phe Ser Val Leu Ile Gly Ser Val Phe Leu Val Met Thr Thr Thr Val
20     25     30
Ala Ala Asp Glu Leu Ser Thr Met Ser Glu Pro Thr Ile Thr Asn His
35     40     45
Ala Gln Gln Gln Ala Gln His Leu Thr Asn Thr Glu Leu Ser Ser Ala
50     55     60
Glu Ser Lys Ser Gln Asp Thr Ser Gln Ile Thr Leu Lys Thr Asn Arg
65     70     75     80
Glu Lys Glu Gln Ser Gln Asp Leu Val Ser Glu Pro Thr Thr Thr Glu
85     90     95
Leu Ala Asp Thr Asp Ala Ala Ser Met Ala Asn Thr Gly Ser Asp Ala
100    105    110
Thr Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val His Asp
115    120    125
Trp Val Lys Thr Lys Gly Ala Trp Asp Lys Gly Tyr Lys Gly Gln Gly
130    135    140
Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His Gln Ser
145    150    155    160
Met Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys Glu Asp
165    170    175
Met Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser Trp Ile
180    185    190
Asn Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser Asp Asn
195    200    205
Ile Lys Glu Asn Gln Phe Glu Asp Phe Asp Glu Asp Trp Glu Asn Phe
210    215    220
Glu Phe Asp Ala Glu Ala Glu Pro Lys Ala Ile Lys Lys His Lys Ile
225    230    235    240
Tyr Arg Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys Thr
245    250    255
Glu Glu Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp Asp
260    265    270
Asp Thr Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val Ala
275    280    285
Gly Asn Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu Gly Ile
290    295    300
Ala Pro Glu Ala Gln Val Met Phe Met Arg Val Phe Ala Asn Asp Ile
305    310    315    320
Met Gly Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp Ala Val
325    330    335
Ala Leu Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala Asn Gly
340    345    350
Ala Gln Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu Lys Ala

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		355					360				365					
Lys	Lys	Ala	Gly	Val	Ser	Val	Val	Val	Ala	Ala	Gly	Asn	Glu	Arg	Val	
	370					375					380					
Tyr	Gly	Ser	Asp	His	Asp	Asp	Pro	Leu	Ala	Thr	Asn	Pro	Asp	Tyr	Gly	
385					390					395					400	
Leu	Val	Gly	Ser	Pro	Ser	Thr	Gly	Arg	Thr	Pro	Thr	Ser	Val	Ala	Ala	
				405					410					415		
Ile	Asn	Ser	Lys	Trp	Val	Ile	Gln	Arg	Leu	Met	Thr	Val	Lys	Glu	Leu	
			420					425					430			
Glu	Asn	Arg	Ala	Asp	Leu	Asn	His	Gly	Lys	Ala	Ile	Tyr	Ser	Glu	Ser	
		435				440						445				
Val	Asp	Phe	Lys	Asp	Ile	Lys	Asp	Ser	Leu	Gly	Tyr	Asp	Lys	Ser	His	
	450					455					460					
Gln	Phe	Ala	Tyr	Val	Lys	Glu	Ser	Thr	Asp	Ala	Gly	Tyr	Asn	Ala	Gln	
465					470					475					480	
Asp	Val	Lys	Gly	Lys	Ile	Ala	Leu	Ile	Glu	Arg	Asp	Pro	Asn	Lys	Thr	
				485					490					495		
Tyr	Asp	Glu	Met	Ile	Ala	Leu	Ala	Lys	Lys	His	Gly	Ala	Leu	Gly	Val	
			500					505					510			
Leu	Ile	Phe	Asn	Asn	Lys	Pro	Gly	Gln	Ser	Asn	Arg	Ser	Met	Arg	Leu	
		515					520					525				
Thr	Ala	Asn	Gly	Met	Gly	Ile	Pro	Ser	Ala	Phe	Ile	Ser	His	Glu	Phe	
	530					535					540					
Gly	Lys	Ala	Met	Ser	Gln	Leu	Asn	Gly	Asn	Gly	Thr	Gly	Ser	Leu	Glu	
545					550					555					560	
Phe	Asp	Ser	Val	Val	Ser	Lys	Ala	Pro	Ser	Gln	Lys	Gly	Asn	Glu	Met	
				565					570					575		
Asn	His	Phe	Ser	Asn	Trp	Gly	Leu	Thr	Ser	Asp	Gly	Tyr	Leu	Lys	Pro	
			580					585					590			
Asp	Ile	Thr	Ala	Pro	Gly	Gly	Asp	Ile	Tyr	Ser	Thr	Tyr	Asn	Asp	Asn	
		595					600					605				
His	Tyr	Gly	Ser	Gln	Thr	Gly	Thr	Ser	Met	Ala	Ser	Pro	Gln	Ile	Ala	
	610					615					620					
Gly	Ala	Ser	Leu	Leu	Val	Lys	Gln	Tyr	Leu	Glu	Lys	Thr	Gln	Pro	Asn	
625					630					635					640	
Leu	Pro	Lys	Glu	Lys	Ile	Ala	Asp	Ile	Val	Lys	Asn	Leu	Leu	Met	Ser	
				645					650					655		
Asn	Ala	Gln	Ile	His	Val	Asn	Pro	Glu	Thr	Lys	Thr	Thr	Thr	Ser	Pro	
			660					665					670			
Arg	Gln	Gln	Gly	Ala	Gly	Leu	Leu	Asn	Ile	Asp	Gly	Ala	Val	Thr	Ser	
		675					680					685				
Gly	Leu	Tyr	Val	Thr	Gly	Lys	Asp	Asn	Tyr	Gly	Ser	Ile	Ser	Leu	Gly	
	690					695				700						
Asn	Ile	Thr	Asp	Thr	Met	Thr	Phe	Asp	Val	Thr	Val	His	Asn	Leu	Ser	
705					710					715					720	
Asn	Lys	Asp	Lys	Thr	Leu	Arg	Tyr	Asp	Thr	Glu	Leu	Leu	Thr	Asp	His	
				725					730					735		
Val	Asp	Pro	Gln	Lys	Gly	Arg	Phe	Thr	Leu	Thr	Ser	His	Ser	Leu	Lys	
		740						745					750			
Thr	Tyr	Gln	Gly	Gly	Glu	Val	Thr	Val	Pro	Ala	Asn	Gly	Lys	Val	Thr	
		755					760					765				
Val	Arg	Val	Thr	Met	Asp	Val	Ser	Gln	Phe	Thr	Lys	Glu	Leu	Thr	Lys	
	770					775					780					
Gln	Met	Pro	Asn	Gly	Tyr	Tyr	Leu	Glu	Gly	Phe	Val	Arg	Phe	Arg	Asp	
785					790					795					800	
Ser	Gln	Asp	Asp	Gln	Leu	Asn	Arg	Val	Asn	Ile	Pro	Phe	Val	Gly	Phe	
				805					810					815		

Lys Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr Arg
 820 825 830
 Leu Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly Pro
 835 840 845
 Lys Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr Leu
 850 855 860
 Gly Ser Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly Leu
 865 870 875 880
 His Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu Glu
 885 890 895
 Lys Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly Asp
 900 905 910
 Asn Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys Tyr
 915 920 925
 Gln Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His Lys
 930 935 940
 Asn Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn Phe
 945 950 955 960
 Asn Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr Ala
 965 970 975
 Phe Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly His Tyr
 980 985 990
 His Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg Gln
 995 1000 1005
 Glu Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu
 1010 1015 1020
 Ser Gln Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu
 1025 1030 1035
 Pro Leu Lys Asp Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val
 1040 1045 1050
 Phe Tyr Leu Glu Arg Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile
 1055 1060 1065
 Asn Asp Ser Tyr Lys Tyr Val Ser Val Glu Asp Asn Lys Thr Phe
 1070 1075 1080
 Val Glu Arg Gln Ala Asp Gly Ser Phe Ile Leu Pro Leu Asp Lys
 1085 1090 1095
 Ala Lys Leu Gly Asp Phe Tyr Tyr Met Val Glu Asp Phe Ala Gly
 1100 1105 1110
 Asn Val Ala Ile Ala Lys Leu Gly Asp His Leu Pro Gln Thr Leu
 1115 1120 1125
 Gly Lys Thr Pro Ile Lys Leu Lys Leu Thr Asp Gly Asn Tyr Gln
 1130 1135 1140
 Thr Lys Glu Thr Leu Lys Asp Asn Leu Glu Met Thr Gln Ser Asp
 1145 1150 1155
 Thr Gly Leu Val Thr Asn Gln Ala Gln Leu Ala Val Val His Arg
 1160 1165 1170
 Asn Gln Pro Gln Ser Gln Leu Thr Lys Met Asn Gln Asp Phe Phe
 1175 1180 1185
 Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp Phe Val Ala Phe Lys
 1190 1195 1200
 Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr Val Asn Val Tyr
 1205 1210 1215
 Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser Ser Gln
 1220 1225 1230
 Ala Gly Ala Ser Val Ser Ala Ile Glu Ser Thr Ala Trp Tyr Gly
 1235 1240 1245
 Ile Thr Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr

1250	Val Val Thr Tyr Arg Asp	1255	Glu His Gly Lys Glu	1260	His Gln Lys Gln
1265	Tyr Thr Ile Ser Val Asn	1270	Asp Lys Lys Pro Met	1275	Ile Thr Gln Gly
1280	Arg Phe Asp Thr Ile Asn	1285	Gly Val Asp His Phe	1290	Thr Pro Asp Lys
1295	Thr Lys Ala Leu Asp Ser	1300	Ser Gly Ile Val Arg	1305	Glu Glu Val Phe
1310	Tyr Leu Ala Lys Lys Asn	1315	Gly Arg Lys Phe Asp	1320	Val Thr Glu Gly
1325	Lys Asp Gly Ile Thr Val	1330	Ser Asp Asn Lys Val	1335	Tyr Ile Pro Lys
1340	Asn Pro Asp Gly Ser Tyr	1345	Thr Ile Ser Lys Arg	1350	Asp Gly Val Thr
1355	Leu Ser Asp Tyr Tyr Tyr	1360	Leu Val Glu Asp Arg	1365	Ala Gly Asn Val
1370	Ser Phe Ala Thr Leu Arg	1375	Asp Leu Lys Ala Val	1380	Gly Lys Asp Lys
1385	Ala Val Val Asn Phe Gly	1390	Leu Asp Leu Pro Val	1395	Pro Glu Asp Lys
1400	Gln Ile Val Asn Phe Thr	1405	Tyr Leu Val Arg Asp	1410	Ala Asp Gly Lys
1415	Pro Ile Glu Asn Leu Glu	1420	Tyr Tyr Asn Asn Ser	1425	Gly Asn Ser Leu
1430	Ile Leu Pro Tyr Gly Lys	1435	Tyr Thr Val Glu Leu	1440	Leu Thr Tyr Asp
1445	Thr Asn Ala Ala Lys Leu	1450	Glu Ser Asp Lys Ile	1455	Val Ser Phe Thr
1460	Leu Ser Ala Asp Asn Asn	1465	Phe Gln Gln Val Thr	1470	Phe Lys Ile Thr
1475	Met Leu Ala Thr Ser Gln	1480	Ile Thr Ala His Phe	1485	Asp His Leu Leu
1490	Pro Glu Gly Ser Arg Val	1495	Ser Leu Lys Thr Ala	1500	Gln Asp Gln Leu
1505	Ile Pro Leu Glu Gln Ser	1510	Leu Tyr Val Pro Lys	1515	Ala Tyr Gly Lys
1520	Thr Val Gln Glu Gly Thr	1525	Tyr Glu Val Val Val	1530	Ser Leu Pro Lys
1535	Gly Tyr Arg Ile Glu Gly	1540	Asn Thr Lys Val Asn	1545	Thr Leu Pro Asn
1550	Glu Val His Glu Leu Ser	1555	Leu Arg Leu Val Lys	1560	Val Gly Asp Ala
1565	Ser Asp Ser Thr Gly Asp	1570	His Lys Val Met Ser	1575	Lys Asn Asn Ser
1580	Gln Ala Leu Thr Ala Ser	1585	Ala Thr Pro Thr Lys	1590	Ser Thr Thr Ser
1595	Ala Thr Ala Lys Ala Leu	1600	Pro Ser Thr Gly Glu	1605	Lys Met Gly Leu
1610	Lys Leu Arg Ile Val Gly	1615	Leu Val Leu Leu Gly	1620	Leu Thr Cys Val
1625	Phe Ser Arg Lys Lys Ser	1630	Lys Lys Asp	1635	
1640		1645			

<210> SEQ ID NO 81

<211> LENGTH: 846

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 81

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gaatctgatac aagcgagatg ggataaagtt gaagaattat tgaaaaaaga caatatcact    180
ttgaagtaca aagaatttac agattactcg caacctaata aggcagttgc taatggtgaa    240
gtcgatatta atgccttcca aactataat ttcttaaata actggaataa ggaaaaataag    300
gaacatttggg tggccattgc tgatacctat atcagcccaa ttaacctttt ctctggaacc    360
agtcaagatg gaaaggctaa atacaaatca gtagctgatac tgccaaatgg tactcaaatt    420
gcagtaccaa atgatgagac caatgaaagc cgtgccctct atgtgctgca atcagctggc    480
ctcattaaat tgaatgtgtc tggatgacaa ttagcaacca ttgccaatat ctacagagaac    540
aaaaagaaat tagatatcaa ggaattagat gctagccaaa cggcacgtgc tttagtagtct    600
gctgatgcag ctgttgtaaa taatagttac gctgttctcg caaaaattga ctacaaaacc    660
tctcttttca aagaaaaagc agatgacaat tcaaaacagt ggattaacat tattgcaggt    720
caaaaagatt gggaaaaaatc agagaaggct gatgctatta aaaaactcat caaggcctac    780
caaatgatg aggtgaagaa agtcgtggaa aaaacttcaa atggtataga tgtatccgta    840
tggttaa                                           846
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<210> SEQ ID NO 82

<211> LENGTH: 281

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 82

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Met Ser Phe Lys Lys Trp Ile Gly Ile Val Gly Ile Ala Leu Ala Ser
1          5          10          15
Thr Val Leu Val Ala Cys Ser Glu Lys Gln Asp Asp Lys Asn Thr Leu
20          25          30
Thr Ile Gly Val Met Thr Lys Thr Glu Ser Asp Gln Ala Arg Trp Asp
35          40          45
Lys Val Glu Glu Leu Leu Lys Lys Asp Asn Ile Thr Leu Lys Tyr Lys
50          55          60
Glu Phe Thr Asp Tyr Ser Gln Pro Asn Lys Ala Val Ala Asn Gly Glu
65          70          75          80
Val Asp Ile Asn Ala Phe Gln His Tyr Asn Phe Leu Asn Asn Trp Asn
85          90          95
Lys Glu Asn Lys Glu His Leu Val Ala Ile Ala Asp Thr Tyr Ile Ser
100         105         110
Pro Ile Asn Leu Phe Ser Gly Thr Ser Gln Asp Gly Lys Ala Lys Tyr
115         120         125
Lys Ser Val Ala Asp Leu Pro Asn Gly Thr Gln Ile Ala Val Pro Asn
130         135         140
Asp Ala Thr Asn Glu Ser Arg Ala Leu Tyr Val Leu Gln Ser Ala Gly
145         150         155         160
Leu Ile Lys Leu Asn Val Ser Gly Asp Gln Leu Ala Thr Ile Ala Asn
165         170         175
Ile Ser Glu Asn Lys Lys Lys Leu Asp Ile Lys Glu Leu Asp Ala Ser
180         185         190
Gln Thr Ala Arg Ala Leu Val Ser Ala Asp Ala Ala Val Val Asn Asn
195         200         205
Ser Tyr Ala Val Pro Ala Lys Ile Asp Tyr Lys Thr Ser Leu Phe Lys
210         215         220
Glu Lys Ala Asp Asp Asn Ser Lys Gln Trp Ile Asn Ile Ile Ala Gly
225         230         235         240
Gln Lys Asp Trp Glu Lys Ser Glu Lys Ala Asp Ala Ile Lys Lys Leu
245         250         255
Ile Lys Ala Tyr Gln Thr Asp Glu Val Lys Lys Val Val Glu Lys Thr
260         265         270
```

Ser Asn Gly Ile Asp Val Ser Val Trp
275 280

<210> SEQ ID NO 83
<211> LENGTH: 402
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 83
ttgcagctat ttaaaggaat actaatggat aatgatatga ggaataaaat gaaaaaagaa 60
gaactcttaa aaattgttgt ggaagcaact gaggaaaagc gtgctaaaga tatttttagcc 120
ttggatttag aggggttaac tagtttgacc gattattttg tgattgcgag tgcaacaaac 180
agtcgtcaat tagaggctat tgcggataat attcgtgaaa aggtaaaaga ggctggtgga 240
gatgctagcc atggtgaagg taatagccaa gcaggctggg tcttgcttga tttgaccgat 300
gtggtggtac atcttttttt agaagacgag cgttaccact ataatcttga aaaattgtgg 360
catgaagcgc ctgctgtggc tctagatgcc tatttagctt aa 402

<210> SEQ ID NO 84
<211> LENGTH: 133
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 84
Met Gln Leu Phe Lys Gly Ile Leu Met Asp Asn Asp Met Arg Asn Lys
1 5 10 15
Met Lys Lys Glu Glu Leu Leu Lys Ile Val Val Glu Ala Thr Glu Glu
20 25 30
Lys Arg Ala Lys Asp Ile Leu Ala Leu Asp Leu Glu Gly Leu Thr Ser
35 40 45
Leu Thr Asp Tyr Phe Val Ile Ala Ser Ala Thr Asn Ser Arg Gln Leu
50 55 60
Glu Ala Ile Ala Asp Asn Ile Arg Glu Lys Val Lys Glu Ala Gly Gly
65 70 75 80
Asp Ala Ser His Val Glu Gly Asn Ser Gln Ala Gly Trp Val Leu Leu
85 90 95
Asp Leu Thr Asp Val Val Val His Leu Phe Leu Glu Asp Glu Arg Tyr
100 105 110
His Tyr Asn Leu Glu Lys Leu Trp His Glu Ala Pro Ala Val Ala Leu
115 120 125
Asp Ala Tyr Leu Ala
130

<210> SEQ ID NO 85
<211> LENGTH: 1515
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 85
ttgaggacaa ctatgaaaaa atatatttta aaccgtatca tgcgatcggt agtgtcggta 60
gttctggttaa cggctttaac atacaccatc gtatatactc tagtacctac cagccttatc 120
tttaaacaag accctaatta taataaaatg acaacaacac cagataaaaa agtagcgtat 180
gaaaatctaa cttttcaacg tatgggttat gtcaattatt tttcaagcaa agaattaaaa 240
gataatgctt ctaaagtaga tagtagtgta acgacagaag caactagtgc taacaaagct 300
atctatgaga agtatattga ttctcttggc aatggctggc agctaaaacg cttccccact 360
agcaaacagt tttatgcaat tcgcaatatt cctatttacg aacgtgtttg gaactttttc 420
tcaaacttag ttgttattga tcacccttgg aagattcagg ataaaagataa tccaaaatta 480
gttaggtata ttcgtctaga aaaagataaa tcagttggct ggtcacttgt tgggttcgggg 540
acaaaacata agtatctcct ctatactaac ggaaaatttc cttatcttca ccaaaacttt 600
gttaccttaa acttagggac atcttatcca acatacagca atattcctgt tcttcaggtc 660
atttcacaag ggcaaggacg aacagctctt caagatgtga ccttcccatc aggtgtcact 720

aagaaatcgt	cagtggatat	ctatagccgt	agctacaaaa	atccaaaatc	attggatgat	780
atcaccaagg	taaactatgg	taagggagat	tcctacacta	aaaccatcaa	taattatgtc	840
gacccatcaa	tgattcacaa	ttcttttgta	attgggtttt	ttgggtgttat	gttttcctat	900
atcgttgggt	tgcctcttgg	tttatttatg	gctcgggtta	aaaataccta	ttttgacagt	960
ttctcaacag	cgaccatgac	cttcattgctt	gctttaccaa	gtattgctgt	tatctatgtt	1020
gttcgcttcc	taggtggcat	ggttgggtta	ccagatagtt	tcccaatgct	gggggcatct	1080
gattcctaaat	cttatatttt	accagccctt	attttaggaa	ttttaaatat	tccaactacg	1140
gttatctggg	tccgtcgcta	tcttggtgac	cttcaggcca	gcgattgggt	acgttttgcg	1200
cgttcaaaaag	gattatcaga	atctgaaatt	tacagagggc	atctcttcaa	aaatgccatg	1260
gtcccaattg	tgtcaggggt	tcctgcaagt	attatccttg	ctattgggtg	tgcaacatta	1320
acagagactg	tctttgcctt	cccgggtatg	ggtaaaatgt	taattgattc	tattaaatct	1380
gctaacaatt	ctatgattgt	tggattaacc	tttatcttca	ctgtcttgct	aattgtttca	1440
cttttactag	gagatattgt	catgaccctt	gtcgatccac	gtattaaatt	gtcaacaaaa	1500
aaaggaggta	agtaa					1515

<210> SEQ ID NO 86

<211> LENGTH: 504

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 86

Met	Arg	Thr	Thr	Met	Lys	Lys	Tyr	Ile	Leu	Asn	Arg	Ile	Met	Arg	Ser
1				5					10				15		
Leu	Val	Ser	Val	Val	Leu	Val	Thr	Ala	Leu	Thr	Tyr	Thr	Ile	Val	Tyr
			20					25					30		
Thr	Leu	Val	Pro	Thr	Ser	Leu	Ile	Phe	Lys	Gln	Asp	Pro	Asn	Tyr	Asn
			35				40					45			
Lys	Met	Thr	Thr	Thr	Pro	Asp	Lys	Lys	Val	Ala	Tyr	Glu	Asn	Leu	Thr
	50					55					60				
Phe	Gln	Arg	Met	Gly	Tyr	Val	Asn	Tyr	Phe	Ser	Ser	Lys	Glu	Leu	Lys
65					70					75				80	
Asp	Asn	Ala	Ser	Lys	Val	Asp	Ser	Ser	Val	Thr	Thr	Glu	Ala	Thr	Ser
				85					90					95	
Ala	Asn	Lys	Ala	Ile	Tyr	Glu	Lys	Tyr	Ile	Asp	Ser	Leu	Gly	Asn	Gly
			100						105				110		
Trp	Gln	Leu	Lys	Arg	Phe	Pro	Thr	Ser	Lys	Gln	Phe	Tyr	Ala	Ile	Arg
	115						120					125			
Asn	Ile	Pro	Ile	Tyr	Glu	Arg	Val	Trp	Asn	Phe	Phe	Ser	Asn	Leu	Val
	130					135					140				
Val	Ile	Asp	His	Pro	Trp	Lys	Ile	Gln	Asp	Lys	Asp	Asn	Pro	Lys	Leu
145					150					155				160	
Ala	Arg	Tyr	Ile	Arg	Leu	Glu	Lys	Asp	Lys	Ser	Val	Gly	Trp	Ser	Leu
				165					170					175	
Val	Gly	Ser	Gly	Thr	Lys	His	Lys	Tyr	Leu	Leu	Tyr	Thr	Asn	Gly	Lys
			180					185					190		
Phe	Pro	Tyr	Leu	His	Gln	Asn	Phe	Val	Thr	Leu	Asn	Leu	Gly	Thr	Ser
	195						200					205			
Tyr	Pro	Thr	Tyr	Ser	Asn	Ile	Pro	Val	Leu	Gln	Val	Ile	Ser	Gln	Gly
	210					215					220				
Gln	Gly	Arg	Thr	Ala	Leu	Gln	Asp	Val	Thr	Phe	Pro	Ser	Gly	Val	Thr
225					230					235				240	
Lys	Lys	Ser	Ser	Val	Asp	Ile	Tyr	Ser	Arg	Ser	Tyr	Lys	Asn	Pro	Lys
				245					250					255	
Ser	Leu	Asp	Asp	Ile	Thr	Lys	Val	Asn	Tyr	Gly	Lys	Gly	Asp	Ser	Tyr
			260					265					270		
Thr	Lys	Thr	Ile	Asn	Asn	Tyr	Val	Asp	Pro	Ser	Met	Ile	His	Asn	Ser
	275						280					285			
Phe	Val	Ile	Gly	Phe	Phe	Gly	Val	Met	Phe	Ser	Tyr	Ile	Val	Gly	Leu

290	295	300
Pro Leu Gly Leu Phe Met	Ala Arg Phe Lys Asn	Thr Tyr Phe Asp Ser
305	310	315
Phe Ser Thr Ala Thr Met	Thr Phe Met Leu Ala	Leu Pro Ser Ile Ala
	325	330
Val Ile Tyr Val Val Arg	Phe Leu Gly Gly Met	Val Gly Leu Pro Asp
	340	345
Ser Phe Pro Met Leu Gly	Ala Ser Asp Pro Lys	Ser Tyr Ile Leu Pro
	355	360
Ala Leu Ile Leu Gly Ile	Leu Asn Ile Pro Thr	Thr Val Ile Trp Phe
	370	375
Arg Arg Tyr Leu Val Asp	Leu Gln Ala Ser Asp	Trp Val Arg Phe Ala
385	390	395
Arg Ser Lys Gly Leu Ser	Glu Ser Glu Ile Tyr	Arg Gly His Leu Phe
	405	410
Lys Asn Ala Met Val Pro	Ile Val Ser Gly Val	Pro Ala Ser Ile Ile
	420	425
Leu Ala Ile Gly Gly Ala	Thr Leu Thr Glu Thr	Val Phe Ala Phe Pro
	435	440
Gly Met Gly Lys Met Leu	Ile Asp Ser Ile Lys	Ser Ala Asn Asn Ser
	450	455
Met Ile Val Gly Leu Thr	Phe Ile Phe Thr Val	Leu Ser Ile Val Ser
465	470	475
Leu Leu Leu Gly Asp Ile	Val Met Thr Leu Val	Asp Pro Arg Ile Lys
	485	490
Leu Ser Thr Lys Lys Gly	Gly Gly Lys	
	500	

<210> SEQ ID NO 87

<211> LENGTH: 1980

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 87

gtgacttttta	tgaagaaaag	taaatggttg	gcagctgtaa	gtgttgcat	cttgctcagta	60
tccgcttttgg	cagcttggtg	taataaaaaat	gcttcagggtg	gctcagaagc	tacaaaaaac	120
tacaagtacg	tttttggttaa	cgatccaaaa	tcattggatt	atattttgac	taatggcggg	180
ggaacgactg	atgtgataac	acaaatgggtt	gatggctctt	tggaaaacga	tgagtatggg	240
aatttagtac	catcacttgc	taaagatttg	aaggtttcaa	aagacgggtc	gacttatact	300
tatactcttc	gcatggtgt	ctcttggtat	acggctgatg	gtgaagaata	tgccccagta	360
acagcagaag	atthttgtgac	tggtttgaag	cacgcgggtg	acgataaatc	agatgctctt	420
tacgttggtg	aagattcaat	aaaaaactta	aaggcttacc	aaaatgggtg	agtagatttt	480
aaagaagttg	gtgtcaaagc	ccttgacgat	aaaactgttc	agtatacttt	gaacaagcct	540
gaaagctact	ggaattcaaa	aacaacttat	agtgtgcttt	tcccagttaa	tgcgaaattt	600
ttgaagtcaa	aaggtaaaga	ttttggtaca	accgatccat	catcaatcct	tgtaaatggg	660
gcttacttct	tgagcgcctt	cacctcaaaa	tcatctatgg	aattccataa	aaatgaaaac	720
tactgggatg	ctaagaatgt	tgggatagaa	tctgttaaata	tgacttactc	agatggttca	780
gacccagggt	cgttctacaa	gaactttgac	aagggtgagt	tcagcgttgc	acgactttac	840
ccaaatgacc	ctacctacaa	atcagctaag	aaaaactatg	ctgataacat	tacttacgga	900
atgttgactg	gagatatccg	tcatttaaca	tggaaatttg	accgtacttc	tttcaaaaac	960
actaagaaaag	accctgcaca	acaagatgcc	ggtaagaaaag	ctcttaacaa	caaggatttt	1020
cgtcaagcta	ttcagtttgc	ttttgaccga	gcgtcattcc	aagcacaaac	tgacgggtcaa	1080
gatgccaaaa	caaaagcctt	acgtaacatg	cttgctccca	caacatttgt	gaccattgga	1140
gaaagtgtatt	ttgggttcaga	agttgaaaag	gaaatggcaa	aacttggtga	tgaatggaaa	1200
gacgttaact	tagctgatgc	tcaagatggg	ttctataatc	ctgaaaaagc	aaaagctgag	1260
tttgcaaaaag	ccaaagaagc	tttaacagct	gaaggtgtaa	ccttcccagt	tcaattagat	1320
taccctgttg	accaagcaaa	cgcagcaact	gttcaggaag	cccagtcctt	caaacaatct	1380
gttgaagcat	ctcttggtaa	agagaatgtc	attgtcaatg	ttcttgaaac	agaaacatca	1440

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actcacgaag cccaaggctt ctatgctgag accccagaac aacaagacta cgatatcatt 1500
tcatcatggg ggggaccaga ctatcaagat ccacggacct accttgacat catgagtcca 1560
gtaggtgggt gatctgttat ccaaaaaactt ggaatcaaag caggtcaaaa taaggatggt 1620
gtggcagctg caggccttga tacctaccaa actcttcttg atgaagcagc agcaattaca 1680
gacgacaacg atgcgcgcta taaagcttac gcaaaagcac aagcctacct tacagataat 1740
gccgtagata ttccagttgt ggcattgggt ggcactccac gagttactaa agccgttcca 1800
tttagcgggg gcttctcttg ggcagggtct aaaggctcct tagcatataa aggaatgaaa 1860
cttcaagaca aacctgtcac agtaaaaacaa tacgaaaaag caaaagaaaa atggatgaaa 1920
gcaaaggcta agtcaaattgc aaaatatgct gagaagttag ctgatcacgt tgaaaaataa 1980

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<210> SEQ ID NO 88

<211> LENGTH: 659

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 88

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Met Thr Phe Met Lys Lys Ser Lys Trp Leu Ala Ala Val Ser Val Ala
1          5          10          15
Ile Leu Ser Val Ser Ala Leu Ala Ala Cys Gly Asn Lys Asn Ala Ser
20          25          30
Gly Gly Ser Glu Ala Thr Lys Thr Tyr Lys Tyr Val Phe Val Asn Asp
35          40          45
Pro Lys Ser Leu Asp Tyr Ile Leu Thr Asn Gly Gly Gly Thr Thr Asp
50          55          60
Val Ile Thr Gln Met Val Asp Gly Leu Leu Glu Asn Asp Glu Tyr Gly
65          70          75          80
Asn Leu Val Pro Ser Leu Ala Lys Asp Trp Lys Val Ser Lys Asp Gly
85          90          95
Leu Thr Tyr Thr Tyr Thr Leu Arg Asp Gly Val Ser Trp Tyr Thr Ala
100          105          110
Asp Gly Glu Glu Tyr Ala Pro Val Thr Ala Glu Asp Phe Val Thr Gly
115          120          125
Leu Lys His Ala Val Asp Asp Lys Ser Asp Ala Leu Tyr Val Val Glu
130          135          140
Asp Ser Ile Lys Asn Leu Lys Ala Tyr Gln Asn Gly Glu Val Asp Phe
145          150          155          160
Lys Glu Val Gly Val Lys Ala Leu Asp Asp Lys Thr Val Gln Tyr Thr
165          170          175
Leu Asn Lys Pro Glu Ser Tyr Trp Asn Ser Lys Thr Thr Tyr Ser Val
180          185          190
Leu Phe Pro Val Asn Ala Lys Phe Leu Lys Ser Lys Gly Lys Asp Phe
195          200          205
Gly Thr Thr Asp Pro Ser Ser Ile Leu Val Asn Gly Ala Tyr Phe Leu
210          215          220
Ser Ala Phe Thr Ser Lys Ser Ser Met Glu Phe His Lys Asn Glu Asn
225          230          235          240
Tyr Trp Asp Ala Lys Asn Val Gly Ile Glu Ser Val Lys Leu Thr Tyr
245          250          255
Ser Asp Gly Ser Asp Pro Gly Ser Phe Tyr Lys Asn Phe Asp Lys Gly
260          265          270
Glu Phe Ser Val Ala Arg Leu Tyr Pro Asn Asp Pro Thr Tyr Lys Ser
275          280          285
Ala Lys Lys Asn Tyr Ala Asp Asn Ile Thr Tyr Gly Met Leu Thr Gly
290          295          300
Asp Ile Arg His Leu Thr Trp Asn Leu Asn Arg Thr Ser Phe Lys Asn
305          310          315          320
Thr Lys Lys Asp Pro Ala Gln Gln Asp Ala Gly Lys Lys Ala Leu Asn
325          330          335

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gaagtactga aattatctag caaatcctcc actatTTTTg ctggacaaac catttacagt      660
tataattaca tgcttaaagg catgccttgt tatcgagaag gcgtggatgg tctTTTTgtt      720
ggttattcta aaaaagccgg tgcttctttt gtagtacta gtgtcgaaaa tcaaattgagg      780
gttattacag tagttttaaa tgctgatcaa agccacgagg atgatttagc tatattttaaa      840
acaaccaatc aattgttgca gtacctttta attaatTTTc aaaaagtcca gtttaattgaa      900
aataataaac cagtaaaaac gttatatgtc ttagacagtc ctgaaaaaac tgtcaaactt      960
gtagcccaaa atagtttatt ttttatcaaa ccaatacata caaagaccaa aaataccgtc     1020
catattacta agaaatcatc cacaatgatc gcacctctat caaagggaca agtcttaggt     1080
agagcaaccc ttcaagataa acatcttatt ggacaagggt atctggatac tcctccttct     1140
atcaatctta tccttcaaaa aaacatttct aaaagtttct ttttaaagggt ctggtggaac     1200
cgttttgtga ggtatgtcaa tacctcttta tag                                     1233

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<210> SEQ ID NO 90

<211> LENGTH: 410

<212> TYPE: PRT

<213> ORGANISM: *Streptococcus pyogenes*

<400> SEQUENCE: 90

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Met Ile Lys Arg Leu Ile Ser Leu Val Val Ile Ala Leu Phe Phe Ala
1           5           10          15
Ala Ser Thr Val Ser Gly Glu Glu Tyr Ser Val Thr Ala Lys His Ala
20          25          30
Ile Ala Val Asp Leu Glu Ser Gly Lys Val Leu Tyr Glu Lys Asp Ala
35          40          45
Lys Glu Val Val Pro Val Ala Ser Val Ser Lys Leu Leu Thr Thr Tyr
50          55          60
Leu Val Tyr Lys Glu Val Ser Lys Gly Lys Leu Asn Trp Asp Ser Pro
65          70          75          80
Val Thr Ile Ser Asn Tyr Pro Tyr Glu Leu Thr Thr Asn Tyr Thr Ile
85          90          95
Ser Asn Val Pro Leu Asp Lys Arg Lys Tyr Thr Val Lys Glu Leu Leu
100         105         110
Ser Ala Leu Val Val Asn Asn Ala Asn Ser Pro Ala Ile Ala Leu Ala
115         120         125
Glu Lys Ile Gly Gly Thr Glu Pro Lys Phe Val Asp Lys Met Lys Lys
130         135         140
Gln Leu Arg Gln Trp Gly Ile Ser Asp Ala Lys Val Val Asn Ser Thr
145         150         155         160
Gly Leu Thr Asn His Phe Leu Gly Ala Asn Thr Tyr Pro Asn Thr Glu
165         170         175
Pro Asp Asp Glu Asn Cys Phe Cys Ala Thr Asp Leu Ala Ile Ile Ala
180         185         190
Arg His Leu Leu Leu Glu Phe Pro Glu Val Leu Lys Leu Ser Ser Lys
195         200         205
Ser Ser Thr Ile Phe Ala Gly Gln Thr Ile Tyr Ser Tyr Asn Tyr Met
210         215         220
Leu Lys Gly Met Pro Cys Tyr Arg Glu Gly Val Asp Gly Leu Phe Val
225         230         235         240
Gly Tyr Ser Lys Lys Ala Gly Ala Ser Phe Val Ala Thr Ser Val Glu
245         250         255
Asn Gln Met Arg Val Ile Thr Val Val Leu Asn Ala Asp Gln Ser His
260         265         270
Glu Asp Asp Leu Ala Ile Phe Lys Thr Thr Asn Gln Leu Leu Gln Tyr
275         280         285
Leu Leu Ile Asn Phe Gln Lys Val Gln Leu Ile Glu Asn Asn Lys Pro
290         295         300
Val Lys Thr Leu Tyr Val Leu Asp Ser Pro Glu Lys Thr Val Lys Leu
305         310         315         320

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Val	Ala	Gln	Asn	Ser	Leu	Phe	Phe	Ile	Lys	Pro	Ile	His	Thr	Lys	Thr
				325					330					335	
Lys	Asn	Thr	Val	His	Ile	Thr	Lys	Lys	Ser	Ser	Thr	Met	Ile	Ala	Pro
			340					345					350		
Leu	Ser	Lys	Gly	Gln	Val	Leu	Gly	Arg	Ala	Thr	Leu	Gln	Asp	Lys	His
		355					360					365			
Leu	Ile	Gly	Gln	Gly	Tyr	Leu	Asp	Thr	Pro	Pro	Ser	Ile	Asn	Leu	Ile
	370					375					380				
Leu	Gln	Lys	Asn	Ile	Ser	Lys	Ser	Phe	Phe	Leu	Lys	Val	Trp	Trp	Asn
385					390					395					400
Arg	Phe	Val	Arg	Tyr	Val	Asn	Thr	Ser	Leu						
				405					410						

<210> SEQ ID NO 91

<211> LENGTH: 471

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 91

atgagtcgta	aaaatcaagc	gcctaaacgc	gaagtattac	cagatccatt	atataactca	60
aaaatcgtaa	cacgtcttat	caaccgtgtt	atgcttgacg	gtaaacgtgg	tacagctgct	120
actatcgttt	acgatgcttt	caacgctatc	aaagaagcaa	caggaaatga	cgctcttgaa	180
gtatttgaaa	cagctatgga	caacatcatg	cctgtacttg	aagtacgcgc	acgccgtgct	240
ggtggttcta	actaccaagt	cccagttgaa	gttcgtccag	aacgtcgtac	aacacttgga	300
cttcgttggt	tggtaaacgc	atcacgtgct	cgtggtgaac	acactatgaa	agatcgtctt	360
gctaaagaaa	tcatggatgc	tgcaaacaac	acaggtgcat	cagttaagaa	acgtgaagac	420
actcacaana	tggctgaagc	taaccgtgcc	tttgctcact	tccgttggtg	a	471

<210> SEQ ID NO 92

<211> LENGTH: 156

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 92

Met	Ser	Arg	Lys	Asn	Gln	Ala	Pro	Lys	Arg	Glu	Val	Leu	Pro	Asp	Pro
1				5					10					15	
Leu	Tyr	Asn	Ser	Lys	Ile	Val	Thr	Arg	Leu	Ile	Asn	Arg	Val	Met	Leu
			20					25				30			
Asp	Gly	Lys	Arg	Gly	Thr	Ala	Ala	Thr	Ile	Val	Tyr	Asp	Ala	Phe	Asn
		35				40					45				
Ala	Ile	Lys	Glu	Ala	Thr	Gly	Asn	Asp	Ala	Leu	Glu	Val	Phe	Glu	Thr
	50					55				60					
Ala	Met	Asp	Asn	Ile	Met	Pro	Val	Leu	Glu	Val	Arg	Ala	Arg	Arg	Val
65				70					75					80	
Gly	Gly	Ser	Asn	Tyr	Gln	Val	Pro	Val	Glu	Val	Arg	Pro	Glu	Arg	Arg
			85					90					95		
Thr	Thr	Leu	Gly	Leu	Arg	Trp	Leu	Val	Asn	Ala	Ser	Arg	Ala	Arg	Gly
		100					105					110			
Glu	His	Thr	Met	Lys	Asp	Arg	Leu	Ala	Lys	Glu	Ile	Met	Asp	Ala	Ala
	115					120						125			
Asn	Asn	Thr	Gly	Ala	Ser	Val	Lys	Lys	Arg	Glu	Asp	Thr	His	Lys	Met
	130					135					140				
Ala	Glu	Ala	Asn	Arg	Ala	Phe	Ala	His	Phe	Arg	Trp				
145				150					155						

<210> SEQ ID NO 93

<211> LENGTH: 2640

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 93

```
atggaaaaaag gagagagaat ggacttagaa caaacgaagc caaaccaagt taagcagaaa      60
attgcttttaa cctcaacaat tgctttattg agtgccagtg taggcgtatc tcaccaagtc      120
aaagcagatg atagagcctc aggagaaacg aaggcgagta atactcacga cgatagttta      180
ccaaaaccag aaacaattca agaggcaaag gcaactattg atgcagttga aaaaactctc      240
agtcaacaaa aagcagaact gacagagctt gctaccgctc tgacaaaaac tactgctgaa      300
atcaaccact taaaagagca gcaagataat gaacaaaaag cttaaaccctc tgcacaagaa      360
atttacacta atactcttgc aagtagtgag gagacgctat tagcccaagg agccgaacat      420
caaagagagt taacagctac tgaaacagag cttcataatg ctcaagcaga tcaacattca      480
aaagagactg cattgtcaga acaaaaagct agcatttcag cagaaactac tcgagctcaa      540
gatttagtgg aacaagtcaa aacgtctgaa caaaatattg ctaagctcaa tgctatgatt      600
agcaatcctg atgctatcac taaagcagct caaacggcta atgataatac aaaagcatta      660
agctcagaat tggagaaggc taaagctgac ttagaaaatc aaaaagctaa agttaaaaag      720
caattgactg aagagttggc agctcagaaa gctgctctag cagaaaaaga ggcagaactt      780
agtcgtctta aatcctcagc tccgtctact caagatagca ttgtgggtaa taataccatg      840
aaagcaccgc aaggctatcc tcttgaagaa cttaaaaaat tagaagctag tggttatatt      900
ggatcagcta gttacaataa ttattacaaa gagcatgcag atcaaattat tgccaaagct      960
agtccaggta atcaattaaa tcaataccaa gatattccag cagatcgtaa tcgctttgtt     1020
gatcccgata atttgacacc agaagtgcaa aatgagctag cgcagtttgc agctcacatg     1080
attaatagtg taagaagaca attaggtcta ccaccagtta ctgttacagc aggatcacia     1140
gaatttgcaa gattacttag taccagctat aagaaaactc atggtaatac aagaccatca     1200
tttgtctacg gacagccagg ggtatcaggg cattatggtg ttgggcctca tgataaaaact     1260
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agtatcaagt atatgctctt tacagatcat ttacacggaa atacatacgg ccatgctatt     1440
aactttttac gtgtagataa acataaccct aatgcgcctg tttaccttgg attttcaacc     1500
agcaatgtag gatctttgaa tgaacacttt gtaatgttcc cagagtctaa cattgctaac     1560
catcaacgct ttaataagac ccctataaaa gccgttggaa gtacaaaaga ttatgcccaa     1620
agagtaggca ctgtatctga tactattgca gcgatcaaag gaaaagtaag ctcattagaa     1680
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caacttcaag gtaaattagc aagcacactt aagcagtcag acagcttaaa tctccaagtg     1800
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gcaactgcacc agacagaagc cttagcagag caagccgcag ccagagtgcac agcactgggtg     1980
gctaaaaaag ctcatattgca atatctaagg gactttaaat tgaatcctaa ccgccttcaa     2040
gtgatacgtg agcgcattga taatactaag caagatttgg ctaaaactac ctcatctttg     2100
ttaaatgcac aagaagcttt agcagcctta caagctaaac aaagcagtct agaagctact     2160
attgctacca cagaacacca gttgactttg cttaaaacct tagctaacga aaaggaatat     2220
cgccacttag acgaagatat agctactgtg cctgatttgc aagtagctcc acctcttacg     2280
ggcgtaaaac cgctatcata tagtaagata gatactactc cgcttggtca agaaatggtt     2340
aaagaaacga aacaactatt agaagcttca gcaagattag ctgctgaaaa tacaagtctt     2400
gtagcagaag cgcttggtgg ccaaacctct gaaatggtag caagtaatgc cattgtgtct     2460
aaaatcacat cttcgattac tcagccctca tctaagacat cttatggctc aggatcttct     2520
acaacgagca atctcatttc tgatgttgat gaaagtactc aaagagctct taaagcagga     2580
gtcgtcatgt tggcagctgt cggcctcaca ggatttaggt tccgtaagga atctaagtga     2640
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<210> SEQ ID NO 94

<211> LENGTH: 879

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 94

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Val Lys Gln Lys Ile Ala Leu Thr Ser Thr Ile Ala Leu Leu Ser Ala
      20             25             30
Ser Val Gly Val Ser His Gln Val Lys Ala Asp Asp Arg Ala Ser Gly
      35             40             45
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Glu	Thr	Lys	Ala	Ser	Asn	Thr	His	Asp	Asp	Ser	Leu	Pro	Lys	Pro	Glu
50						55					60				
Thr	Ile	Gln	Glu	Ala	Lys	Ala	Thr	Ile	Asp	Ala	Val	Glu	Lys	Thr	Leu
65					70					75					80
Ser	Gln	Gln	Lys	Ala	Glu	Leu	Thr	Glu	Leu	Ala	Thr	Ala	Leu	Thr	Lys
				85					90					95	
Thr	Thr	Ala	Glu	Ile	Asn	His	Leu	Lys	Glu	Gln	Gln	Asp	Asn	Glu	Gln
			100					105					110		
Lys	Ala	Leu	Thr	Ser	Ala	Gln	Glu	Ile	Tyr	Thr	Asn	Thr	Leu	Ala	Ser
		115					120					125			
Ser	Glu	Glu	Thr	Leu	Leu	Ala	Gln	Gly	Ala	Glu	His	Gln	Arg	Glu	Leu
130						135					140				
Thr	Ala	Thr	Glu	Thr	Glu	Leu	His	Asn	Ala	Gln	Ala	Asp	Gln	His	Ser
145					150					155					160
Lys	Glu	Thr	Ala	Leu	Ser	Glu	Gln	Lys	Ala	Ser	Ile	Ser	Ala	Glu	Thr
				165					170					175	
Thr	Arg	Ala	Gln	Asp	Leu	Val	Glu	Gln	Val	Lys	Thr	Ser	Glu	Gln	Asn
			180				185						190		
Ile	Ala	Lys	Leu	Asn	Ala	Met	Ile	Ser	Asn	Pro	Asp	Ala	Ile	Thr	Lys
		195					200					205			
Ala	Ala	Gln	Thr	Ala	Asn	Asp	Asn	Thr	Lys	Ala	Leu	Ser	Ser	Glu	Leu
		210				215					220				
Glu	Lys	Ala	Lys	Ala	Asp	Leu	Glu	Asn	Gln	Lys	Ala	Lys	Val	Lys	Lys
225					230					235					240
Gln	Leu	Thr	Glu	Glu	Leu	Ala	Ala	Gln	Lys	Ala	Ala	Leu	Ala	Glu	Lys
				245					250					255	
Glu	Ala	Glu	Leu	Ser	Arg	Leu	Lys	Ser	Ser	Ala	Pro	Ser	Thr	Gln	Asp
			260					265					270		
Ser	Ile	Val	Gly	Asn	Asn	Thr	Met	Lys	Ala	Pro	Gln	Gly	Tyr	Pro	Leu
		275					280					285			
Glu	Glu	Leu	Lys	Lys	Leu	Glu	Ala	Ser	Gly	Tyr	Ile	Gly	Ser	Ala	Ser
290						295					300				
Tyr	Asn	Asn	Tyr	Tyr	Lys	Glu	His	Ala	Asp	Gln	Ile	Ile	Ala	Lys	Ala
305					310					315					320
Ser	Pro	Gly	Asn	Gln	Leu	Asn	Gln	Tyr	Gln	Asp	Ile	Pro	Ala	Asp	Arg
			325						330					335	
Asn	Arg	Phe	Val	Asp	Pro	Asp	Asn	Leu	Thr	Pro	Glu	Val	Gln	Asn	Glu
			340					345					350		
Leu	Ala	Gln	Phe	Ala	Ala	His	Met	Ile	Asn	Ser	Val	Arg	Arg	Gln	Leu
		355					360					365			
Gly	Leu	Pro	Pro	Val	Thr	Val	Thr	Ala	Gly	Ser	Gln	Glu	Phe	Ala	Arg
		370				375					380				
Leu	Leu	Ser	Thr	Ser	Tyr	Lys	Lys	Thr	His	Gly	Asn	Thr	Arg	Pro	Ser
385					390					395					400
Phe	Val	Tyr	Gly	Gln	Pro	Gly	Val	Ser	Gly	His	Tyr	Gly	Val	Gly	Pro
				405					410					415	
His	Asp	Lys	Thr	Ile	Ile	Glu	Asp	Ser	Ala	Gly	Ala	Ser	Gly	Leu	Ile
			420					425					430		
Arg	Asn	Asp	Asp	Asn	Met	Tyr	Glu	Asn	Ile	Gly	Ala	Phe	Asn	Asp	Val
		435					440					445			
His	Thr	Val	Asn	Gly	Ile	Lys	Arg	Gly	Ile	Tyr	Asp	Ser	Ile	Lys	Tyr
		450				455					460				
Met	Leu	Phe	Thr	Asp	His	Leu	His	Gly	Asn	Thr	Tyr	Gly	His	Ala	Ile
465					470					475					480
Asn	Phe	Leu	Arg	Val	Asp	Lys	His	Asn	Pro	Asn	Ala	Pro	Val	Tyr	Leu
				485					490					495	
Gly	Phe	Ser	Thr	Ser	Asn	Val	Gly	Ser	Leu	Asn	Glu	His	Phe	Val	Met

				500						505					510				
Phe	Pro	Glu	Ser	Asn	Ile	Ala	Asn	His	Gln	Arg	Phe	Asn	Lys	Thr	Pro				
		515						520					525						
Ile	Lys	Ala	Val	Gly	Ser	Thr	Lys	Asp	Tyr	Ala	Gln	Arg	Val	Gly	Thr				
		530						535					540						
Val	Ser	Asp	Thr	Ile	Ala	Ala	Ile	Lys	Gly	Lys	Val	Ser	Ser	Leu	Glu				
545					550					555					560				
Asn	Arg	Leu	Ser	Ala	Ile	His	Gln	Glu	Ala	Asp	Ile	Met	Ala	Ala	Gln				
				565					570					575					
Ala	Lys	Val	Ser	Gln	Leu	Gln	Gly	Lys	Leu	Ala	Ser	Thr	Leu	Lys	Gln				
			580					585					590						
Ser	Asp	Ser	Leu	Asn	Leu	Gln	Val	Arg	Gln	Leu	Asn	Asp	Thr	Lys	Gly				
		595						600					605						
Ser	Leu	Arg	Thr	Glu	Leu	Leu	Ala	Ala	Lys	Ala	Lys	Gln	Ala	Gln	Leu				
	610					615						620							
Glu	Ala	Thr	Arg	Asp	Gln	Ser	Leu	Ala	Lys	Leu	Ala	Ser	Leu	Lys	Ala				
625					630					635					640				
Ala	Leu	His	Gln	Thr	Glu	Ala	Leu	Ala	Glu	Gln	Ala	Ala	Ala	Arg	Val				
			645						650					655					
Thr	Ala	Leu	Val	Ala	Lys	Lys	Ala	His	Leu	Gln	Tyr	Leu	Arg	Asp	Phe				
			660					665					670						
Lys	Leu	Asn	Pro	Asn	Arg	Leu	Gln	Val	Ile	Arg	Glu	Arg	Ile	Asp	Asn				
		675					680					685							
Thr	Lys	Gln	Asp	Leu	Ala	Lys	Thr	Thr	Ser	Ser	Leu	Leu	Asn	Ala	Gln				
	690					695						700							
Glu	Ala	Leu	Ala	Ala	Leu	Gln	Ala	Lys	Gln	Ser	Ser	Leu	Glu	Ala	Thr				
705					710					715					720				
Ile	Ala	Thr	Thr	Glu	His	Gln	Leu	Thr	Leu	Leu	Lys	Thr	Leu	Ala	Asn				
			725						730					735					
Glu	Lys	Glu	Tyr	Arg	His	Leu	Asp	Glu	Asp	Ile	Ala	Thr	Val	Pro	Asp				
			740					745					750						
Leu	Gln	Val	Ala	Pro	Pro	Leu	Thr	Gly	Val	Lys	Pro	Leu	Ser	Tyr	Ser				
		755					760						765						
Lys	Ile	Asp	Thr	Thr	Pro	Leu	Val	Gln	Glu	Met	Val	Lys	Glu	Thr	Lys				
	770					775						780							
Gln	Leu	Leu	Glu	Ala	Ser	Ala	Arg	Leu	Ala	Ala	Glu	Asn	Thr	Ser	Leu				
785					790					795					800				
Val	Ala	Glu	Ala	Leu	Val	Gly	Gln	Thr	Ser	Glu	Met	Val	Ala	Ser	Asn				
			805						810					815					
Ala	Ile	Val	Ser	Lys	Ile	Thr	Ser	Ser	Ile	Thr	Gln	Pro	Ser	Ser	Lys				
			820					825					830						
Thr	Ser	Tyr	Gly	Ser	Gly	Ser	Ser	Thr	Thr	Ser	Asn	Leu	Ile	Ser	Asp				
		835					840						845						
Val	Asp	Glu	Ser	Thr	Gln	Arg	Ala	Leu	Lys	Ala	Gly	Val	Val	Met	Leu				
	850					855					860								
Ala	Ala	Val	Gly	Leu	Thr	Gly	Phe	Arg	Phe	Arg	Lys	Glu	Ser	Lys					
865					870					875									

<210> SEQ ID NO 95

<211> LENGTH: 1320

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 95

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gcttggtggcg	gaaagagcca	gaaagaggct	ggtgcaagta	aatctgatac	tgctaagaca	120
gaaatcacat	gggtgggcttt	cccgtcttc	acgcaagaaa	aagctgaaga	tggtgtggga	180
acctatgaga	agaaattgat	tgctgccttt	gagaaagcta	atccagaaat	caaggtaaaa	240

ttggaacca	ttgattttac	atctggtcct	gagaaaatca	caactgctat	tgaagctgga	300
acagctcctg	atgtcctctt	tgatgctcca	ggtcgtatca	ttcaatatgg	taaaaatggg	360
aaattggctg	acttgaatga	cttgttcaca	gaagagttta	ccaaagatgt	taacaatgac	420
aaattgattc	aagcctcaaa	agcaggagat	acagcttaca	tgtatcctat	cagctctgct	480
ccattctaca	tggcgttgaa	taaaaaaatg	ctcaaagatg	ctggcgtcct	tgatcttggtg	540
aaagaggggtt	ggacaacaga	tgattttgaa	aaagtcttga	aagcattgaa	ggacaaagga	600
tataacccag	gttcttttctt	tgctaattggt	caagggtggtg	accaaggacc	acgtgccttc	660
tttgctaacc	tttatagtag	tcatattacc	gatgacaaag	taaccaaata	caccacagat	720
gatgctaact	ctattaaaagc	catgaccaag	atttccaatt	ggattaaaga	tggtttaagt	780
atgaatggct	ctcagtacga	tggttcagct	gatattcaaa	actttgcgaa	tggccaaact	840
tcctttacca	ttcttttggc	gcctgcacaa	ccaggcatcc	aagctaaatt	gttagaagct	900
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tacctcgtaa	atggttttgc	ggtctttaat	aacaaagatg	aacaaaaagt	cgctgcctct	1020
aagacattta	tccaatttat	cgctgatgat	aaagaatggg	gacctaaaaa	tgttgttcgt	1080
acaggtgctt	tccctgtaag	aacttcttat	ggggatcttt	acaaagacaa	acgaatggaa	1140
aaaattgctg	aatggacaaa	attctactca	ccatactata	acacgattga	tgggtttgct	1200
gaaatgagaa	ctcttttggtt	cccaatgggt	caagccgtct	ctaattggtga	tgaaaagcca	1260
gaagatgctt	tgaaagcctt	cactgaaaaa	gcaaacaaga	caatcaaaaa	aacacaataa	1320

<210> SEQ ID NO 96

<211> LENGTH: 439

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 96

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Leu	Gly	Leu	Ala	Ala	Cys	Gly	Gly	Lys	Ser	Gln	Lys	Glu	Ala	Gly	Ala
		20						25					30		
Ser	Lys	Ser	Asp	Thr	Ala	Lys	Thr	Glu	Ile	Thr	Trp	Trp	Ala	Phe	Pro
		35					40					45			
Val	Phe	Thr	Gln	Glu	Lys	Ala	Glu	Asp	Gly	Val	Gly	Thr	Tyr	Glu	Lys
	50					55					60				
Lys	Leu	Ile	Ala	Ala	Phe	Glu	Lys	Ala	Asn	Pro	Glu	Ile	Lys	Val	Lys
65					70					75					80
Leu	Glu	Thr	Ile	Asp	Phe	Thr	Ser	Gly	Pro	Glu	Lys	Ile	Thr	Thr	Ala
				85					90					95	
Ile	Glu	Ala	Gly	Thr	Ala	Pro	Asp	Val	Leu	Phe	Asp	Ala	Pro	Gly	Arg
			100					105					110		
Ile	Ile	Gln	Tyr	Gly	Lys	Asn	Gly	Lys	Leu	Ala	Asp	Leu	Asn	Asp	Leu
		115					120					125			
Phe	Thr	Glu	Glu	Phe	Thr	Lys	Asp	Val	Asn	Asn	Asp	Lys	Leu	Ile	Gln
	130					135					140				
Ala	Ser	Lys	Ala	Gly	Asp	Thr	Ala	Tyr	Met	Tyr	Pro	Ile	Ser	Ser	Ala
145					150					155					160
Pro	Phe	Tyr	Met	Ala	Leu	Asn	Lys	Lys	Met	Leu	Lys	Asp	Ala	Gly	Val
			165						170					175	
Leu	Asp	Leu	Val	Lys	Glu	Gly	Trp	Thr	Thr	Asp	Asp	Phe	Glu	Lys	Val
			180						185					190	
Leu	Lys	Ala	Leu	Lys	Asp	Lys	Gly	Tyr	Asn	Pro	Gly	Ser	Phe	Phe	Ala
		195					200					205			
Asn	Gly	Gln	Gly	Gly	Asp	Gln	Gly	Pro	Arg	Ala	Phe	Phe	Ala	Asn	Leu
	210					215						220			
Tyr	Ser	Ser	His	Ile	Thr	Asp	Asp	Lys	Val	Thr	Lys	Tyr	Thr	Thr	Asp
225					230					235					240
Asp	Ala	Asn	Ser	Ile	Lys	Ala	Met	Thr	Lys	Ile	Ser	Asn	Trp	Ile	Lys
				245					250					255	
Asp	Gly	Leu	Met	Met	Asn	Gly	Ser	Gln	Tyr	Asp	Gly	Ser	Ala	Asp	Ile

				260					265				270				
Gln	Asn	Phe	Ala	Asn	Gly	Gln	Thr	Ser	Phe	Thr	Ile	Leu	Trp	Ala	Pro		
		275					280					285					
Ala	Gln	Pro	Gly	Ile	Gln	Ala	Lys	Leu	Leu	Glu	Ala	Ser	Lys	Val	Asp		
	290					295					300						
Tyr	Leu	Glu	Ile	Pro	Phe	Pro	Ser	Asp	Asp	Gly	Lys	Pro	Glu	Leu	Glu		
305					310					315					320		
Tyr	Leu	Val	Asn	Gly	Phe	Ala	Val	Phe	Asn	Asn	Lys	Asp	Glu	Gln	Lys		
			325					330					335				
Val	Ala	Ala	Ser	Lys	Thr	Phe	Ile	Gln	Phe	Ile	Ala	Asp	Asp	Lys	Glu		
		340						345				350					
Trp	Gly	Pro	Lys	Asn	Val	Val	Arg	Thr	Gly	Ala	Phe	Pro	Val	Arg	Thr		
	355						360					365					
Ser	Tyr	Gly	Asp	Leu	Tyr	Lys	Asp	Lys	Arg	Met	Glu	Lys	Ile	Ala	Glu		
	370					375					380						
Trp	Thr	Lys	Phe	Tyr	Ser	Pro	Tyr	Tyr	Asn	Thr	Ile	Asp	Gly	Phe	Ala		
385					390				395						400		
Glu	Met	Arg	Thr	Leu	Trp	Phe	Pro	Met	Val	Gln	Ala	Val	Ser	Asn	Gly		
			405					410				415					
Asp	Glu	Lys	Pro	Glu	Asp	Ala	Leu	Lys	Ala	Phe	Thr	Glu	Lys	Ala	Asn		
		420						425				430					
Lys	Thr	Ile	Lys	Lys	Thr	Gln											
	435																

<210> SEQ ID NO 97

<211> LENGTH: 1788

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 97

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gtcattgctg	ttgccgttat	cttagcaact	tatttacaag	taaaagctcc	tgtcttctta	120
ggagagtcct	tgactgagtt	gggaaaaatc	ggtcaggctt	attacgttgc	taagatgagt	180
ggccagacac	atttttagccc	tgatttatca	gcttttaatg	ccgtgatgtt	taagcttttg	240
atgactttatt	tcttttactgt	tttagctaata	ctaatatata	gtttcttact	tacacgtgtt	300
gtctcacatt	cgactaaccg	catgcgcaag	ggcttatttg	gtaaattaga	acgtttaacc	360
gtcgcctttt	ttgaccgcca	taaagatggg	gagattcttt	ctcgtttcac	gagtgatttg	420
gataatatcc	aaaactcgct	gaaccaatcc	ttgattcaag	tggtgactaa	tattgccctt	480
tacatcggcc	tggtctggat	gatgtttagg	caagatagcc	gtttagcttt	gttaaccatc	540
gcatcaaccc	cagttgctct	cattttttta	gtgattaaca	tccgtttggc	aagaaaatac	600
accaatatcc	aacagcaaga	agtcagtgtc	ttaaagtctt	ttatggatga	aaccatttca	660
ggacaaaagg	ctattattgt	acaagggtgc	caagaagata	cgatgacagc	ctttttaaag	720
cataatgaaa	gggttcgaca	agccaccttc	aaacgccgtc	tgttctcagg	acaattattt	780
ccagtcatga	atggaatgag	ccttattaac	acggctatcg	tgatttttgt	cggttcaaca	840
attgtcctca	gtgacaaatc	tatgccagca	gcggcagcgc	ttggtttagt	ggttactttt	900
gtacaatatt	cccagcaata	ttaccaaccc	atgatgcaaa	tcgcgtctag	ttggggagaa	960
ttgcagctgg	cctttaccgg	tgctcaccgt	attcaagaaa	tgtttgatga	aaccgaagaa	1020
gttcgtccac	aaaatgcacc	agcgttcacc	agcttaaaag	aagcagtggc	gattaaccac	1080
gtcgattttg	ggtatcttcc	tgggcaaaaa	gttttatcag	atgtgtcaat	cgttgcaccc	1140
aagggcaaaa	tgattgccgt	ggttggaccg	acaggttctg	gaaagaccac	tattatgaac	1200
ttgattaacc	gtttctacga	tgtggatgca	ggttcgatta	cctttgatgg	ccgtgatatt	1260
cgtgactacg	atttggatag	tcttcgtcaa	aaggtaggga	ttgtgttgca	agagtcagtt	1320
cttttttcag	gaaccattac	ggataatatt	cgttttgggt	atcagaccat	tagtcaagac	1380
atggttgaaa	ctgctgcgcg	tgcgacccat	attcatgact	ttatcatgtc	cttaccaaaa	1440
gggtacaata	cctatgtctc	agatgatgac	aatgtctttt	caacagggtc	aaagcagttg	1500
atttctattg	ctaggacgct	actgactgac	cctgaaagtgt	tgatttttga	tgaggccact	1560
tcaaatgttg	atacggttac	cgaaagtaaa	attcaacggg	ccatggaagc	tatcgtggca	1620
ggtcgaacta	gctttgtcat	tgctcaccgc	ctcaaaacca	ttttaaatgc	cgatcacatt	1680

attgtgttga aagatggcaa ggtcattgag caaggaaatc atcatgagct attgcatcaa 1740
aaaggctttt atgccgaatt gtatcacaat caatttgtct ttgaatag 1788

<210> SEQ ID NO 98

<211> LENGTH: 595

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 98

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1				5					10					15	
Phe	Ser	Phe	Thr	Val	Ile	Ala	Val	Ala	Val	Ile	Leu	Ala	Thr	Tyr	Leu
			20					25					30		
Gln	Val	Lys	Ala	Pro	Val	Phe	Leu	Gly	Glu	Ser	Leu	Thr	Glu	Leu	Gly
		35					40					45			
Lys	Ile	Gly	Gln	Ala	Tyr	Tyr	Val	Ala	Lys	Met	Ser	Gly	Gln	Thr	His
	50					55					60				
Phe	Ser	Pro	Asp	Leu	Ser	Ala	Phe	Asn	Ala	Val	Met	Phe	Lys	Leu	Leu
65					70					75				80	
Met	Thr	Tyr	Phe	Phe	Thr	Val	Leu	Ala	Asn	Leu	Ile	Tyr	Ser	Phe	Leu
			85						90					95	
Leu	Thr	Arg	Val	Val	Ser	His	Ser	Thr	Asn	Arg	Met	Arg	Lys	Gly	Leu
			100					105					110		
Phe	Gly	Lys	Leu	Glu	Arg	Leu	Thr	Val	Ala	Phe	Phe	Asp	Arg	His	Lys
		115					120					125			
Asp	Gly	Glu	Ile	Leu	Ser	Arg	Phe	Thr	Ser	Asp	Leu	Asp	Asn	Ile	Gln
	130					135					140				
Asn	Ser	Leu	Asn	Gln	Ser	Leu	Ile	Gln	Val	Val	Thr	Asn	Ile	Ala	Leu
145					150					155				160	
Tyr	Ile	Gly	Leu	Val	Trp	Met	Met	Phe	Arg	Gln	Asp	Ser	Arg	Leu	Ala
			165						170					175	
Leu	Leu	Thr	Ile	Ala	Ser	Thr	Pro	Val	Ala	Leu	Ile	Phe	Leu	Val	Ile
			180					185					190		
Asn	Ile	Arg	Leu	Ala	Arg	Lys	Tyr	Thr	Asn	Ile	Gln	Gln	Gln	Glu	Val
		195					200					205			
Ser	Ala	Leu	Asn	Ala	Phe	Met	Asp	Glu	Thr	Ile	Ser	Gly	Gln	Lys	Ala
	210					215					220				
Ile	Ile	Val	Gln	Gly	Val	Gln	Glu	Asp	Thr	Met	Thr	Ala	Phe	Leu	Lys
225					230					235				240	
His	Asn	Glu	Arg	Val	Arg	Gln	Ala	Thr	Phe	Lys	Arg	Arg	Leu	Phe	Ser
			245						250				255		
Gly	Gln	Leu	Phe	Pro	Val	Met	Asn	Gly	Met	Ser	Leu	Ile	Asn	Thr	Ala
			260					265					270		
Ile	Val	Ile	Phe	Val	Gly	Ser	Thr	Ile	Val	Leu	Ser	Asp	Lys	Ser	Met
		275					280					285			
Pro	Ala	Ala	Ala	Ala	Leu	Gly	Leu	Val	Val	Thr	Phe	Val	Gln	Tyr	Ser
	290					295					300				
Gln	Gln	Tyr	Tyr	Gln	Pro	Met	Met	Gln	Ile	Ala	Ser	Ser	Trp	Gly	Glu
305					310					315				320	
Leu	Gln	Leu	Ala	Phe	Thr	Gly	Ala	His	Arg	Ile	Gln	Glu	Met	Phe	Asp
			325						330				335		
Glu	Thr	Glu	Glu	Val	Arg	Pro	Gln	Asn	Ala	Pro	Ala	Phe	Thr	Ser	Leu
			340					345					350		
Lys	Glu	Ala	Val	Ala	Ile	Asn	His	Val	Asp	Phe	Gly	Tyr	Leu	Pro	Gly
		355					360					365			
Gln	Lys	Val	Leu	Ser	Asp	Val	Ser	Ile	Val	Ala	Pro	Lys	Gly	Lys	Met
	370						375				380				
Ile	Ala	Val	Val	Gly	Pro	Thr	Gly	Ser	Gly	Lys	Thr	Thr	Ile	Met	Asn

385		390		395		400									
Leu	Ile	Asn	Arg	Phe	Tyr	Asp	Val	Asp	Ala	Gly	Ser	Ile	Thr	Phe	Asp
				405					410					415	
Gly	Arg	Asp	Ile	Arg	Asp	Tyr	Asp	Leu	Asp	Ser	Leu	Arg	Gln	Lys	Val
			420					425					430		
Gly	Ile	Val	Leu	Gln	Glu	Ser	Val	Leu	Phe	Ser	Gly	Thr	Ile	Thr	Asp
		435					440					445			
Asn	Ile	Arg	Phe	Gly	Asp	Gln	Thr	Ile	Ser	Gln	Asp	Met	Val	Glu	Thr
	450				455					460					
Ala	Ala	Arg	Ala	Thr	His	Ile	His	Asp	Phe	Ile	Met	Ser	Leu	Pro	Lys
465				470					475					480	
Gly	Tyr	Asn	Thr	Tyr	Val	Ser	Asp	Asp	Asp	Asn	Val	Phe	Ser	Thr	Gly
			485					490						495	
Gln	Lys	Gln	Leu	Ile	Ser	Ile	Ala	Arg	Thr	Leu	Leu	Thr	Asp	Pro	Glu
		500					505						510		
Val	Leu	Ile	Leu	Asp	Glu	Ala	Thr	Ser	Asn	Val	Asp	Thr	Val	Thr	Glu
	515				520							525			
Ser	Lys	Ile	Gln	Arg	Ala	Met	Glu	Ala	Ile	Val	Ala	Gly	Arg	Thr	Ser
	530				535					540					
Phe	Val	Ile	Ala	His	Arg	Leu	Lys	Thr	Ile	Leu	Asn	Ala	Asp	His	Ile
545				550					555					560	
Ile	Val	Leu	Lys	Asp	Gly	Lys	Val	Ile	Glu	Gln	Gly	Asn	His	His	Glu
			565				570						575		
Leu	Leu	His	Gln	Lys	Gly	Phe	Tyr	Ala	Glu	Leu	Tyr	His	Asn	Gln	Phe
		580					585						590		
Val	Phe	Glu													
	595														

<210> SEQ ID NO 99

<211> LENGTH: 1728

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 99

ttggaaacga	tattacaaac	aaaattacca	gtagctcaac	tggtggagca	gctaacggag	60
tggctaacta	aaactttctc	aggtctattt	gatattatgc	aagtagttgg	tagctttttg	120
atggattgga	tgaccaaaac	actttttatt	atccaccctg	tactttttat	tgttctagta	180
acagcagggg	tgtttttctc	tgctaagaaa	aaatggcctt	tgccaacctt	taccttggtt	240
ggattgctct	ttattttaca	tcaaggggta	tggaaagcag	taatgaatac	ctttactctg	300
gtgttagtag	ctagtttgat	ttcggtagct	attgggtatt	cgtctgggat	ttggatggct	360
aaaaatgcca	ctgtccgtca	gattgtgaat	cctatttttg	actttatgca	aaccatgccg	420
gcttttggtt	acttgattcc	tgccgttgcc	ttttttggta	ttggtagtgt	gcctggagta	480
tttgcttcag	tcattcttgc	cttaccacca	acggttcgtt	tcacaaattt	ggccattcgt	540
gacattccaa	cagaattgat	tgaggcctca	gatgcctttg	ggtcaactgg	gaaacaaaag	600
ctctttaaag	tggaattgcc	tttagctaaa	aatactatta	tggcaggtgt	taatcagacc	660
atgatgttag	ccctttccat	ggtagtaaca	ggctccatga	ttggtgctcc	tggttttagga	720
cgtgaagtct	tgtcagccct	tcaacacgct	gatattggta	gtggatttgt	cagtggctct	780
gccttggtta	tcttggcgat	tgtgcttgac	cgtagtacac	agttgttcaa	tagcaaacct	840
caagaaaaag	ccaaagctgg	caaaaccaat	aaatggattg	gtttagcagc	ccttgctgtc	900
tttttgatag	ctgcttttag	acgcggtatt	atggctatga	cttctgggtat	ggcagataag	960
ggtgaaactg	ttaacatcgc	ttacgtgcag	tgggattctg	aggttgcctc	aactcatgtg	1020
attgcagaag	ttttgaaaaa	cgaaggttac	catgtgacct	tgactccgct	tgacaatgcc	1080
gttatgtggc	aaaccgttgc	aaatgggaac	gctgattttt	caactagtgc	ttggttgcca	1140
gtcaccatg	gccaacaata	tcagaaatac	aagtcaaaat	tagatgattt	aggacctaac	1200
ctaaaagggg	ccaaacttgg	tttagctgtt	ccaaaataca	tgacagatgt	caatagtatt	1260
gaggacttaa	cgaacaagc	cgatcaaaaa	atcacaggga	tcgaaccagg	tgagggtatc	1320
atggcagcag	cccaaaagac	tctaaaagag	tatcataatc	tatctagtgt	ggagttagtg	1380
gcggcatcaa	caggagccat	gacgacttcc	ttggatcaag	cgatcaagaa	aaaagatcct	1440

attgttgga	cagcttggtc	accacactgg	atgtttgcc	agtatgactt	gaagtacctt	1500
aaagatccta	aagaaatctt	tggctcgact	gagaacatca	ataccattgc	tcgtaaaggc	1560
ttgaaaaaag	aacttcctaaa	tgtctacaaa	atcattgata	agttccactg	gacccaaaaa	1620
gatatggaag	cagtcattgct	tgacatcaac	aaaggcatga	gtccagaagc	tgccgcaaaa	1680
aaatgggtag	aggcaaacaa	atctaaagta	tcaagttgga	caaaataa		1728

<210> SEQ ID NO 100

<211> LENGTH: 575

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 100

Met	Glu	Thr	Ile	Leu	Gln	Thr	Lys	Leu	Pro	Val	Ala	Gln	Leu	Val	Glu
1				5					10				15		
Gln	Leu	Thr	Glu	Trp	Leu	Thr	Lys	Thr	Phe	Ser	Gly	Leu	Phe	Asp	Ile
			20					25				30			
Met	Gln	Val	Val	Gly	Ser	Phe	Leu	Met	Asp	Trp	Met	Thr	Lys	Thr	Leu
		35					40					45			
Leu	Phe	Ile	His	Pro	Leu	Leu	Phe	Ile	Val	Leu	Val	Thr	Ala	Gly	Met
	50					55					60				
Phe	Phe	Leu	Ala	Lys	Lys	Lys	Trp	Pro	Leu	Pro	Thr	Phe	Thr	Leu	Leu
65				70						75				80	
Gly	Leu	Leu	Phe	Ile	Tyr	Asn	Gln	Gly	Leu	Trp	Lys	Gln	Leu	Met	Asn
				85					90				95		
Thr	Phe	Thr	Leu	Val	Leu	Val	Ala	Ser	Leu	Ile	Ser	Val	Leu	Ile	Gly
			100					105					110		
Ile	Pro	Leu	Gly	Ile	Trp	Met	Ala	Lys	Asn	Ala	Thr	Val	Arg	Gln	Ile
	115					120						125			
Val	Asn	Pro	Ile	Leu	Asp	Phe	Met	Gln	Thr	Met	Pro	Ala	Phe	Val	Tyr
	130					135					140				
Leu	Ile	Pro	Ala	Val	Ala	Phe	Phe	Gly	Ile	Gly	Met	Val	Pro	Gly	Val
145				150						155				160	
Phe	Ala	Ser	Val	Ile	Phe	Ala	Leu	Pro	Pro	Thr	Val	Arg	Phe	Thr	Asn
				165					170					175	
Leu	Ala	Ile	Arg	Asp	Ile	Pro	Thr	Glu	Leu	Ile	Glu	Ala	Ser	Asp	Ala
			180					185					190		
Phe	Gly	Ser	Thr	Gly	Lys	Gln	Lys	Leu	Phe	Lys	Val	Glu	Leu	Pro	Leu
	195					200						205			
Ala	Lys	Asn	Thr	Ile	Met	Ala	Gly	Val	Asn	Gln	Thr	Met	Met	Leu	Ala
	210					215					220				
Leu	Ser	Met	Val	Val	Thr	Gly	Ser	Met	Ile	Gly	Ala	Pro	Gly	Leu	Gly
225				230						235				240	
Arg	Glu	Val	Leu	Ser	Ala	Leu	Gln	His	Ala	Asp	Ile	Gly	Ser	Gly	Phe
				245					250					255	
Val	Ser	Gly	Leu	Ala	Leu	Val	Ile	Leu	Ala	Ile	Val	Leu	Asp	Arg	Met
			260					265					270		
Thr	Gln	Leu	Phe	Asn	Ser	Lys	Pro	Gln	Glu	Lys	Ala	Lys	Ala	Gly	Lys
	275					280						285			
Thr	Asn	Lys	Trp	Ile	Gly	Leu	Ala	Ala	Leu	Ala	Val	Phe	Leu	Ile	Ala
	290					295					300				
Ala	Leu	Gly	Arg	Gly	Ile	Met	Ala	Met	Thr	Ser	Gly	Met	Ala	Asp	Lys
305				310						315				320	
Gly	Glu	Thr	Val	Asn	Ile	Ala	Tyr	Val	Gln	Trp	Asp	Ser	Glu	Val	Ala
				325					330					335	
Ser	Thr	His	Val	Ile	Ala	Glu	Val	Leu	Lys	Asn	Glu	Gly	Tyr	His	Val
			340					345					350		
Thr	Leu	Thr	Pro	Leu	Asp	Asn	Ala	Val	Met	Trp	Gln	Thr	Val	Ala	Asn
	355						360						365		

Gly	Asn	Ala	Asp	Phe	Ser	Thr	Ser	Ala	Trp	Leu	Pro	Val	Thr	His	Gly
370						375					380				
Gln	Gln	Tyr	Gln	Lys	Tyr	Lys	Ser	Lys	Leu	Asp	Asp	Leu	Gly	Pro	Asn
385				390					395						400
Leu	Lys	Gly	Thr	Lys	Leu	Gly	Leu	Ala	Val	Pro	Lys	Tyr	Met	Thr	Asp
			405					410					415		
Val	Asn	Ser	Ile	Glu	Asp	Leu	Ser	Lys	Gln	Ala	Asp	Gln	Lys	Ile	Thr
			420					425					430		
Gly	Ile	Glu	Pro	Gly	Ala	Gly	Ile	Met	Ala	Ala	Ala	Gln	Lys	Thr	Leu
		435					440					445			
Lys	Glu	Tyr	His	Asn	Leu	Ser	Ser	Trp	Glu	Leu	Val	Ala	Ala	Ser	Thr
	450					455					460				
Gly	Ala	Met	Thr	Thr	Ser	Leu	Asp	Gln	Ala	Ile	Lys	Lys	Lys	Asp	Pro
465					470					475					480
Ile	Val	Val	Thr	Ala	Trp	Ser	Pro	His	Trp	Met	Phe	Ala	Lys	Tyr	Asp
				485					490					495	
Leu	Lys	Tyr	Leu	Lys	Asp	Pro	Lys	Glu	Ile	Phe	Gly	Ser	Thr	Glu	Asn
			500					505					510		
Ile	Asn	Thr	Ile	Ala	Arg	Lys	Gly	Leu	Lys	Lys	Glu	Leu	Pro	Asn	Val
	515						520						525		
Tyr	Lys	Ile	Ile	Asp	Lys	Phe	His	Trp	Thr	Gln	Lys	Asp	Met	Glu	Ala
	530					535					540				
Val	Met	Leu	Asp	Ile	Asn	Lys	Gly	Met	Ser	Pro	Glu	Ala	Ala	Ala	Lys
545					550				555						560
Lys	Trp	Val	Glu	Ala	Asn	Lys	Ser	Lys	Val	Ser	Ser	Trp	Thr	Lys	
				565					570					575	

<210> SEQ ID NO 101

<211> LENGTH: 1725

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 101

atgaaggaca	tgtctaataa	aaaaacattt	aaaaaataca	gtcgcgtcgc	tgggctactg	60
acggcagctc	ttatcattgg	taaccttggt	actgctaata	ctgaatcgaa	caaacaaaac	120
actgctagta	cagaaaccac	aacgacaaat	gagcaaccaa	agccagaaa	tagtgagcta	180
actactgaaa	aagcagggtc	gaaaacggat	gatatgctta	actctaacga	tatgattaag	240
cttgctccca	aagaaatgcc	actagaatct	gcagaaaaag	aagaaaaaaa	gtcagaagac	300
aaaaaaaaaga	gcgaagaaga	tcacactgaa	gaaatcaatg	acaagattta	ttcactaaat	360
tataatgagc	ttgaagtact	tgctaaaaat	ggtgaaacca	ttgaaaattt	tgttcctaaa	420
gaaggcggtta	agaaagctga	taaattttatt	gtcattgaaa	gaaagaaaaa	aaatatcaac	480
actacaccag	tcgatatttc	cattattgac	tctgtcactg	ataggaccta	tccagcagcc	540
cttcagctgg	ctaataaagg	ttttaccgaa	aacaaaccag	acgcggtagt	caccaagcga	600
aaccacaaaa	aatccatat	tgattttacca	ggtatgggag	acaaagcaac	ggttgaggtc	660
aatgacccta	cctatgcca	tgttttcaaca	gctattgata	atcttggtta	ccaatggcat	720
gataattatt	ctgggtggtaa	tacgcttcct	gccagaacac	aatatactga	atcaatggta	780
tattctaagt	cacagattga	agcagctcta	aatgttaata	gcaaaatctt	agatgggtact	840
ttaggcattg	atttcaagtc	gattttcaaaa	ggtgaaaaga	aggtgatgat	tgcagcatac	900
aagcaaattt	tttacaccgt	atcagcaaac	cttcctaata	atcctgcgga	tgtgtttgat	960
aaatcgggtga	ccttttaaaga	gttgcaacga	aaagggtgtca	gcaatgaagc	tccgccactc	1020
tttgtgagta	acgtagccta	tggtcgaact	gtttttgtca	aactagaaac	aagttctaaa	1080
agtaatgatg	ttgaagcggc	cttttagtgca	gctctaaaag	gaacagatgt	taaaactaat	1140
ggaaaatatt	ctgatatctt	agaaaatagc	tcattttacag	ctgtcgtttt	aggaggagat	1200
gctgcagagc	acaataaggt	agtcacaaaa	gacttttgatg	ttattagaaa	cgttatcaaa	1260
gacaatgcta	ccttcagtag	aaaaaaccca	gcttatccta	tttcatacac	cagtgttttc	1320
cttaaaaata	ataaaattgc	gggtgtcaat	aacagaactg	aatacgttga	aacaacatct	1380
accgagtaca	ctagtggaaa	aattaacctg	tctcatcaag	gcgcgtatgt	tgctcaatat	1440
gaaatccttt	gggatgaaat	caattatgat	gacaaaggaa	aagaagtgat	tacaaaacga	1500

cgttgggaca	acaactggta	tagtaagaca	tcaccattta	gcacagttat	cccactagga	1560
gctaattcac	gaaatatccg	tatcatggct	agagagtgc	ctggccttagc	ttgggaatgg	1620
tggcgaaaag	tgatcgacga	aagagatgtg	aaactgtcta	aagaaatcaa	tgtcaatatc	1680
tcaggatcaa	ccttgagccc	atatggttcg	attacttata	agtag		1725

<210> SEQ ID NO 102

<211> LENGTH: 574

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 102

Met	Lys	Asp	Met	Ser	Asn	Lys	Lys	Thr	Phe	Lys	Lys	Tyr	Ser	Arg	Val
1				5					10					15	
Ala	Gly	Leu	Leu	Thr	Ala	Ala	Leu	Ile	Gly	Asn	Leu	Val	Thr	Ala	
		20						25				30			
Asn	Ala	Glu	Ser	Asn	Lys	Gln	Asn	Thr	Ala	Ser	Thr	Glu	Thr	Thr	Thr
		35					40					45			
Thr	Asn	Glu	Gln	Pro	Lys	Pro	Glu	Ser	Ser	Glu	Leu	Thr	Thr	Glu	Lys
	50					55					60				
Ala	Gly	Gln	Lys	Thr	Asp	Asp	Met	Leu	Asn	Ser	Asn	Asp	Met	Ile	Lys
65					70					75				80	
Leu	Ala	Pro	Lys	Glu	Met	Pro	Leu	Glu	Ser	Ala	Glu	Lys	Glu	Glu	Lys
				85					90				95		
Lys	Ser	Glu	Asp	Lys	Lys	Lys	Ser	Glu	Glu	Asp	His	Thr	Glu	Glu	Ile
			100					105					110		
Asn	Asp	Lys	Ile	Tyr	Ser	Leu	Asn	Tyr	Asn	Glu	Leu	Glu	Val	Leu	Ala
		115					120					125			
Lys	Asn	Gly	Glu	Thr	Ile	Glu	Asn	Phe	Val	Pro	Lys	Glu	Gly	Val	Lys
	130					135					140				
Lys	Ala	Asp	Lys	Phe	Ile	Val	Ile	Glu	Arg	Lys	Lys	Lys	Asn	Ile	Asn
145					150					155				160	
Thr	Thr	Pro	Val	Asp	Ile	Ser	Ile	Ile	Asp	Ser	Val	Thr	Asp	Arg	Thr
				165					170					175	
Tyr	Pro	Ala	Ala	Leu	Gln	Leu	Ala	Asn	Lys	Gly	Phe	Thr	Glu	Asn	Lys
			180					185					190		
Pro	Asp	Ala	Val	Val	Thr	Lys	Arg	Asn	Pro	Gln	Lys	Ile	His	Ile	Asp
	195						200					205			
Leu	Pro	Gly	Met	Gly	Asp	Lys	Ala	Thr	Val	Glu	Val	Asn	Asp	Pro	Thr
	210					215					220				
Tyr	Ala	Asn	Val	Ser	Thr	Ala	Ile	Asp	Asn	Leu	Val	Asn	Gln	Trp	His
225					230					235				240	
Asp	Asn	Tyr	Ser	Gly	Gly	Asn	Thr	Leu	Pro	Ala	Arg	Thr	Gln	Tyr	Thr
				245					250					255	
Glu	Ser	Met	Val	Tyr	Ser	Lys	Ser	Gln	Ile	Glu	Ala	Ala	Leu	Asn	Val
			260					265					270		
Asn	Ser	Lys	Ile	Leu	Asp	Gly	Thr	Leu	Gly	Ile	Asp	Phe	Lys	Ser	Ile
		275					280					285			
Ser	Lys	Gly	Glu	Lys	Lys	Val	Met	Ile	Ala	Ala	Tyr	Lys	Gln	Ile	Phe
	290					295					300				
Tyr	Thr	Val	Ser	Ala	Asn	Leu	Pro	Asn	Asn	Pro	Ala	Asp	Val	Phe	Asp
305					310					315				320	
Lys	Ser	Val	Thr	Phe	Lys	Glu	Leu	Gln	Arg	Lys	Gly	Val	Ser	Asn	Glu
				325					330					335	
Ala	Pro	Pro	Leu	Phe	Val	Ser	Asn	Val	Ala	Tyr	Gly	Arg	Thr	Val	Phe
			340					345					350		
Val	Lys	Leu	Glu	Thr	Ser	Ser	Lys	Ser	Asn	Asp	Val	Glu	Ala	Ala	Phe
	355						360					365			
Ser	Ala	Ala	Leu	Lys	Gly	Thr	Asp	Val	Lys	Thr	Asn	Gly	Lys	Tyr	Ser

370	375	380
Asp Ile Leu Glu Asn Ser Ser Phe Thr Ala Val Val Leu Gly Gly Asp		
385	390	395
Ala Ala Glu His Asn Lys Val Val Thr Lys Asp Phe Asp Val Ile Arg		400
	405	410
Asn Val Ile Lys Asp Asn Ala Thr Phe Ser Arg Lys Asn Pro Ala Tyr		415
	420	425
Pro Ile Ser Tyr Thr Ser Val Phe Leu Lys Asn Asn Lys Ile Ala Gly		430
	435	440
Val Asn Asn Arg Thr Glu Tyr Val Glu Thr Thr Ser Thr Glu Tyr Thr		445
	450	455
Ser Gly Lys Ile Asn Leu Ser His Gln Gly Ala Tyr Val Ala Gln Tyr		460
465	470	475
Glu Ile Leu Trp Asp Glu Ile Asn Tyr Asp Asp Lys Gly Lys Glu Val		480
	485	490
Ile Thr Lys Arg Arg Trp Asp Asn Asn Trp Tyr Ser Lys Thr Ser Pro		495
	500	505
Phe Ser Thr Val Ile Pro Leu Gly Ala Asn Ser Arg Asn Ile Arg Ile		510
	515	520
Met Ala Arg Glu Cys Thr Gly Leu Ala Trp Glu Trp Trp Arg Lys Val		525
	530	535
Ile Asp Glu Arg Asp Val Lys Leu Ser Lys Glu Ile Asn Val Asn Ile		540
545	550	555
Ser Gly Ser Thr Leu Ser Pro Tyr Gly Ser Ile Thr Tyr Lys		560
	565	570

<210> SEQ ID NO 103

<211> LENGTH: 648

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 103

atgaaaaaat	ctatattaag	aatttttagct	attgggttatt	tacttatgag	tttttgtttg	60
ttagactccg	tagaggcaga	aaacctcact	gcaagcatta	atattgaagt	tattaatcaa	120
gttgatggtg	ctaccaacaa	acaatcctct	gacatagatg	aaacgtttat	gtttgtaatt	180
gaagcggttag	ataaagaaag	tcctttacct	aattcggtaa	ctacttctgt	taagggaaat	240
gggaaaacat	catttgaaca	gttgactttt	tcagaagttg	gacaatatca	ttataaaaatt	300
catcaactgt	taggtaagaa	tagtcaatat	cattatgatg	aaacagtata	tgaagttggt	360
atttacgtat	tgtataatga	gcaaagtggg	gctttagaaa	ctaacctagt	ttctaacaaa	420
cttgagagaaa	ccgaaaaaatc	ggagcttatt	tttaaacaag	aatatagtga	aaaaacaccg	480
gaacctcatc	aaccagatac	aactgagaag	gaaaaaacctc	agaaaaaacg	taatgggtatt	540
ttgccatcaa	ctggtgaaat	ggtgagttac	gtatctgctt	taggaattgt	cttagtggct	600
accattactt	tgtattctat	ttataaaaag	ctaaagacaa	gcaaatag		648

<210> SEQ ID NO 104

<211> LENGTH: 215

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 104

Met Lys Lys Ser Ile Leu Arg Ile Leu Ala Ile Gly Tyr Leu Leu Met	
1	15
Ser Phe Cys Leu Leu Asp Ser Val Glu Ala Glu Asn Leu Thr Ala Ser	
	30
Ile Asn Ile Glu Val Ile Asn Gln Val Asp Val Ala Thr Asn Lys Gln	
	45
Ser Ser Asp Ile Asp Glu Thr Phe Met Phe Val Ile Glu Ala Leu Asp	
	60
Lys Glu Ser Pro Leu Pro Asn Ser Val Thr Thr Ser Val Lys Gly Asn	

65		70		75		80									
Gly	Lys	Thr	Ser	Phe	Glu	Gln	Leu	Thr	Phe	Ser	Glu	Val	Gly	Gln	Tyr
				85					90					95	
His	Tyr	Lys	Ile	His	Gln	Leu	Leu	Gly	Lys	Asn	Ser	Gln	Tyr	His	Tyr
			100					105					110		
Asp	Glu	Thr	Val	Tyr	Glu	Val	Val	Ile	Tyr	Val	Leu	Tyr	Asn	Glu	Gln
		115					120					125			
Ser	Gly	Ala	Leu	Glu	Thr	Asn	Leu	Val	Ser	Asn	Lys	Leu	Gly	Glu	Thr
	130					135					140				
Glu	Lys	Ser	Glu	Leu	Ile	Phe	Lys	Gln	Glu	Tyr	Ser	Glu	Lys	Thr	Pro
145					150					155					160
Glu	Pro	His	Gln	Pro	Asp	Thr	Thr	Glu	Lys	Glu	Lys	Pro	Gln	Lys	Lys
			165					170					175		
Arg	Asn	Gly	Ile	Leu	Pro	Ser	Thr	Gly	Glu	Met	Val	Ser	Tyr	Val	Ser
		180						185					190		
Ala	Leu	Gly	Ile	Val	Leu	Val	Ala	Thr	Ile	Thr	Leu	Tyr	Ser	Ile	Tyr
	195						200					205			
Lys	Lys	Leu	Lys	Thr	Ser	Lys									
	210					215									

<210> SEQ ID NO 105

<211> LENGTH: 2313

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 105

atgaggtatt	ttatggtgaa	atggaacacg	aaacaaaagc	gtataagtca	tcaaagatta	60
gggtctcttg	atttggggcc	ggtgctatta	cgtacgttga	gactactgtc	taactttttt	120
tatattgtta	tcttcctttt	tggaatgatg	ggatttggta	tggcatttgg	gtatttggct	180
agtcagattg	aatctgttaa	ggtaccaagt	aaagaaaagt	tagtcaaaca	agttgaatca	240
ttaacgatga	tttcgcaa	gaactattct	gataatagtt	taatttctac	tttagatacg	300
gatttacttc	gaacaccagt	agctaattgat	gcgatttcag	agaatatcaa	aaaagctatt	360
gtatcaacag	aagacgaaca	ttttcaagaa	cataaaggta	tcgtgccaaa	agctgttttt	420
cgggcaacat	tggcttctgt	attgggattt	ggagaagcta	gtggagggtc	gaccttaaca	480
cagcaattag	tcaagcaaca	agttttggga	gacgatccca	catttaagcg	caagtctaag	540
gagatcgttt	acgctcttgc	cttagagcgt	tatatgtcca	aagacaatat	cttatgtgat	600
tatcttaatg	tttcaccttt	tggccgtaac	aacaagggtc	aaaatattgc	tggtgttgaa	660
gaagctgcgc	gtggcatttt	tggcgtttct	gccaaaagatt	taacggtgcc	acaggcgagca	720
tttttggcgg	gtcttccgca	gagtcctatt	gtttactctc	cttatttgtc	aacgggacaa	780
ctgaaatcag	aaaaggacat	ggcttatggc	atcaagcgtc	agcaaaatgt	tctctttaac	840
atgtaccgta	cagggtgttct	gtctaaaaaa	gaatacgagg	actataaggc	ttatccgatt	900
caaaaggatt	ttattcaacc	gggaagtgca	atagtaaata	atcacgatta	cctttattac	960
acggtgttag	cggatgctaa	gaaagccatg	tatagctatt	tgattaagcg	agataagggtg	1020
tctagtcgtg	acttgaaaaa	tgacgagact	aaggctgctt	atgaagagag	agccttaaca	1080
gaattgcaac	aggggtggcta	taccatcacc	acaaccatta	ataagcctat	ttacaatgcg	1140
atgcagacag	cggcagctca	gtttggtggc	ttgttagatg	atggcactgg	tacagttcaa	1200
atgggaaatg	tcttgacaga	caatgcgact	ggtgctgtgt	taggttttgt	tggtggtaga	1260
gattatgctc	tgaatcaaaa	taatcatgct	ttcaatacag	ttagatcgcc	aggttctagc	1320
attaaaccga	taatcgctta	tggtcctgct	attgatcaag	gtttaatggg	gagtgttagc	1380
gttttgtcta	attaccaaac	aacttactcg	agtggccaaa	aaatcatgca	tgctgatagt	1440
gaaggaacag	ccatgatgcc	acttcaagag	gccctaaata	cttcttgga	catcccagct	1500
ttttggacac	agaaattact	gcgtgaaaaa	ggtgtcgatg	tcgaaaatta	tatgacaaaa	1560
atgggttata	agattgcaga	ctactcgatt	gaaagtgttac	ctctaggggg	cggatttgaa	1620
gtctcggttg	ctcaacaaa	caatgcttac	caaagtcttt	caaacaatgg	cttatatcaa	1680
aagcaataaa	ttgtagataa	gattactgct	agcgatggta	cagtcgttta	caaacaatgaa	1740
aataagccaa	ttcgtatttt	ttctgcagca	acagctacga	ttttacaaga	attgttgaga	1800
gggtccgatta	cttcaggcgc	tacgactact	ttcaagaacc	gtttggcggc	tattaatccg	1860
tggtcttgcta	atgctgattg	gattgggtaag	accggaacaa	ctgagaatta	tacggatggt	1920

tggctagtcc	tgtctactcc	aaaagttact	ttaggcgggtt	gggcaggaca	tgatgacaat	1980
acctcattag	cgccattaac	aggatataac	aataattcta	attatcttgc	ctatttagct	2040
aatgccatta	atcaggccga	tcccaatgtt	attggagtag	ggcaacgctt	caacttagat	2100
ccaggagtca	ttaaggcgaa	tgtcttgaag	tcaacaggtt	tacaaccagg	aactgttaat	2160
gtcaatggac	atactttttc	tgttggtgga	gaaatgacca	ccagtctatg	gtcccaaaaa	2220
ggaccggggg	ctatgactta	ccgatttgct	attggtggca	cggatgccga	ttatcaaaaa	2280
gcctggggga	acttcggggtt	cagaaaaaat	tag			2313

<210> SEQ ID NO 106

<211> LENGTH: 770

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 106

Met	Arg	Tyr	Phe	Met	Val	Lys	Trp	Asn	Thr	Lys	Gln	Lys	Arg	Ile	Ser
1				5					10					15	
His	Gln	Arg	Leu	Gly	Leu	Leu	Asp	Leu	Gly	Pro	Val	Leu	Leu	Arg	Thr
			20					25						30	
Leu	Arg	Leu	Leu	Ser	Asn	Phe	Phe	Tyr	Ile	Val	Ile	Phe	Leu	Phe	Gly
			35				40					45			
Met	Met	Gly	Phe	Gly	Met	Ala	Phe	Gly	Tyr	Leu	Ala	Ser	Gln	Ile	Glu
	50					55					60				
Ser	Val	Lys	Val	Pro	Ser	Lys	Glu	Ser	Leu	Val	Lys	Gln	Val	Glu	Ser
65					70					75				80	
Leu	Thr	Met	Ile	Ser	Gln	Met	Asn	Tyr	Ser	Asp	Asn	Ser	Leu	Ile	Ser
			85						90					95	
Thr	Leu	Asp	Thr	Asp	Leu	Leu	Arg	Thr	Pro	Val	Ala	Asn	Asp	Ala	Ile
			100					105					110		
Ser	Glu	Asn	Ile	Lys	Lys	Ala	Ile	Val	Ser	Thr	Glu	Asp	Glu	His	Phe
		115					120					125			
Gln	Glu	His	Lys	Gly	Ile	Val	Pro	Lys	Ala	Val	Phe	Arg	Ala	Thr	Leu
	130					135					140				
Ala	Ser	Val	Leu	Gly	Phe	Gly	Glu	Ala	Ser	Gly	Gly	Ser	Thr	Leu	Thr
145					150					155				160	
Gln	Gln	Leu	Val	Lys	Gln	Gln	Val	Leu	Gly	Asp	Asp	Pro	Thr	Phe	Lys
			165						170					175	
Arg	Lys	Ser	Lys	Glu	Ile	Val	Tyr	Ala	Leu	Ala	Leu	Glu	Arg	Tyr	Met
			180					185					190		
Ser	Lys	Asp	Asn	Ile	Leu	Cys	Asp	Tyr	Leu	Asn	Val	Ser	Pro	Phe	Gly
		195					200					205			
Arg	Asn	Asn	Lys	Gly	Gln	Asn	Ile	Ala	Gly	Val	Glu	Glu	Ala	Ala	Arg
	210					215					220				
Gly	Ile	Phe	Gly	Val	Ser	Ala	Lys	Asp	Leu	Thr	Val	Pro	Gln	Ala	Ala
225					230					235				240	
Phe	Leu	Ala	Gly	Leu	Pro	Gln	Ser	Pro	Ile	Val	Tyr	Ser	Pro	Tyr	Leu
			245						250					255	
Ser	Thr	Gly	Gln	Leu	Lys	Ser	Glu	Lys	Asp	Met	Ala	Tyr	Gly	Ile	Lys
			260					265					270		
Arg	Gln	Gln	Asn	Val	Leu	Phe	Asn	Met	Tyr	Arg	Thr	Gly	Val	Leu	Ser
		275					280					285			
Lys	Lys	Glu	Tyr	Glu	Asp	Tyr	Lys	Ala	Tyr	Pro	Ile	Gln	Lys	Asp	Phe
	290					295					300				
Ile	Gln	Pro	Gly	Ser	Ala	Ile	Val	Asn	Asn	His	Asp	Tyr	Leu	Tyr	Tyr
305					310					315				320	
Thr	Val	Leu	Ala	Asp	Ala	Lys	Lys	Ala	Met	Tyr	Ser	Tyr	Leu	Ile	Lys
			325						330					335	
Arg	Asp	Lys	Val	Ser	Ser	Arg	Asp	Leu	Lys	Asn	Asp	Glu	Thr	Lys	Ala
			340					345					350		

Ala	Tyr	Glu	Glu	Arg	Ala	Leu	Thr	Glu	Leu	Gln	Gln	Gly	Gly	Tyr	Thr		
		355					360					365					
Ile	Thr	Thr	Thr	Ile	Asn	Lys	Pro	Ile	Tyr	Asn	Ala	Met	Gln	Thr	Ala		
		370				375					380						
Ala	Ala	Gln	Phe	Gly	Gly	Leu	Leu	Asp	Asp	Gly	Thr	Gly	Thr	Val	Gln		
385					390					395					400		
Met	Gly	Asn	Val	Leu	Thr	Asp	Asn	Ala	Thr	Gly	Ala	Val	Leu	Gly	Phe		
			405						410					415			
Val	Gly	Gly	Arg	Asp	Tyr	Ala	Leu	Asn	Gln	Asn	Asn	His	Ala	Phe	Asn		
			420					425					430				
Thr	Val	Arg	Ser	Pro	Gly	Ser	Ser	Ile	Lys	Pro	Ile	Ile	Ala	Tyr	Gly		
		435					440					445					
Pro	Ala	Ile	Asp	Gln	Gly	Leu	Met	Gly	Ser	Ala	Ser	Val	Leu	Ser	Asn		
		450				455					460						
Tyr	Pro	Thr	Thr	Tyr	Ser	Ser	Gly	Gln	Lys	Ile	Met	His	Ala	Asp	Ser		
465				470						475					480		
Glu	Gly	Thr	Ala	Met	Met	Pro	Leu	Gln	Glu	Ala	Leu	Asn	Thr	Ser	Trp		
				485					490						495		
Asn	Ile	Pro	Ala	Phe	Trp	Thr	Gln	Lys	Leu	Leu	Arg	Glu	Lys	Gly	Val		
			500					505					510				
Asp	Val	Glu	Asn	Tyr	Met	Thr	Lys	Met	Gly	Tyr	Lys	Ile	Ala	Asp	Tyr		
		515					520					525					
Ser	Ile	Glu	Ser	Leu	Pro	Leu	Gly	Gly	Gly	Ile	Glu	Val	Ser	Val	Ala		
		530				535					540						
Gln	Gln	Thr	Asn	Ala	Tyr	Gln	Met	Leu	Ser	Asn	Asn	Gly	Leu	Tyr	Gln		
545				550						555					560		
Lys	Gln	Tyr	Ile	Val	Asp	Lys	Ile	Thr	Ala	Ser	Asp	Gly	Thr	Val	Val		
				565					570						575		
Tyr	Lys	His	Glu	Asn	Lys	Pro	Ile	Arg	Ile	Phe	Ser	Ala	Ala	Thr	Ala		
			580					585					590				
Thr	Ile	Leu	Gln	Glu	Leu	Leu	Arg	Gly	Pro	Ile	Thr	Ser	Gly	Ala	Thr		
		595					600					605					
Thr	Thr	Phe	Lys	Asn	Arg	Leu	Ala	Ala	Ile	Asn	Pro	Trp	Leu	Ala	Asn		
		610				615					620						
Ala	Asp	Trp	Ile	Gly	Lys	Thr	Gly	Thr	Thr	Glu	Asn	Tyr	Thr	Asp	Val		
625				630						635					640		
Trp	Leu	Val	Leu	Ser	Thr	Pro	Lys	Val	Thr	Leu	Gly	Gly	Trp	Ala	Gly		
				645					650					655			
His	Asp	Asp	Asn	Thr	Ser	Leu	Ala	Pro	Leu	Thr	Gly	Tyr	Asn	Asn	Asn		
			660				665						670				
Ser	Asn	Tyr	Leu	Ala	Tyr	Leu	Ala	Asn	Ala	Ile	Asn	Gln	Ala	Asp	Pro		
		675					680					685					
Asn	Val	Ile	Gly	Val	Gly	Gln	Arg	Phe	Asn	Leu	Asp	Pro	Gly	Val	Ile		
		690				695					700						
Lys	Ala	Asn	Val	Leu	Lys	Ser	Thr	Gly	Leu	Gln	Pro	Gly	Thr	Val	Asn		
705				710						715					720		
Val	Asn	Gly	His	Thr	Phe	Ser	Val	Gly	Gly	Glu	Met	Thr	Thr	Ser	Leu		
			725					730						735			
Trp	Ser	Gln	Lys	Gly	Pro	Gly	Ala	Met	Thr	Tyr	Arg	Phe	Ala	Ile	Gly		
		740					745					750					
Gly	Thr	Asp	Ala	Asp	Tyr	Gln	Lys	Ala	Trp	Gly	Asn	Phe	Gly	Phe	Arg		
		755				760						765					
Lys	Asn																
		770															

<210> SEQ ID NO 107

<211> LENGTH: 366

<212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 107
 atggctcgta ttgctggagt tgatattcca aatgataaac gcgtagtaat ttcacttact 60
 tatgttttacg gaattggtct tgcaacatct aaaaaaatct tagcagctgc aggtatttct 120
 gaagatatcc gtgttaaaga tttaacatca gatcaagaag atgctatccg tcgtgaagtg 180
 gatgcaatca aagttgaagg tgaccttcga cgtgaagtaa acatgaacat taaacgtttg 240
 atggaaatcg gttcataccg tggaatccgt catcgtcgtg gacttcctgt ccgtggacaa 300
 aatactaaaa acaatgctcg cactcgtaaa gggaaagctg ttgcgattgc aggtaagaaa 360
 aaataa 366

<210> SEQ ID NO 108
 <211> LENGTH: 121
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 108
 Met Ala Arg Ile Ala Gly Val Asp Ile Pro Asn Asp Lys Arg Val Val
 1 5 10 15
 Ile Ser Leu Thr Tyr Val Tyr Gly Ile Gly Leu Ala Thr Ser Lys Lys
 20 25 30
 Ile Leu Ala Ala Ala Gly Ile Ser Glu Asp Ile Arg Val Lys Asp Leu
 35 40 45
 Thr Ser Asp Gln Glu Asp Ala Ile Arg Arg Glu Val Asp Ala Ile Lys
 50 55 60
 Val Glu Gly Asp Leu Arg Arg Glu Val Asn Met Asn Ile Lys Arg Leu
 65 70 75 80
 Met Glu Ile Gly Ser Tyr Arg Gly Ile Arg His Arg Arg Gly Leu Pro
 85 90 95
 Val Arg Gly Gln Asn Thr Lys Asn Asn Ala Arg Thr Arg Lys Gly Lys
 100 105 110
 Ala Val Ala Ile Ala Gly Lys Lys Lys
 115 120

<210> SEQ ID NO 109
 <211> LENGTH: 369
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 109
 atgattcaac aagaaactcg cttgaaaagtt gctgataata gcggtgctcg tgagatcttg 60
 actatcaaag tacttggtgg ttcaggacgt aaattcgcta acatcggtga cgtaatcggt 120
 gcttctgtaa aacaagctac tcctggtgga gcagttaaaa aaggtgatgt gggttaaagct 180
 gttatcgttc gtacaaaaaac tgggtgcacgc cgtccagacg gttcatacat caaatttgac 240
 gacaatgctg ctgtaatcat ccgtgatgat aaaactcctc gcggaactcg tatctttggc 300
 ccagttgcac gcgaattgcg tgagggtggc tacatgaaga tcgtatcact tgcaccagaa 360
 gtacttttaa 369

<210> SEQ ID NO 110
 <211> LENGTH: 122
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 110
 Met Ile Gln Gln Glu Thr Arg Leu Lys Val Ala Asp Asn Ser Gly Ala
 1 5 10 15
 Arg Glu Ile Leu Thr Ile Lys Val Leu Gly Gly Ser Gly Arg Lys Phe
 20 25 30
 Ala Asn Ile Gly Asp Val Ile Val Ala Ser Val Lys Gln Ala Thr Pro
 35 40 45

Gly	Gly	Ala	Val	Lys	Lys	Gly	Asp	Val	Val	Lys	Ala	Val	Ile	Val	Arg
50						55					60				
Thr	Lys	Thr	Gly	Ala	Arg	Arg	Pro	Asp	Gly	Ser	Tyr	Ile	Lys	Phe	Asp
65					70					75					80
Asp	Asn	Ala	Ala	Val	Ile	Ile	Arg	Asp	Asp	Lys	Thr	Pro	Arg	Gly	Thr
				85					90					95	
Arg	Ile	Phe	Gly	Pro	Val	Ala	Arg	Glu	Leu	Arg	Glu	Gly	Gly	Tyr	Met
			100					105					110		
Lys	Ile	Val	Ser	Leu	Ala	Pro	Glu	Val	Leu						
		115					120								

<210> SEQ ID NO 111
 <211> LENGTH: 834
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 111

gtgggtatta	aagtttataa	accaacgaca	aatggccgtc	gtaacatgac	ttctttggat	60
ttcgcgga	tcacaacaag	cacgcctgag	aaatcattgc	ttgtttctct	taagagcaaa	120
gctggtcgta	acaacaatgg	tcgcatcaca	gttcgtcacc	aaggtgggtg	acacaaacgt	180
cattaccgtt	tgatcgactt	caaacgtaac	aaagatggcg	ttgaagcagt	tgtaaaaaca	240
atcgaatacg	atccaaaccg	tactgcaaac	atcgcaactt	tacattacac	tgacgggtgtg	300
aaagcttaca	tcattgcacc	taaaggtctt	gaagtaggtc	aacgtattgt	ttctgggtcca	360
gatgcagata	tcaaagttgg	taacgcactt	ccattagcaa	acattcctgt	cggtacagtt	420
gttcacaata	ttgagttgaa	acctggtaaa	ggtggagaac	ttgttcgtgc	agctggagct	480
tctgctcaag	tacttgggtca	agaaggtaaa	tacgttcttg	ttcgtcttca	atcaggcgaa	540
gttcgtatga	ttcttgggtac	atgccgtgca	actatcggtg	ctgttggtaa	cgaacaacaa	600
tcacttggtta	acattgggtaa	agcaggacgt	agccgttgga	aaggtatccg	cccaacagtt	660
cgtgggttctg	taatgaaccc	taacgatcac	ccacacggtg	gtggtgaagg	taaagcacca	720
gttggacgta	aagcgccatc	aactccatgg	ggtaaaccag	cgcttggtct	taaaactcgt	780
aacaagaaa	ctaaatcaga	caaacttatc	gttcgtcgtc	gtaacgaaaa	ataa	834

<210> SEQ ID NO 112
 <211> LENGTH: 277
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 112

Met	Gly	Ile	Lys	Val	Tyr	Lys	Pro	Thr	Thr	Asn	Gly	Arg	Arg	Asn	Met
1			5						10					15	
Thr	Ser	Leu	Asp	Phe	Ala	Glu	Ile	Thr	Thr	Ser	Thr	Pro	Glu	Lys	Ser
		20						25				30			
Leu	Leu	Val	Ser	Leu	Lys	Ser	Lys	Ala	Gly	Arg	Asn	Asn	Asn	Gly	Arg
		35				40					45				
Ile	Thr	Val	Arg	His	Gln	Gly	Gly	Gly	His	Lys	Arg	His	Tyr	Arg	Leu
	50				55				60						
Ile	Asp	Phe	Lys	Arg	Asn	Lys	Asp	Gly	Val	Glu	Ala	Val	Val	Lys	Thr
65				70					75					80	
Ile	Glu	Tyr	Asp	Pro	Asn	Arg	Thr	Ala	Asn	Ile	Ala	Leu	Val	His	Tyr
			85				90						95		
Thr	Asp	Gly	Val	Lys	Ala	Tyr	Ile	Ile	Ala	Pro	Lys	Gly	Leu	Glu	Val
		100					105					110			
Gly	Gln	Arg	Ile	Val	Ser	Gly	Pro	Asp	Ala	Asp	Ile	Lys	Val	Gly	Asn
	115					120					125				
Ala	Leu	Pro	Leu	Ala	Asn	Ile	Pro	Val	Gly	Thr	Val	Val	His	Asn	Ile
	130				135					140					
Glu	Leu	Lys	Pro	Gly	Lys	Gly	Gly	Glu	Leu	Val	Arg	Ala	Ala	Gly	Ala
145				150					155					160	
Ser	Ala	Gln	Val	Leu	Gly	Gln	Glu	Gly	Lys	Tyr	Val	Leu	Val	Arg	Leu

Gln	Ser	Gly	Glu	Val	Arg	Met	Ile	Leu	Gly	Thr	Cys	Arg	Ala	Thr	Ile
			180					185					190		
Gly	Thr	Val	Gly	Asn	Glu	Gln	Gln	Ser	Leu	Val	Asn	Ile	Gly	Lys	Ala
		195					200					205			
Gly	Arg	Ser	Arg	Trp	Lys	Gly	Ile	Arg	Pro	Thr	Val	Arg	Gly	Ser	Val
	210					215					220				
Met	Asn	Pro	Asn	Asp	His	Pro	His	Gly	Gly	Gly	Glu	Gly	Lys	Ala	Pro
225				230						235					240
Val	Gly	Arg	Lys	Ala	Pro	Ser	Thr	Pro	Trp	Gly	Lys	Pro	Ala	Leu	Gly
			245						250					255	
Leu	Lys	Thr	Arg	Asn	Lys	Lys	Ala	Lys	Ser	Asp	Lys	Leu	Ile	Val	Arg
		260						265					270		
Arg	Arg	Asn	Glu	Lys											
		275													

<210> SEQ ID NO 113

<211> LENGTH: 627

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 113

atgacaaaag	gaatcttagg	gaaaaaagtg	ggaatgactc	aaattttcac	tgaatcaggc	60
gaattcatcc	ctgttactgt	cattgaagca	actccaaacg	ttgtgcttca	agttaaaact	120
gttgaaacag	acggttatga	agcagttcag	gttggttttg	atgacaaacg	tgaagtcttg	180
agtaacaaac	ctgccaaaag	ccatgttgca	aaagcaaaca	cagctcctaa	gcgcttcatt	240
cgtgaattca	aaaacattga	aggcttagaa	gttggtgcag	aattatctgt	agaacaattt	300
gaagctgggtg	atgttggtga	cgtcacaggg	atatcaaaaag	gtaaaagggtt	ccaagggtgtt	360
atcaaacgcc	atggtcaatc	acgtggctct	atggctcacg	gttctcgtta	ccatcgtcgc	420
ccagggttcta	tgggacctgt	tgcgcctaac	cgcgttttca	aaaacaaacg	cttggcagga	480
cgtatgggtg	gtaaccgtgt	aacagttcaa	aaccttgaaa	ttgtacaagt	tatcccagaa	540
aagaacgtta	tccttggtta	aggtaacgta	ccagggtgcta	agaaatctct	tatcactatc	600
aagtcagcag	ttaaagctgc	taaataa				627

<210> SEQ ID NO 114

<211> LENGTH: 208

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 114

Met	Thr	Lys	Gly	Ile	Leu	Gly	Lys	Lys	Val	Gly	Met	Thr	Gln	Ile	Phe
1				5					10					15	
Thr	Glu	Ser	Gly	Glu	Phe	Ile	Pro	Val	Thr	Val	Ile	Glu	Ala	Thr	Pro
		20					25					30			
Asn	Val	Val	Leu	Gln	Val	Lys	Thr	Val	Glu	Thr	Asp	Gly	Tyr	Glu	Ala
		35				40					45				
Val	Gln	Val	Gly	Phe	Asp	Asp	Lys	Arg	Glu	Val	Leu	Ser	Asn	Lys	Pro
	50				55				60						
Ala	Lys	Gly	His	Val	Ala	Lys	Ala	Asn	Thr	Ala	Pro	Lys	Arg	Phe	Ile
65				70					75					80	
Arg	Glu	Phe	Lys	Asn	Ile	Glu	Gly	Leu	Glu	Val	Gly	Ala	Glu	Leu	Ser
			85				90						95		
Val	Glu	Gln	Phe	Glu	Ala	Gly	Asp	Val	Val	Asp	Val	Thr	Gly	Ile	Ser
		100					105					110			
Lys	Gly	Lys	Gly	Phe	Gln	Gly	Val	Ile	Lys	Arg	His	Gly	Gln	Ser	Arg
		115				120					125				
Gly	Pro	Met	Ala	His	Gly	Ser	Arg	Tyr	His	Arg	Arg	Pro	Gly	Ser	Met
	130					135				140					
Gly	Pro	Val	Ala	Pro	Asn	Arg	Val	Phe	Lys	Asn	Lys	Arg	Leu	Ala	Gly

145		150		155		160									
Arg	Met	Gly	Gly	Asn	Arg	Val	Thr	Val	Gln	Asn	Leu	Glu	Ile	Val	Gln
		165		170		175									
Val	Ile	Pro	Glu	Lys	Asn	Val	Ile	Leu	Val	Lys	Gly	Asn	Val	Pro	Gly
		180		185		190									
Ala	Lys	Lys	Ser	Leu	Ile	Thr	Ile	Lys	Ser	Ala	Val	Lys	Ala	Ala	Lys
		195		200		205									

<210> SEQ ID NO 115
 <211> LENGTH: 309
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 115

atggcaaaaca	aaaaaatccg	tatccgtttg	aaagcgtacg	aacaccgtac	acttgataca	60
gcggcagaaa	aaatcgttga	aactgcaaca	cgtacagggtg	ctacagttgc	tggaaccagtt	120
ccatttccaa	ctgaacgcag	tctttacaca	attattcgtg	cgactcacia	atacaaagat	180
tctcgcaaac	aatttgaaat	gcgtacacac	aaacgtttgg	tagacatcat	caatccaaca	240
caaaaaactg	ttgatgcttt	gatgaaactt	gatcttccaa	gtggtgtcaa	cgtagaaatc	300
aaacttttaa						309

<210> SEQ ID NO 116
 <211> LENGTH: 102
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 116

Met	Ala	Asn	Lys	Lys	Ile	Arg	Ile	Arg	Leu	Lys	Ala	Tyr	Glu	His	Arg
1			5						10				15		
Thr	Leu	Asp	Thr	Ala	Ala	Glu	Lys	Ile	Val	Glu	Thr	Ala	Thr	Arg	Thr
		20					25					30			
Gly	Ala	Thr	Val	Ala	Gly	Pro	Val	Pro	Leu	Pro	Thr	Glu	Arg	Ser	Leu
		35				40					45				
Tyr	Thr	Ile	Ile	Arg	Ala	Thr	His	Lys	Tyr	Lys	Asp	Ser	Arg	Glu	Gln
	50				55				60						
Phe	Glu	Met	Arg	Thr	His	Lys	Arg	Leu	Val	Asp	Ile	Ile	Asn	Pro	Thr
65				70					75				80		
Gln	Lys	Thr	Val	Asp	Ala	Leu	Met	Lys	Leu	Asp	Leu	Pro	Ser	Gly	Val
			85					90					95		
Asn	Val	Glu	Ile	Lys	Leu										
			100												

<210> SEQ ID NO 117
 <211> LENGTH: 372
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 117

atgaagaagc	ctagtattgt	tcaattaaat	aatcattata	ttaagaaaga	gaatctcaaa	60
aaaaaatttg	aagaagaaga	atctcaaaaa	agaaatcggt	ttatgggatg	gatccttgta	120
agtatgatgt	ttttatttat	tttgccaact	tataatcttg	tcaaaagtta	tgttgatttt	180
gaaaagcaaa	atcaacaggt	ggttaaatta	aaaaaagagt	ataatgaatt	gtcagagagt	240
acaaaaaaag	aaaaacaatt	agcagaacga	ctaaaagatg	ataattttgt	caaaaaatat	300
gctaggggcaa	aatactatgt	atcgcggtgaa	ggagaaatga	tttatcctat	tccaggacta	360
ttaccaaaat	ga					372

<210> SEQ ID NO 118
 <211> LENGTH: 123
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 118

```
Met Lys Lys Pro Ser Ile Val Gln Leu Asn Asn His Tyr Ile Lys Lys
 1           5           10           15
Glu Asn Leu Lys Lys Lys Phe Glu Glu Glu Glu Ser Gln Lys Arg Asn
          20           25           30
Arg Phe Met Gly Trp Ile Leu Val Ser Met Met Phe Leu Phe Ile Leu
          35           40           45
Pro Thr Tyr Asn Leu Val Lys Ser Tyr Val Asp Phe Glu Lys Gln Asn
          50           55           60
Gln Gln Val Val Lys Leu Lys Lys Glu Tyr Asn Glu Leu Ser Glu Ser
65           70           75           80
Thr Lys Lys Glu Lys Gln Leu Ala Glu Arg Leu Lys Asp Asp Asn Phe
          85           90           95
Val Lys Lys Tyr Ala Arg Ala Lys Tyr Tyr Leu Ser Arg Glu Gly Glu
          100          105          110
Met Ile Tyr Pro Ile Pro Gly Leu Leu Pro Lys
          115          120
```

<210> SEQ ID NO 119

<211> LENGTH: 1224

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 119

```
atgccaaagta tgaaacatat cttaaaatcc ttaagtattt tactaattgg attttttagga      60
ggattaatag caattattac attcaataat ctctaccac attctccatc aaaaataaat      120
tcaggtaagg caacaactag taatatgggtt ttaacaaca caaccaatac tactaaagct      180
gtcaaagctg ttcaaaatgc agttgtatca gttattaatt atcaagataa cccttcttca      240
tcccttttcta acccttatac aaaactcttt ggagaagggc gttcaaaaga gaataaggat      300
gctgaattat ctatttttag tgaaggatct ggggtcattt atcgaaaaga tggcaactcc      360
gcttacgttg ttactaataa ccatgttatc gacggagcta aacgaattga aattcttatg      420
gcagacggat ctaaagttgt tgggtgaatta gttggagctg atacttattc ggatttagct      480
gttggttaaga tctcttcaga taagataaaa acagtagctg aatttgcaga ttctacaaaa      540
ctaaatgttg gagaagttgc tattgctatc ggcagcccac taggaacaca atacgctaata      600
tctgttactc aaggaaatcgt ctctagttta agtcgtactg taacttttaa aaacgagaat      660
ggtgagactg tctcaacaaa tgctattcag acagatgctg ctattaaccc tggaaactct      720
ggtggaccac taattaatat tgagggggcaa gtaatcggaa ttaattcaag taaaatttct      780
tctaccccaa ctggtagcaa cggtaatagt ggtgctgttg aaggaattgg ttttgctatc      840
ccatctactg atgttattaa aattattaaa caactagaaa ctaatggtga agttatcaga      900
cctgctcttg gaatatccat ggtcaattta aatgacttat ccacaaatgc tcttagtcaa      960
attaatattc caactagtgt aactggtggt attgtagtag cagaagttaa ggaaggaatg     1020
ccggcatctg gcaaacttgc tcagtacgat gtgattacag aaattgatgg caaaacagtt     1080
aattcaatta gtgatttaca aagtagtcta tacggacacg atattaatga tactattaaa     1140
gtaacttttt atagaggaac tacaaagaaa aaagcagata tcaaattaac aaaaactact     1200
caagatttga ctaaaacgca gtaa                                     1224
```

<210> SEQ ID NO 120

<211> LENGTH: 407

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 120

```
Met Pro Ser Met Lys His Ile Leu Lys Ser Leu Ser Ile Leu Leu Ile
 1           5           10           15
Gly Phe Leu Gly Gly Leu Ile Ala Ile Thr Phe Asn Asn Leu Tyr
          20           25           30
Pro His Ser Pro Ser Lys Ile Asn Ser Gly Lys Ala Thr Thr Ser Asn
          35           40           45
Met Val Phe Asn Asn Thr Thr Asn Thr Thr Lys Ala Val Lys Ala Val
```

50		55		60
Gln Asn Ala Val Val Ser Val Ile Asn Tyr Gln Asp Asn Pro Ser Ser				
65		70		75
Ser Leu Ser Asn Pro Tyr Thr Lys Leu Phe Gly Glu Gly Arg Ser Lys				
	85		90	95
Glu Asn Lys Asp Ala Glu Leu Ser Ile Phe Ser Glu Gly Ser Gly Val				
	100		105	110
Ile Tyr Arg Lys Asp Gly Asn Ser Ala Tyr Val Val Thr Asn Asn His				
	115		120	125
Val Ile Asp Gly Ala Lys Arg Ile Glu Ile Leu Met Ala Asp Gly Ser				
	130		135	140
Lys Val Val Gly Glu Leu Val Gly Ala Asp Thr Tyr Ser Asp Leu Ala				
145		150		155
Val Val Lys Ile Ser Ser Asp Lys Ile Lys Thr Val Ala Glu Phe Ala				
	165		170	175
Asp Ser Thr Lys Leu Asn Val Gly Glu Val Ala Ile Ala Ile Gly Ser				
	180		185	190
Pro Leu Gly Thr Gln Tyr Ala Asn Ser Val Thr Gln Gly Ile Val Ser				
	195		200	205
Ser Leu Ser Arg Thr Val Thr Leu Lys Asn Glu Asn Gly Glu Thr Val				
210		215		220
Ser Thr Asn Ala Ile Gln Thr Asp Ala Ala Ile Asn Pro Gly Asn Ser				
225		230		235
Gly Gly Pro Leu Ile Asn Ile Glu Gly Gln Val Ile Gly Ile Asn Ser				
	245		250	255
Ser Lys Ile Ser Ser Thr Pro Thr Gly Ser Asn Gly Asn Ser Gly Ala				
	260		265	270
Val Glu Gly Ile Gly Phe Ala Ile Pro Ser Thr Asp Val Ile Lys Ile				
	275		280	285
Ile Lys Gln Leu Glu Thr Asn Gly Glu Val Ile Arg Pro Ala Leu Gly				
290		295		300
Ile Ser Met Val Asn Leu Asn Asp Leu Ser Thr Asn Ala Leu Ser Gln				
305		310		315
Ile Asn Ile Pro Thr Ser Val Thr Gly Gly Ile Val Val Ala Glu Val				
	325		330	335
Lys Glu Gly Met Pro Ala Ser Gly Lys Leu Ala Gln Tyr Asp Val Ile				
	340		345	350
Thr Glu Ile Asp Gly Lys Thr Val Asn Ser Ile Ser Asp Leu Gln Ser				
	355		360	365
Ser Leu Tyr Gly His Asp Ile Asn Asp Thr Ile Lys Val Thr Phe Tyr				
370		375		380
Arg Gly Thr Thr Lys Lys Lys Ala Asp Ile Lys Leu Thr Lys Thr Thr				
385		390		395
Gln Asp Leu Thr Lys Thr Gln				400
	405			

<210> SEQ ID NO 121

<211> LENGTH: 1560

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 121

gtgatcgagt taaacgatga attcatccga aaagagacga tagaactggc caacgatggc	60
ccacgagtac acaccactca atatgaaact aaagtacctc ggcttcataa atgctatctg	120
cttttcttta gcattattat cagttcttta acaattgcag tacctttttt aacagatgca	180
gccaatgggc ttcagtccca aaacttatat ataggaatga tgttaacgaa ggggcaactt	240
ccctatagtg ctgctttttac aacaggaggg ctcttttact ttgttatcat tgcattaagt	300
tattatttgg gatcgacact ttggctagtc tttgttcagg tgttttgttt ttacttatct	360

ggtttatatc	tttataaaact	cattaattat	atgacaggct	ttcaaaaagt	ggctttaact	420
ttttcaatta	gctactat	ttt	attatctg	ttt	gtatcctact	480
caactggcta	tgccatttat	attaatatcg	gcttgggttt	taactaagta	ttttgcctgt	540
ttagtgaaag	atgaggcatt	tattcttttt	ggctttgtag	gtgctcttgc	aatgctaatt	600
gacccgagta	cccttatctt	ttgggtctttt	gcttgtgtga	cagttttttc	ttataatata	660
agccaaaagc	atcttgcaag	agggtttttat	caactgctag	cttcgatttt	tggaatgatt	720
ttagtttttt	acacagcagg	atatttcatt	ttgaacttac	aagtgcataa	tccttatatta	780
tcacaaacga	tgatttatcc	ttttactttt	tttaaatcag	gaaacttatc	gttgcttttt	840
ggactggcta	ttcagttg	cttcgctttg	gggcttggtc	ttttgacggg	aatggagaat	900
gtcattaggc	gatttaaaaa	caattctgat	agggtcgtca	agtggctatt	tgatcatggtc	960
attctagaat	ctatacttgt	ggctatat	ttcacaagact	atcgccccta	tcactcttta	1020
cctcttttac	cttttggatt	aattttgact	gctattcctg	ttggctatca	gtatggata	1080
ggattaggtc	agagtagtca	tcgcagacgt	catggtaaaa	atgggtgttg	tcgagtaatg	1140
atgatttatc	ttaagagaca	cttttat	ccaattttaa	ttgtagggac	aataactaatc	1200
tgttctactt	attgtttcat	tagtagtatt	cctcttaatc	aggagcgtga	tcataattgct	1260
agttatttag	aacagaaaact	aaataaaaact	caatctattt	atgtttggga	tgatacttct	1320
aaaattttatt	tggacagtaa	agctaaatct	gtttctcaat	ttagtctctcc	tgacatcaat	1380
acgcaaaaag	agagtcacg	aaaaatatta	gaagatgaac	tattagaaaa	taaggctgct	1440
tatatcgttg	ttaatcgcta	taaaaacctg	cctaaaaatca	ttcaaaaagt	attatctact	1500
aattacaaag	tagataaaca	gataacgaca	aaaagt	ttgtttatca	gaaaaagtaa	1560

<210> SEQ ID NO 122

<211> LENGTH: 519

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 122

Met	Ile	Glu	Leu	Asn	Asp	Glu	Phe	Ile	Arg	Lys	Glu	Thr	Ile	Glu	Leu
1				5					10					15	
Ala	Asn	Asp	Gly	Pro	Arg	Val	His	Thr	Thr	Gln	Tyr	Glu	Thr	Lys	Val
			20					25					30		
Pro	Arg	Leu	His	Lys	Cys	Tyr	Leu	Phe	Phe	Ser	Ile	Ile	Ile	Ser	
		35					40				45				
Ser	Leu	Thr	Ile	Ala	Val	Pro	Phe	Leu	Thr	Asp	Ala	Ala	Asn	Gly	Leu
		50				55				60					
Gln	Ser	Gln	Asn	Leu	Tyr	Ile	Gly	Met	Met	Leu	Thr	Lys	Gly	Gln	Leu
65					70					75					80
Pro	Tyr	Ser	Ala	Ala	Phe	Thr	Thr	Gly	Gly	Leu	Phe	Tyr	Phe	Val	Ile
			85					90						95	
Ile	Ala	Leu	Ser	Tyr	Tyr	Leu	Gly	Ser	Thr	Leu	Trp	Leu	Val	Phe	Val
			100					105					110		
Gln	Val	Phe	Cys	Phe	Tyr	Leu	Ser	Gly	Leu	Tyr	Leu	Tyr	Lys	Leu	Ile
		115					120					125			
Asn	Tyr	Met	Thr	Gly	Phe	Gln	Lys	Val	Ala	Leu	Thr	Phe	Ser	Ile	Ser
		130				135					140				
Tyr	Tyr	Leu	Leu	Ser	Val	Ser	Leu	Gly	Phe	Gly	Gly	Leu	Tyr	Pro	Thr
145					150					155					160
Gln	Leu	Ala	Met	Pro	Phe	Ile	Leu	Ile	Ser	Ala	Trp	Phe	Leu	Thr	Lys
			165						170					175	
Tyr	Phe	Ala	Cys	Leu	Val	Lys	Asp	Glu	Ala	Phe	Ile	Leu	Phe	Gly	Phe
		180						185				190			
Val	Gly	Ala	Leu	Ala	Met	Leu	Ile	Asp	Pro	Ser	Thr	Leu	Ile	Phe	Trp
		195					200					205			
Ser	Phe	Ala	Cys	Val	Thr	Val	Phe	Ser	Tyr	Asn	Ile	Ser	Gln	Lys	His
		210				215					220				
Leu	Ala	Arg	Gly	Phe	Tyr	Gln	Leu	Leu	Ala	Ser	Ile	Phe	Gly	Met	Ile
225					230					235					240
Leu	Val	Phe	Tyr	Thr	Ala	Gly	Tyr	Phe	Ile	Leu	Asn	Leu	Gln	Val	Leu

				245					250					255			
Asn	Pro	Tyr	Leu	Ser	Gln	Thr	Met	Ile	Tyr	Pro	Phe	Thr	Phe	Phe	Lys		
			260					265					270				
Ser	Gly	Asn	Leu	Ser	Leu	Leu	Phe	Gly	Leu	Ala	Ile	Gln	Leu	Phe	Phe		
		275					280					285					
Ala	Leu	Gly	Leu	Gly	Leu	Leu	Thr	Gly	Met	Glu	Asn	Val	Ile	Arg	Arg		
	290					295				300							
Phe	Lys	Asn	Asn	Ser	Asp	Arg	Val	Val	Lys	Trp	Leu	Phe	Val	Met	Val		
305				310					315					320			
Ile	Leu	Glu	Ser	Ile	Leu	Val	Ala	Ile	Phe	Ser	Gln	Asp	Tyr	Arg	Pro		
			325					330					335				
Tyr	His	Leu	Leu	Pro	Leu	Leu	Pro	Phe	Gly	Leu	Ile	Leu	Thr	Ala	Ile		
		340						345					350				
Pro	Val	Gly	Tyr	Gln	Tyr	Gly	Ile	Gly	Leu	Gly	Gln	Ser	Ser	His	Arg		
	355					360					365						
Arg	Arg	His	Gly	Lys	Asn	Gly	Val	Gly	Arg	Val	Met	Met	Ile	Tyr	Leu		
	370				375					380							
Lys	Arg	His	Phe	Tyr	Leu	Pro	Ile	Leu	Ile	Val	Gly	Thr	Ile	Leu	Ile		
385				390					395					400			
Cys	Ser	Thr	Tyr	Cys	Phe	Ile	Ser	Ser	Ile	Pro	Leu	Asn	Gln	Glu	Arg		
		405				410							415				
Asp	His	Ile	Ala	Ser	Tyr	Leu	Glu	Gln	Lys	Leu	Asn	Lys	Thr	Gln	Ser		
		420				425						430					
Ile	Tyr	Val	Trp	Asp	Asp	Thr	Ser	Lys	Ile	Tyr	Leu	Asp	Ser	Lys	Ala		
	435					440					445						
Lys	Ser	Val	Ser	Gln	Phe	Ser	Ser	Pro	Asp	Ile	Asn	Thr	Gln	Lys	Glu		
	450					455					460						
Ser	His	Arg	Lys	Ile	Leu	Glu	Asp	Glu	Leu	Leu	Glu	Asn	Lys	Ala	Ala		
465				470					475					480			
Tyr	Ile	Val	Val	Asn	Arg	Tyr	Lys	Asn	Leu	Pro	Lys	Ile	Ile	Gln	Lys		
		485						490						495			
Val	Leu	Ser	Thr	Asn	Tyr	Lys	Val	Asp	Lys	Gln	Ile	Thr	Thr	Lys	Ser		
		500						505					510				
Phe	Ile	Val	Tyr	Gln	Lys	Lys											
		515															

<210> SEQ ID NO 123

<211> LENGTH: 3075

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 123

atgacgaagg	gtattcgatt	tcaattgctt	ggcagtcctt	acatttttct	tgatgacaaa	60
gaacaatttt	ttgcctttgc	caaagcaaat	gctctccttt	attacttagt	ggttaatgga	120
tctgttagcc	gcgaggtggc	ggcgagtcta	ctttgggaaa	ataagaacac	gcaaacagcg	180
aaaaagaatt	tacgaaacgc	tatctaccag	gtcaataaaag	tcttgcaagc	tgatgtgatt	240
atttgtccca	atcgcaacct	gctggttttg	aataaaaacac	ttgatatcaa	aacagatatt	300
aacctttttc	tggctgatcc	gctagctcac	ttagaactct	accaagggga	gtttttgcag	360
ggctttttacc	ttaaaagtgg	tgaggaattt	gatcctttggg	tttcaaaaat	gcgtatgcag	420
tatgaacagg	tatacctaaa	agcgtgttac	caaaaaattg	aagaaaagct	ctcttttagat	480
gccattgaag	atgtcgagga	acatttataaa	cagcttattg	aacgtgatga	atttgaagag	540
aaaaattatc	agctcttgat	gaggctttat	cagcagggga	attgtcctgg	taaggatcatc	600
gaaacttatt	atcagttggc	taatgtgttg	gataaggagc	tagggattca	gccaaagtttg	660
caaagccaac	agatttatca	ggaagtggtc	gctaaagatc	gtaatgaacg	caaaatcaag	720
catttttttgc	gcaacagtaa	tcattttttg	gggcggattg	atgagattaa	gcagctggaa	780
aacttttttg	ccaactgttt	ggcctgccaa	gaggtaggag	ctctgctctt	aattggtgat	840
acagggattg	ggaaacgaac	cctagccaga	caggtcttag	ccaatcaaac	ccaaacgttt	900
caaattgtca	cagctaaatg	ttttcgtgaa	gaggctatgg	attccttatt	gccttggcgt	960

aatatcttag	atggcctggg	agatttggtg	attcaaaacc	gcttattgac	caccaaagct	1020
tggaaggctg	ctcttaaacg	ctgttttcct	gtggcaacca	tttttcaaga	agataacaac	1080
caacccttta	tcaaggacca	caccagcttg	ttggtttcct	ttattgttga	tattttacaa	1140
catttggcag	aaatcaaggc	gctggtaatc	cttattgagg	attgtcactg	gatggatgag	1200
gatagtttga	ccttgttgca	acgggtcatg	aatcaattgg	tccactatcc	gattgctttt	1260
gtcttgacca	agcatctagg	aacgactcct	gagctcggtc	tttgtttgaa	tgctttgatg	1320
agtcaagggc	gttttagaaag	catttgtttg	gagcctttta	atcggcaaga	aagtttggtt	1380
tatattaaca	gtcaactggg	tagtcagcca	gtgacggcag	aagaaatgga	gcacctctat	1440
caagccagcc	aaggcaaccc	tttctttttg	tcagaataca	ctcaggccct	actgcgtcac	1500
gaaaaatttg	tgcttttaac	gcctgccatt	aaggctaagt	tggttcttaa	actagctaata	1560
ctaagtagtc	gtgatgacgc	attgttaaac	tatttgcctt	gttgctggag	gcctatccct	1620
ataaatcccc	tcgctcaatt	gatgttactg	cctttagaag	aagtgatcga	gatgggtgat	1680
tttcgtgggc	actactatat	tttggtagaa	gaaagcgtag	gagaggaagt	gttgatttca	1740
tttcgtcagc	ggattattca	actctatagt	tatgaccggt	tatcctttgtc	aaaaaggcgt	1800
ttattgcacg	gacaaattgc	caaacggtta	gaagatttac	tgctattttt	gacaccaagc	1860
cctcacttat	tagatgacat	tgcttacctat	tatcaggaat	cacggcaggt	gattaaggct	1920
ttggaataca	accttaacta	tctagatgct	accttgccat	ttcagcatga	gctgtttccc	1980
atattattcaa	agagtattgg	ctccttgga	aagtcagatc	gtgacctatca	acgcttaatg	2040
gaagagcagt	ttgataagat	tcgtcaaagc	attgcggatt	tggaactgac	ctatgataat	2100
aaccgtgatt	tccagcagtt	gcttattcgt	ttttcttacc	ttgaaggccg	ttatgatatt	2160
cgaacagggg	ggatcaaga	agggattaaa	cacattcaaa	aggtcacgc	tttggcaacc	2220
gagctaaaac	agccctcctt	cttgctagaa	ggctatcgcc	agttaattca	ttactgtatc	2280
caagtggaaa	acaagccaga	aatgcgttat	tacactagtc	tttcattgga	ggcagcgggt	2340
gctgctaatac	attttgaggc	cattgcgatt	agtttgcggt	taaacggtct	ctatcatttg	2400
attattggggg	agttaaatga	ggcagagcgt	ctgcttcaac	agtcgattga	cttcttcaag	2460
gtgacgccag	gcttgcaagc	taactatgcg	attcagattg	ctgctgcctt	agattatttg	2520
ggggagattg	cccagattcg	ctatcagttt	gaaaaggccg	ttgcttatca	aaaacaagcc	2580
attgccttga	ccgaaaacaa	gccagctgag	ttatcggcga	gtatttttta	tattggatta	2640
gggatttcct	acttttat	agctgatttt	gaacaagctg	agcaaactct	gagtttggct	2700
aaggaagcct	tggtcaatca	tagttatcct	tggaagaaaa	cgcaacttga	aatttacctg	2760
gctatgattc	aatggaaaaa	gggcaattat	cagccagcct	tgaccctact	tgattacaga	2820
gaaaccttga	tgtctaggta	tcgcaatccg	cgtgataagg	gcttggtttt	ctatttgatg	2880
gctgtgggtca	agtaccaatt	gatatttcaa	ggagctaccc	taagtcagca	ggaaaaagaa	2940
atggcagacc	acctgttgtc	agaatccttt	gagtattatt	atgagattgc	tagtactaac	3000
ctcaaccctt	accgagattg	tcat ttgggtg	agtgaagtga	acgatttgcg	tcaacaatta	3060
tctgctaaaa	gctaa					3075

<210> SEQ ID NO 124

<211> LENGTH: 1024

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 124

Met	Thr	Lys	Gly	Ile	Arg	Phe	Gln	Leu	Leu	Gly	Ser	Pro	His	Ile	Phe
1				5				10						15	
Leu	Asp	Asp	Lys	Glu	Gln	Phe	Phe	Ala	Phe	Ala	Lys	Ala	Asn	Ala	Leu
			20					25					30		
Leu	Tyr	Tyr	Leu	Val	Val	Asn	Gly	Ser	Val	Ser	Arg	Glu	Val	Ala	Ala
			35				40						45		
Ser	Leu	Leu	Trp	Glu	Asn	Lys	Asn	Thr	Gln	Thr	Ala	Lys	Lys	Asn	Leu
			50			55					60				
Arg	Asn	Ala	Ile	Tyr	Gln	Val	Asn	Lys	Val	Leu	Gln	Ala	Asp	Val	Ile
65					70					75				80	
Ile	Cys	Pro	Asn	Arg	Asn	Leu	Leu	Val	Leu	Asn	Lys	Thr	Leu	Asp	Ile
			85					90						95	
Lys	Thr	Asp	Ile	Asn	Leu	Phe	Leu	Ala	Asp	Pro	Leu	Ala	His	Leu	Glu
			100					105					110		
Leu	Tyr	Gln	Gly	Glu	Phe	Leu	Gln	Gly	Phe	Tyr	Leu	Lys	Ser	Gly	Glu

		115					120				125						
Glu	Phe	Asp	Leu	Trp	Val	Ser	Lys	Met	Arg	Met	Gln	Tyr	Glu	Gln	Val		
	130						135					140					
Tyr	Leu	Lys	Ala	Cys	Tyr	Gln	Lys	Ile	Glu	Glu	Lys	Leu	Ser	Leu	Asp		
145					150					155					160		
Ala	Ile	Glu	Asp	Val	Glu	Glu	His	Leu	Lys	Gln	Leu	Ile	Glu	Arg	Asp		
			165						170					175			
Glu	Phe	Glu	Glu	Lys	Asn	Tyr	Gln	Leu	Leu	Met	Arg	Leu	Tyr	Gln	Gln		
			180					185					190				
Gly	Asn	Cys	Pro	Gly	Lys	Val	Ile	Glu	Thr	Tyr	Tyr	Gln	Leu	Ala	Asn		
	195						200					205					
Val	Leu	Asp	Lys	Glu	Leu	Gly	Ile	Gln	Pro	Ser	Leu	Gln	Ser	Gln	Gln		
	210					215						220					
Ile	Tyr	Gln	Glu	Val	Val	Ala	Lys	Asp	Arg	Asn	Glu	Arg	Lys	Ile	Lys		
225					230					235					240		
His	Phe	Leu	Arg	Asn	Ser	Asn	His	Phe	Leu	Gly	Arg	Ile	Asp	Glu	Ile		
			245					250					255				
Lys	Gln	Leu	Glu	Asn	Phe	Phe	Ala	Asn	Cys	Leu	Ala	Cys	Gln	Glu	Val		
			260					265					270				
Gly	Ala	Leu	Leu	Leu	Ile	Gly	Asp	Thr	Gly	Ile	Gly	Lys	Arg	Thr	Leu		
	275					280						285					
Ala	Arg	Gln	Val	Leu	Ala	Asn	Gln	Thr	Gln	Thr	Phe	Gln	Ile	Val	Thr		
	290				295						300						
Ala	Lys	Cys	Phe	Arg	Glu	Glu	Ala	Met	Asp	Ser	Leu	Leu	Pro	Trp	Arg		
305					310				315					320			
Asn	Ile	Leu	Asp	Gly	Leu	Gly	Asp	Leu	Val	Ile	Gln	Asn	Arg	Leu	Leu		
			325					330					335				
Thr	Thr	Lys	Ala	Trp	Lys	Ala	Ala	Leu	Lys	Arg	Cys	Phe	Pro	Val	Ala		
		340					345						350				
Thr	Ile	Phe	Gln	Glu	Asp	Asn	Asn	Gln	Pro	Phe	Ile	Lys	Asp	His	Thr		
	355					360						365					
Ser	Leu	Leu	Val	Ser	Phe	Ile	Val	Asp	Ile	Leu	Gln	His	Leu	Ala	Glu		
	370					375					380						
Ile	Lys	Ala	Leu	Val	Ile	Leu	Ile	Glu	Asp	Cys	His	Trp	Met	Asp	Glu		
385					390				395					400			
Asp	Ser	Leu	Thr	Leu	Leu	Gln	Arg	Val	Met	Asn	Gln	Leu	Val	His	Tyr		
			405					410					415				
Pro	Ile	Ala	Phe	Val	Leu	Thr	Lys	His	Leu	Gly	Thr	Thr	Pro	Glu	Leu		
		420					425						430				
Gly	Leu	Cys	Leu	Asn	Ala	Leu	Met	Ser	Gln	Gly	Arg	Leu	Glu	Ser	Ile		
	435					440						445					
Cys	Leu	Glu	Pro	Phe	Asn	Arg	Gln	Glu	Ser	Leu	Val	Tyr	Ile	Asn	Ser		
	450				455						460						
Gln	Leu	Gly	Ser	Gln	Pro	Val	Thr	Ala	Glu	Glu	Met	Glu	His	Leu	Tyr		
465					470				475					480			
Gln	Ala	Ser	Gln	Gly	Asn	Pro	Phe	Phe	Leu	Ser	Glu	Tyr	Thr	Gln	Ala		
			485					490					495				
Leu	Leu	Arg	His	Glu	Lys	Phe	Val	Pro	Leu	Thr	Pro	Ala	Ile	Lys	Ala		
		500					505						510				
Lys	Leu	Gly	Leu	Lys	Leu	Ala	Asn	Leu	Ser	Ser	Arg	Asp	Asp	Ala	Leu		
	515					520						525					
Leu	Asn	Tyr	Leu	Ser	Cys	Cys	Arg	Arg	Pro	Ile	Pro	Leu	Asn	Thr	Leu		
	530				535						540						
Ala	Gln	Leu	Met	Leu	Leu	Pro	Leu	Glu	Glu	Val	Ile	Glu	Met	Val	Asp		
545					550				555					560			
Asn	Leu	Gly	His	Tyr	Tyr	Ile	Leu	Val	Glu	Glu	Ser	Val	Gly	Glu	Glu		
			565					570					575				

Val	Leu	Ile	Ser	Phe	Arg	Gln	Arg	Ile	Gln	Leu	Tyr	Ser	Tyr	Asp	
			580					585				590			
Arg	Leu	Ser	Leu	Ser	Lys	Arg	Arg	Leu	Leu	His	Gly	Gln	Ile	Ala	Lys
		595					600					605			
Arg	Leu	Glu	Asp	Leu	Leu	Pro	Ile	Leu	Thr	Pro	Ser	Pro	His	Leu	Leu
	610					615					620				
Asp	Asp	Ile	Ala	Tyr	His	Tyr	Gln	Glu	Ser	Arg	Gln	Val	Ile	Lys	Ala
625					630					635					640
Leu	Glu	Tyr	Asn	Leu	Asn	Tyr	Leu	Asp	Ala	Thr	Leu	Pro	Phe	Gln	His
				645					650					655	
Glu	Leu	Phe	Pro	Ile	Tyr	Ser	Lys	Ser	Ile	Gly	Ser	Leu	Glu	Lys	Ser
			660					665					670		
Asp	Arg	Asp	His	Gln	Arg	Leu	Met	Glu	Glu	Gln	Phe	Asp	Lys	Ile	Arg
		675					680					685			
Gln	Ser	Ile	Ala	Asp	Leu	Glu	Leu	Thr	Tyr	Asp	Asn	Asn	Arg	Asp	Phe
		690				695					700				
Gln	Gln	Leu	Leu	Ile	Arg	Phe	Ser	Tyr	Leu	Glu	Gly	Arg	Tyr	Asp	Ile
705				710						715					720
Arg	Thr	Gly	Arg	Tyr	Gln	Glu	Gly	Ile	Lys	His	Ile	Gln	Lys	Val	Ile
				725					730					735	
Ala	Leu	Ala	Thr	Glu	Leu	Lys	Gln	Pro	Ser	Phe	Leu	Leu	Glu	Gly	Tyr
			740					745					750		
Arg	Gln	Leu	Ile	His	Tyr	Cys	Ile	Gln	Val	Glu	Asn	Lys	Pro	Glu	Met
		755					760					765			
Arg	Tyr	Tyr	Thr	Ser	Leu	Ser	Leu	Glu	Ala	Ala	Val	Ala	Ala	Asn	His
	770					775					780				
Phe	Glu	Ala	Ile	Ala	Ile	Ser	Leu	Arg	Leu	Asn	Gly	Leu	Tyr	His	Leu
785					790					795					800
Ile	Ile	Gly	Glu	Leu	Asn	Glu	Ala	Glu	Arg	Leu	Leu	Gln	Gln	Ser	Ile
				805					810					815	
Asp	Phe	Phe	Lys	Val	Thr	Pro	Gly	Leu	Gln	Ala	Asn	Tyr	Ala	Ile	Gln
			820					825					830		
Ile	Ala	Ala	Ala	Leu	Asp	Tyr	Leu	Gly	Glu	Ile	Ala	Gln	Ile	Arg	Tyr
		835					840					845			
Gln	Phe	Glu	Lys	Ala	Val	Ala	Tyr	Gln	Lys	Gln	Ala	Ile	Ala	Leu	Thr
	850					855					860				
Glu	Asn	Lys	Pro	Ala	Glu	Leu	Ser	Ala	Ser	Ile	Phe	Tyr	Ile	Gly	Leu
865					870					875					880
Gly	Ile	Ser	Tyr	Phe	Tyr	Leu	Ala	Asp	Phe	Glu	Gln	Ala	Glu	Gln	Ile
				885					890					895	
Leu	Ser	Leu	Ala	Lys	Glu	Ala	Leu	Val	Asn	His	Ser	Tyr	Pro	Trp	Lys
			900					905					910		
Glu	Thr	Gln	Leu	Glu	Ile	Tyr	Leu	Ala	Met	Ile	Gln	Trp	Lys	Lys	Gly
		915					920					925			
Asn	Tyr	Gln</													

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<210> SEQ ID NO 125
<211> LENGTH: 561
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 125
atgtctctaa ttggaaaaga aattgctgaa ttttcagctc aagcttatca cgatggaaaa      60
ttcatcactg ttacaaatga agacgttaaa ggaaaatggg cagttttttg tttctaccca      120
gcgacttttt catttgtttg cccaactgaa ctcggtgacc ttcaagagca atacgaaaca      180
ctgaaatctc ttggtgtaga agtttattct gtctctactg atactcattt tgttcataaa      240
gcttggcatg atgattcaga tgtggttggc actatcacat accctatgat tggtgaccct      300
tcacacctta tttcacaagc ctttgaagtg cttggcgaag acggacttgc tcaacgtgga      360
acatttatcg ttgatccaga tggattatc caaatgatgg aaattaatgc tgatggtatt      420
ggacgtgacg ctagcacctt gattgataaa attcacgctg cccaatacgt ccgtaaacad      480
ccaggtgaag tttgtccagc taaatggaaa gaaggcgtg aaactttgac accaagtctt      540
gatttagttg gtaaaattta a                                     561

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<210> SEQ ID NO 126
<211> LENGTH: 186
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 126
Met Ser Leu Ile Gly Lys Glu Ile Ala Glu Phe Ser Ala Gln Ala Tyr
1      5      10      15
His Asp Gly Lys Phe Ile Thr Val Thr Asn Glu Asp Val Lys Gly Lys
20     25     30
Trp Ala Val Phe Cys Phe Tyr Pro Ala Asp Phe Ser Phe Val Cys Pro
35     40     45
Thr Glu Leu Gly Asp Leu Gln Glu Gln Tyr Glu Thr Leu Lys Ser Leu
50     55     60
Gly Val Glu Val Tyr Ser Val Ser Thr Asp Thr His Phe Val His Lys
65     70     75     80
Ala Trp His Asp Asp Ser Asp Val Val Gly Thr Ile Thr Tyr Pro Met
85     90     95
Ile Gly Asp Pro Ser His Leu Ile Ser Gln Ala Phe Glu Val Leu Gly
100    105    110
Glu Asp Gly Leu Ala Gln Arg Gly Thr Phe Ile Val Asp Pro Asp Gly
115    120    125
Ile Ile Gln Met Met Glu Ile Asn Ala Asp Gly Ile Gly Arg Asp Ala
130    135    140
Ser Thr Leu Ile Asp Lys Ile His Ala Ala Gln Tyr Val Arg Lys His
145    150    155    160
Pro Gly Glu Val Cys Pro Ala Lys Trp Lys Glu Gly Ala Glu Thr Leu
165    170    175
Thr Pro Ser Leu Asp Leu Val Gly Lys Ile
180    185

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<210> SEQ ID NO 127
<211> LENGTH: 2445
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 127
atgattatgt attcaacgaa gatgcaagac atttttagac aggcgcagtt ccaagctgct      60
cgcttttgata gccattgcct ggaaacttgg catgttttgt tagctatggt agctgtagat      120
aattcttttag caaatatgat tttaagtga tatgatgcc aagtcgccat agaagaatat      180
gaagctgcag ctatttttagc catgggcaaa acccctaaag aacagttgtc tcgtgtagac      240
ttcagacctc aatctaaaac tttgactaac ttgttagctt ttgcgcaggc tattagccaa      300

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atcactaggg	atcaagaagt	cggctctgag	catgtcttat	ttgctatttt	attgaatcca	360
gatattatgg	cgagtcgttt	gttagaaata	gctggctatc	agataaaaaga	taacggcaat	420
gggcagccgc	gattagctga	cttgcgaaaa	gcaatagaac	gtcatgcagg	ttacagtaag	480
gaaatgatca	aggctattca	cgaactacgt	aagcctaaaa	aaacgaaaac	acaagggacc	540
ttttcagata	tgatgaagcc	accaagtaca	gctgggtgagt	tgagtgattt	cacaagagat	600
ttgactgaaa	tggcaagaca	aggtttgta	gaatcgggtga	ttggacgtga	ccaagaagta	660
tctcgtatga	ttcagggtact	aagtcgtaaa	acgaaaaaca	atcctgtctt	ggtaggtgat	720
gcagggtgttg	gtaaaactgc	gcttgcttat	ggccttgctc	aacggattgc	aaatggcgct	780
attccttatg	aacttaagga	gatgcgtgtc	ctagaattag	acatgatgag	tgtggttagca	840
ggaacccggt	ttcgtgggga	ttttgaagag	cgcatgaatc	aaatcattga	tgatattgaa	900
gctgatggtc	agattattct	ttttgttgat	gaactacata	ctattatggg	ttctggcagt	960
ggtattgaca	gtacacttga	tgcggctaac	attttaaaaac	cagcattatc	gcgcggcact	1020
cttcatatgg	ttggagcaac	aactcaagaa	gaataccaaa	aacatattga	aaaagatgca	1080
gctctttcgc	gtcgttttgc	taaaatatta	attgaagaac	ctaatacaga	agatgcttat	1140
cagattttga	tgggcctaaa	attatcttat	gagacctacc	ataatgtctc	gatatcaaat	1200
gaggcagtta	aaacagctgt	aaaaatggca	caccgttatt	taaccagtaa	aaatctccct	1260
gattcagcta	tgcatttact	agatgaagct	agtgtgctg	tgcaaaacat	ggtgaaaaaa	1320
tcagcacctg	agactttaac	accaatagac	caagctctta	tcaatggtga	tatgaaaaaa	1380
gtatctcgcc	tcttagctaa	agaagcaaaa	ggtcagatga	gaaaaccaac	accggtgaca	1440
gaagatgata	ttttggcaac	cttgagtaag	ttatcgggaa	ttccacttga	aaaactgacg	1500
caagctgata	gtaaaaaata	cctcaattta	gaaaaagaac	tgcataagcg	tgtgattggg	1560
caggatgctg	ctgttacggc	tattttcaaga	gccattcgtc	gtaatcagtc	aggtattcga	1620
acaggaaaac	gtcctatttg	atcatttatg	tttcttggcc	caacaggagt	aggtaagaca	1680
gaactagcaa	aggcccttgc	agaagttctc	tttgatgatg	aagcagcgct	tattcgtttt	1740
gatatgtctg	agtacatgga	aaaattcgca	gcgtctaggc	ttaatggagc	acctcctggt	1800
tatgtcgggt	atgatgaagg	aggatgaactg	acacagaaag	ttagaaataa	accttattca	1860
gtcttgcttt	ttgatgaagt	ggaaaaagca	catcctgata	tttttaacgt	tctccttcaa	1920
gtattagatg	atggtatatt	gactgatagt	cgtgggcgta	aggtcgattt	ttcaaatact	1980
attattatca	tgaccagcaa	tcttggcgca	acagccctgc	gcgatgataa	aacggtcggg	2040
tttgggggtca	aagacattca	ccaagaccat	caagctatgg	agaaacgtat	tttagaagaa	2100
ttaagaaaaa	cttaccgccc	agaatttatc	aatcgtattg	atgaaaaagt	ggtctttcat	2160
agtctgaccc	aagataacat	gcgcgatgtg	gttaaaatca	tggtacagcc	cctgattact	2220
acattggcag	aaaaaggtat	tacccttaaa	attcagcctt	tggccttgaa	acatttgtcc	2280
gaggtcgggt	atgatgagca	tatgggggca	agaccattac	gtcgaacgct	gcaaactgag	2340
atagaagata	agctatcaga	gcttattctt	tctcgagaat	tgacaagtgg	gcatacgcta	2400
aaaattggat	tatcacatgg	caaattaacg	tttcacatag	cttaa		2445

<210> SEQ ID NO 128

<211> LENGTH: 814

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 128

Met	Ile	Met	Tyr	Ser	Thr	Lys	Met	Gln	Asp	Ile	Phe	Arg	Gln	Ala	Gln
1				5				10						15	
Phe	Gln	Ala	Ala	Arg	Phe	Asp	Ser	His	Cys	Leu	Glu	Thr	Trp	His	Val
		20				25						30			
Leu	Leu	Ala	Met	Val	Ala	Val	Asp	Asn	Ser	Leu	Ala	Asn	Met	Ile	Leu
		35				40					45				
Ser	Glu	Tyr	Asp	Ala	Gln	Val	Ala	Ile	Glu	Glu	Tyr	Glu	Ala	Ala	Ala
	50					55					60				
Ile	Leu	Ala	Met	Gly	Lys	Thr	Pro	Lys	Glu	Gln	Leu	Ser	Arg	Val	Asp
65				70					75					80	
Phe	Arg	Pro	Gln	Ser	Lys	Thr	Leu	Thr	Asn	Leu	Leu	Ala	Phe	Ala	Gln
			85					90						95	
Ala	Ile	Ser	Gln	Ile	Thr	Arg	Asp	Gln	Glu	Val	Gly	Ser	Glu	His	Val
			100					105					110		
Leu	Phe	Ala	Ile	Leu	Leu	Asn	Pro	Asp	Ile	Met	Ala	Ser	Arg	Leu	Leu

		115					120				125				
Glu	Ile	Ala	Gly	Tyr	Gln	Ile	Lys	Asp	Asn	Gly	Asn	Gly	Gln	Pro	Arg
	130						135					140			
Leu	Ala	Asp	Leu	Arg	Lys	Ala	Ile	Glu	Arg	His	Ala	Gly	Tyr	Ser	Lys
145					150					155					160
Glu	Met	Ile	Lys	Ala	Ile	His	Glu	Leu	Arg	Lys	Pro	Lys	Lys	Thr	Lys
			165						170						175
Thr	Gln	Gly	Thr	Phe	Ser	Asp	Met	Met	Lys	Pro	Pro	Ser	Thr	Ala	Gly
		180						185					190		
Glu	Leu	Ser	Asp	Phe	Thr	Arg	Asp	Leu	Thr	Glu	Met	Ala	Arg	Gln	Gly
	195						200					205			
Leu	Leu	Glu	Ser	Val	Ile	Gly	Arg	Asp	Gln	Glu	Val	Ser	Arg	Met	Ile
	210					215					220				
Gln	Val	Leu	Ser	Arg	Lys	Thr	Lys	Asn	Asn	Pro	Val	Leu	Val	Gly	Asp
225					230					235					240
Ala	Gly	Val	Gly	Lys	Thr	Ala	Leu	Ala	Tyr	Gly	Leu	Ala	Gln	Arg	Ile
			245						250					255	
Ala	Asn	Gly	Ala	Ile	Pro	Tyr	Glu	Leu	Lys	Glu	Met	Arg	Val	Leu	Glu
	260						265						270		
Leu	Asp	Met	Met	Ser	Val	Val	Ala	Gly	Thr	Arg	Phe	Arg	Gly	Asp	Phe
	275						280					285			
Glu	Glu	Arg	Met	Asn	Gln	Ile	Ile	Asp	Asp	Ile	Glu	Ala	Asp	Gly	Gln
	290				295					300					
Ile	Ile	Leu	Phe	Val	Asp	Glu	Leu	His	Thr	Ile	Met	Gly	Ser	Gly	Ser
305					310					315					320
Gly	Ile	Asp	Ser	Thr	Leu	Asp	Ala	Ala	Asn	Ile	Leu	Lys	Pro	Ala	Leu
			325						330					335	
Ser	Arg	Gly	Thr	Leu	His	Met	Val	Gly	Ala	Thr	Thr	Gln	Glu	Glu	Tyr
	340							345					350		
Gln	Lys	His	Ile	Glu	Lys	Asp	Ala	Ala	Leu	Ser	Arg	Arg	Phe	Ala	Lys
	355						360					365			
Ile	Leu	Ile	Glu	Glu	Pro	Asn	Thr	Glu	Asp	Ala	Tyr	Gln	Ile	Leu	Met
	370				375					380					
Gly	Leu	Lys	Leu	Ser	Tyr	Glu	Thr	Tyr	His	Asn	Val	Ser	Ile	Ser	Asn
385					390					395					400
Glu	Ala	Val	Lys	Thr	Ala	Val	Lys	Met	Ala	His	Arg	Tyr	Leu	Thr	Ser
			405						410					415	
Lys	Asn	Leu	Pro	Asp	Ser	Ala	Ile	Asp	Leu	Leu	Asp	Glu	Ala	Ser	Ala
	420							425					430		
Ala	Val	Gln	Asn	Met	Val	Lys	Lys	Ser	Ala	Pro	Glu	Thr	Leu	Thr	Pro
	435						440					445			
Ile	Asp	Gln	Ala	Leu	Ile	Asn	Gly	Asp	Met	Lys	Lys	Val	Ser	Arg	Leu
	450					455				460					
Leu	Ala	Lys	Glu	Ala	Lys	Gly	Gln	Met	Arg	Lys	Pro	Thr	Pro	Val	Thr
465					470					475					480
Glu	Asp	Asp	Ile	Leu	Ala	Thr	Leu	Ser	Lys	Leu	Ser	Gly	Ile	Pro	Leu
			485						490					495	
Glu	Lys	Leu	Thr	Gln	Ala	Asp	Ser	Lys	Lys	Tyr	Leu	Asn	Leu	Glu	Lys
	500						505						510		
Glu	Leu	His	Lys	Arg	Val	Ile	Gly	Gln	Asp	Ala	Ala	Val	Thr	Ala	Ile
	515						520					525			
Ser	Arg	Ala	Ile	Arg	Arg	Asn	Gln	Ser	Gly	Ile	Arg	Thr	Gly	Lys	Arg
	530					535				540					
Pro	Ile	Gly	Ser	Phe	Met	Phe	Leu	Gly	Pro	Thr	Gly	Val	Gly	Lys	Thr
545					550					555					560
Glu	Leu	Ala	Lys	Ala	Leu	Ala	Glu	Val	Leu	Phe	Asp	Asp	Glu	Ala	Ala
			565						570					575	

Leu	Ile	Arg	Phe	Asp	Met	Ser	Glu	Tyr	Met	Glu	Lys	Phe	Ala	Ala	Ser		
			580					585					590				
Arg	Leu	Asn	Gly	Ala	Pro	Pro	Gly	Tyr	Val	Gly	Tyr	Asp	Glu	Gly	Gly		
		595					600					605					
Glu	Leu	Thr	Gln	Lys	Val	Arg	Asn	Lys	Pro	Tyr	Ser	Val	Leu	Leu	Phe		
	610					615					620						
Asp	Glu	Val	Glu	Lys	Ala	His	Pro	Asp	Ile	Phe	Asn	Val	Leu	Leu	Gln		
625					630					635					640		
Val	Leu	Asp	Asp	Gly	Ile	Leu	Thr	Asp	Ser	Arg	Gly	Arg	Lys	Val	Asp		
			645					650					655				
Phe	Ser	Asn	Thr	Ile	Ile	Ile	Met	Thr	Ser	Asn	Leu	Gly	Ala	Thr	Ala		
		660					665						670				
Leu	Arg	Asp	Asp	Lys	Thr	Val	Gly	Phe	Gly	Val	Lys	Asp	Ile	His	Gln		
	675						680					685					
Asp	His	Gln	Ala	Met	Glu	Lys	Arg	Ile	Leu	Glu	Glu	Leu	Arg	Lys	Thr		
	690					695					700						
Tyr	Arg	Pro	Glu	Phe	Ile	Asn	Arg	Ile	Asp	Glu	Lys	Val	Val	Phe	His		
705					710					715					720		
Ser	Leu	Thr	Gln	Asp	Asn	Met	Arg	Asp	Val	Val	Lys	Ile	Met	Val	Gln		
			725					730					735				
Pro	Leu	Ile	Thr	Thr	Leu	Ala	Glu	Lys	Gly	Ile	Thr	Leu	Lys	Ile	Gln		
		740					745						750				
Pro	Leu	Ala	Leu	Lys	His	Leu	Ser	Glu	Val	Gly	Tyr	Asp	Glu	His	Met		
	755					760						765					
Gly	Ala	Arg	Pro	Leu	Arg	Arg	Thr	Leu	Gln	Thr	Glu	Ile	Glu	Asp	Lys		
	770				775						780						
Leu	Ser	Glu	Leu	Ile	Leu	Ser	Arg	Glu	Leu	Thr	Ser	Gly	His	Thr	Leu		
785					790					795					800		
Lys	Ile	Gly	Leu	Ser	His	Gly	Lys	Leu	Thr	Phe	His	Ile	Ala				
			805						810								

<210> SEQ ID NO 129

<211> LENGTH: 1725

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 129

gtgaactatc	taggttttctt	cgaaaatcca	ttagccattt	atgatataat	agtaaagaaa	60
aacatagaaa	gttgggggtct	gttgatgacc	aaaccatttc	atcataagaa	actaaaacaa	120
ataactataa	tagctgcaac	tagccttttt	ttattcctga	tcggtggtgc	cttttactac	180
tctaaaaatc	attgtattaa	tgcctatctt	aaagctcgat	cggcccaatc	aggaccagtt	240
tttgagaata	tcaaagcata	tctagtctgg	gatgatacta	atgagcagat	cacaaatgac	300
gaggcgatgt	atactaagtt	tagaagggtat	agtcagaaaag	aattgaggca	aaaaaagcag	360
gattttaaag	ccgctagtca	agatagtgcc	gttcaagtaa	agtctgttgg	tcgtcgtttt	420
tggatttttc	ctgattatcg	gattgccata	aaacccatgg	atttaacgat	aaaaacgaat	480
gtgcctcaag	cagacgttct	tttaaataca	aaaaaagttg	ctgtttctga	ttcagaacag	540
ttctcagtca	agcttgatcg	gctaccaacg	gcagaatata	ccgcaagtat	cagaggcaaa	600
cacaacgggc	gaaacattaa	agtcaacaaa	tcatatgatg	gtgataatcc	cgtgctagat	660
ttgagtgtgt	cttttagaac	tttttttggt	acaagcaatg	ctaagcaagg	agatctttac	720
ttcgatgata	accatattgg	cacattaaaa	gatgggtcaat	tacaagtaga	agattaccct	780
gttacagaaa	acgcacaagc	ttatatgaaa	acaacattcc	cagatggtga	gttaagatca	840
caaaaatatg	ctctagctga	tgttgaagaa	ggagcaaccc	tggagatttt	agttacagat	900
cttttagaag	aggacaaggc	aggggagcta	ttagtatcag	cttttgatca	gctgatgcac	960
tacctcagta	caggtaaga	ctcatctaac	ttacgtagcg	tctttgaggc	agggcttagc	1020
aacgcatttt	ataggggatt	gaaagagtcc	ataaaaagcga	aatttcagac	agatacaaga	1080
aaagccagcc	gtctcaatat	tccatctatc	cttttgacaa	caatgactca	agtgggtaaa	1140
acaacttacg	tgcttgattt	cacagctacc	tacgaatttt	tgtatgacaa	gtcaacagat	1200
cctgagcagc	atacctctgg	acatattaat	caagacttga	ctggaaaagt	gactgtaaaa	1260

aaagttggac	agcattacct	tatcagccag	tccggctcca	aaaatattac	tgttgttaaa	1320
gaggacaatc	aactcaaagc	gccatctgtc	tttcctgagt	ctattttggg	aacgtggaca	1380
ggccaagcca	atggtttgag	catccatatg	tctctagcat	cagatggaac	aattacgact	1440
aaagttgaag	atcaaaaagg	caaccgttct	aaagaaactc	ggacagctaa	aattagtaaa	1500
gttgaagaca	aaggcaatgg	tttttatctt	tatacgccag	atcctggaag	tgacataagc	1560
gccttagttc	cagaaggagg	attggggggg	gcaaagtgtc	aatatgctta	tggtttcaaa	1620
atatctggta	aaacagcctc	tccagtgggtg	tggcaggcag	cattaacaca	tgaatttgat	1680
tataccaagc	cacttttcggg	agtaactttg	caaaagcaac	cataa		1725

<210> SEQ ID NO 130
 <211> LENGTH: 574
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 130

Met	Asn	Tyr	Leu	Gly	Phe	Phe	Glu	Asn	Pro	Leu	Ala	Ile	Tyr	Asp	Ile
1				5					10					15	
Ile	Val	Lys	Lys	Asn	Ile	Glu	Ser	Trp	Gly	Leu	Leu	Met	Thr	Lys	Pro
			20					25					30		
Phe	His	His	Lys	Lys	Leu	Lys	Gln	Ile	Thr	Ile	Ile	Ala	Ala	Thr	Ser
			35				40					45			
Leu	Phe	Leu	Phe	Leu	Ile	Gly	Gly	Ala	Phe	Tyr	Tyr	Ser	Lys	Asn	His
			50			55					60				
Cys	Ile	Asn	Ala	Tyr	Leu	Lys	Ala	Arg	Ser	Ala	Gln	Ser	Gly	Pro	Val
65				70				75						80	
Phe	Glu	Asn	Ile	Lys	Ala	Tyr	Leu	Val	Trp	Asp	Asp	Thr	Asn	Glu	Gln
				85				90					95		
Ile	Thr	Asn	Asp	Glu	Ala	Met	Tyr	Thr	Lys	Phe	Arg	Arg	Tyr	Ser	Gln
			100					105					110		
Lys	Glu	Leu	Arg	Gln	Lys	Lys	Gln	Asp	Leu	Lys	Ala	Ala	Ser	Gln	Asp
			115				120					125			
Ser	Ala	Val	Gln	Val	Lys	Ser	Val	Gly	Arg	Arg	Phe	Trp	Ile	Phe	Pro
			130			135					140				
Asp	Tyr	Arg	Ile	Ala	Ile	Lys	Pro	Met	Asp	Leu	Thr	Ile	Lys	Thr	Asn
145				150					155					160	
Val	Pro	Gln	Ala	Asp	Val	Leu	Leu	Asn	Gln	Lys	Lys	Val	Ala	Val	Ser
				165					170					175	
Asp	Ser	Glu	Gln	Phe	Ser	Val	Lys	Leu	Asp	Arg	Leu	Pro	Thr	Ala	Glu
			180				185						190		
Tyr	Thr	Ala	Ser	Ile	Arg	Gly	Lys	His	Asn	Gly	Arg	Asn	Ile	Lys	Val
			195			200						205			
Asn	Lys	Ser	Tyr	Asp	Gly	Asp	Asn	Pro	Val	Leu	Asp	Leu	Ser	Val	Ser
			210		215						220				
Phe	Arg	Thr	Phe	Leu	Val	Thr	Ser	Asn	Ala	Lys	Gln	Gly	Asp	Leu	Tyr
225				230					235					240	
Phe	Asp	Asp	Asn	His	Ile	Gly	Thr	Leu	Lys	Asp	Gly	Gln	Leu	Gln	Val
			245					250					255		
Glu	Asp	Tyr	Pro	Val	Thr	Glu	Asn	Ala	Gln	Ala	Tyr	Met	Lys	Thr	Thr
			260					265					270		
Phe	Pro	Asp	Gly	Glu	Leu	Arg	Ser	Gln	Lys	Tyr	Ala	Leu	Ala	Asp	Val
			275				280					285			
Glu	Glu	Gly	Ala	Thr	Leu	Glu	Ile	Leu	Val	Thr	Asp	Leu	Leu	Glu	Glu
			290			295					300				
Asp	Lys	Ala	Gly	Glu	Leu	Leu	Val	Ser	Ala	Phe	Asp	Gln	Leu	Met	His
305				310						315				320	
Tyr	Leu	Ser	Thr	Gly	Gln	Asp	Ser	Ser	Asn	Leu	Arg	Ser	Val	Phe	Glu
				325					330				335		
Ala	Gly	Ser	Ser	Asn	Ala	Phe	Tyr	Arg	Gly	Leu	Lys	Glu	Ser	Ile	Lys

			340					345					350				
Ala	Lys	Phe	Gln	Thr	Asp	Thr	Arg	Lys	Ala	Ser	Arg	Leu	Asn	Ile	Pro		
		355					360					365					
Ser	Ile	Leu	Leu	Thr	Thr	Met	Thr	Gln	Val	Gly	Lys	Thr	Thr	Tyr	Val		
	370					375					380						
Leu	Asp	Phe	Thr	Ala	Thr	Tyr	Glu	Phe	Leu	Tyr	Asp	Lys	Ser	Thr	Asp		
385					390					395					400		
Pro	Glu	Gln	His	Thr	Ser	Gly	His	Ile	Asn	Gln	Asp	Leu	Thr	Gly	Lys		
			405						410					415			
Val	Thr	Val	Lys	Lys	Val	Gly	Gln	His	Tyr	Leu	Ile	Ser	Gln	Ser	Gly		
		420					425						430				
Ser	Lys	Asn	Ile	Thr	Val	Val	Lys	Glu	Asp	Asn	Gln	Leu	Lys	Ala	Pro		
	435					440						445					
Ser	Val	Phe	Pro	Glu	Ser	Ile	Leu	Gly	Thr	Trp	Thr	Gly	Gln	Ala	Asn		
	450					455					460						
Gly	Leu	Ser	Ile	His	Met	Ser	Leu	Ala	Ser	Asp	Gly	Thr	Ile	Thr	Thr		
465				470						475					480		
Lys	Val	Glu	Asp	Gln	Lys	Gly	Asn	Arg	Ser	Lys	Glu	Thr	Arg	Thr	Ala		
			485				490							495			
Lys	Ile	Ser	Lys	Val	Glu	Asp	Lys	Gly	Asn	Gly	Phe	Tyr	Leu	Tyr	Thr		
		500					505						510				
Pro	Asp	Pro	Gly	Ser	Asp	Ile	Ser	Ala	Leu	Val	Pro	Glu	Gly	Gly	Leu		
	515					520						525					
Gly	Gly	Ala	Asn	Val	Lys	Tyr	Ala	Tyr	Gly	Phe	Lys	Ile	Ser	Gly	Lys		
	530				535						540						
Thr	Ala	Ser	Pro	Val	Val	Trp	Gln	Ala	Ala	Leu	Thr	His	Glu	Phe	Asp		
545				550						555					560		
Tyr	Thr	Lys	Pro	Leu	Ser	Gly	Val	Thr	Leu	Gln	Lys	Gln	Pro				
			565						570								

<210> SEQ ID NO 131

<211> LENGTH: 954

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 131

atgagaaaaag	aggctcaaaa	ggacatgaaa	caaatgaata	aactcattac	aggagtggta	60
acgctggcga	cagtcgtgac	cttatcagct	tgtcaatcat	cacacaacaa	caccaaactc	120
gtctcgatga	aaggagacac	catcactgtc	agtgacttct	acaatgagac	caaaaacaca	180
gaactcgcac	aaaaagccat	gttaagcttg	gtgattagcc	gcgtttttga	gacacaatat	240
gccaaacaaag	tctctgacaa	agaggttgaa	aaagcctata	aacaaaccgc	agaccaatac	300
ggtacatcct	ttaagacagt	cctagcacaa	tcaggcttaa	cgccagaaac	ctataaaaaa	360
caaattcgcc	tcacaaaatt	agtcgaatat	gccgtcaaag	aacaagccaa	aaacgaaacc	420
atctcaaaaa	aagactaccg	tcaggcctat	gacgcttata	ccccaaccat	gaccgcagaa	480
atcatgcagt	ttgaaaaaga	agaggatgcc	aaagcagcgc	ttgaagccgt	caaagctgaa	540
ggggcagact	ttgcagctat	tgccaaaagaa	aaaaccactg	cagccgataa	aaaaacaacc	600
tatacgtttg	actcaggcga	aacaacccta	ccagcagaag	tagttagagc	tgcatcaggc	660
ctcaaagaag	ggaacagatc	agaaatcatc	acagcgcttg	atccagccac	ctcaaaacgc	720
acctaccata	tcatcaaaag	caccaaataa	gcaactaaaa	aagcagactg	gaaagcgtac	780
caaaaacgct	tgaaagacat	catcgtgact	ggcaaattaa	aagaccctga	cttccaaaac	840
aaagtcatcg	ctaaagctct	tgataaagca	aatgtcaaaa	tcaaagacaa	agcatttgcc	900
aatatcttag	cccagtttgc	aaaacctaac	caaaaacaac	ctgccccaaa	atag	954

<210> SEQ ID NO 132

<211> LENGTH: 317

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 132

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 134

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Met Thr Gly Gln Lys Lys Leu Ala Asn Leu Lys Lys Thr Asp Lys Lys
1          5          10          15
Gln Ile Ile Val Arg Lys Thr Val Asp Ala Ser Val Lys Leu Lys Val
20          25          30
Ser Lys Gln Lys Glu His Phe Ile Met Lys Phe Lys Lys Val Leu Val
35          40          45
Ile Pro Ala Leu Ala Leu Ala Ala Thr Cys Phe Leu Thr Ala Cys Gly
50          55          60
Thr Lys Lys Asp Ser Lys Lys Glu Glu Val Lys Glu Ile Lys Met Ser
65          70          75          80
Asp Ile Lys Asp Asp Ala Val Ser Lys Lys Thr Lys Val Val Asp Gly
85          90          95
Glu Glu Val Thr Glu Tyr Thr Thr Lys Asp Gly Asn Val Ile Gln Ile
100          105          110
Pro Ala Gly Asn Glu Glu Gly Met Glu Ser Lys Asp Ala Gly Gly Ser
115          120          125
Gly Ala Pro Ala Lys Asn
130
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<210> SEQ ID NO 135

<211> LENGTH: 1269

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 135

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atgtttcagt taagaaaaaa aatgacgcgc aaacaattag ccttggtgag tgctggagtg      60
ttgacctgtg tggttggtgg tagctacttg ataatgaacc atcaacaaca agaaattgtc      120
tctagtgtca acaaagtaaa agccttaacc ataaaaagaag ccatggaaca aggaaaagat      180
atcagcttga ccttagctgg cgaagtaaca gctaacaaca gcagcaaagt caaaatcgac      240
tcaagtaaa gagaaagtaa agaggtcttt gttaaaaaaag gcgatgttgt caaagtagga      300
caacccttgt ttagctatga aacgtcacag cggttaacgg ctcaaagttc agaatttgat      360
gttcaaacca aagccaatca gctccaagtt gctaaaacca atgcagcatt gaagtgggaa      420
acctacaatc gcaaggtcaa tgaaatcaac accctaaaat ctcgctacaa cactgcacca      480
gatgagagct tactagagca aattcgcagc gcagaagaca gtgtatccca agcactaagc      540
gatgccaaaa cagcagatag cgatgtcaaa accgctcaaa tcgaactcga taaagctaata      600
gctactgcca caacggaaaa aggtaaaacta gagtatgaca ccgttaagtc agacaccgca      660
ggaaccattg ttagtctaaa tactgatttg ccaaatcaat caaaatccaa aaaagaaaat      720
gaaactttta tggaaattat cgacaaatca aaaatgttag tcaaaggtaa cattagttaa      780
tttgaccgtg acaagttaaa aatcgggtcaa aaagtcgaag tgattgaccg caaagacaac      840
tctaaaaaat ggactggaaa agtaacccaa gttggcaacc tcaaagcaga ggaaaaaggc      900
caaggtcaag gccaaggtgg caatgaccaa caagataatc caaaccaagc aaaattccct      960
tatgttattg aacttgacca atcagacaag cagccactca ttggctcaca cacctatggt      1020
aatgtgctca acaatgttcc agaagctggc aagatcgtat tgaaagaaac ctttacaatg      1080
gcagaaaatg gaaaaaccta tgtgtggaaa gttgataaaa acaaggtcaa aaaacaagaa      1140
atcaagacta agcccttctc aaaagggttat gttgaggtaa caagtggctt gactatgcaa      1200
gataagattg ctgagccgct tcttggcatg aaagacggtg tggaggtagg aagtattggt      1260
aaaccttaa                                     1269
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<210> SEQ ID NO 136

<211> LENGTH: 422

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 136

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Met Phe Gln Leu Arg Lys Lys Met Thr Arg Lys Gln Leu Ala Leu Leu
1          5          10          15
Ser Ala Gly Val Leu Thr Cys Val Val Gly Gly Ser Tyr Leu Ile Met
```

			20					25				30					
Asn	His	Gln	Gln	Gln	Glu	Ile	Val	Ser	Ser	Val	Asn	Lys	Val	Lys	Ala		
		35					40					45					
Leu	Thr	Ile	Lys	Glu	Ala	Met	Glu	Gln	Gly	Lys	Asp	Ile	Ser	Leu	Thr		
	50					55					60						
Leu	Ala	Gly	Glu	Val	Thr	Ala	Asn	Asn	Ser	Ser	Lys	Val	Lys	Ile	Asp		
65					70					75					80		
Ser	Ser	Lys	Gly	Glu	Val	Lys	Glu	Val	Phe	Val	Lys	Lys	Gly	Asp	Val		
			85						90					95			
Val	Lys	Val	Gly	Gln	Pro	Leu	Phe	Ser	Tyr	Glu	Thr	Ser	Gln	Arg	Leu		
			100					105					110				
Thr	Ala	Gln	Ser	Ser	Glu	Phe	Asp	Val	Gln	Thr	Lys	Ala	Asn	Gln	Leu		
		115					120					125					
Gln	Val	Ala	Lys	Thr	Asn	Ala	Ala	Leu	Lys	Trp	Glu	Thr	Tyr	Asn	Arg		
	130					135					140						
Lys	Val	Asn	Glu	Ile	Asn	Thr	Leu	Lys	Ser	Arg	Tyr	Asn	Thr	Ala	Pro		
145					150					155					160		
Asp	Glu	Ser	Leu	Leu	Glu	Gln	Ile	Arg	Ser	Ala	Glu	Asp	Ser	Val	Ser		
			165					170						175			
Gln	Ala	Leu	Ser	Asp	Ala	Lys	Thr	Ala	Asp	Ser	Asp	Val	Lys	Thr	Ala		
		180					185					190					
Gln	Ile	Glu	Leu	Asp	Lys	Ala	Asn	Ala	Thr	Ala	Thr	Thr	Glu	Lys	Gly		
	195						200					205					
Lys	Leu	Glu	Tyr	Asp	Thr	Val	Lys	Ser	Asp	Thr	Ala	Gly	Thr	Ile	Val		
	210				215						220						
Ser	Leu	Asn	Thr	Asp	Leu	Pro	Asn	Gln	Ser	Lys	Ser	Lys	Lys	Glu	Asn		
225					230					235					240		
Glu	Thr	Phe	Met	Glu	Ile	Ile	Asp	Lys	Ser	Lys	Met	Leu	Val	Lys	Gly		
			245					250						255			
Asn	Ile	Ser	Glu	Phe	Asp	Arg	Asp	Lys	Leu	Lys	Ile	Gly	Gln	Lys	Val		
		260					265						270				
Glu	Val	Ile	Asp	Arg	Lys	Asp	Asn	Ser	Lys	Lys	Trp	Thr	Gly	Lys	Val		
	275						280					285					
Thr	Gln	Val	Gly	Asn	Leu	Lys	Ala	Glu	Glu	Lys	Gly	Gln	Gly	Gln	Gly		
	290					295					300						
Gln	Gly	Gly	Asn	Asp	Gln	Gln	Asp	Asn	Pro	Asn	Gln	Ala	Lys	Phe	Pro		
305					310					315					320		
Tyr	Val	Ile	Glu	Leu	Asp	Gln	Ser	Asp	Lys	Gln	Pro	Leu	Ile	Gly	Ser		
			325					330						335			
His	Thr	Tyr	Val	Asn	Val	Leu	Asn	Asn	Val	Pro	Glu	Ala	Gly	Lys	Ile		
		340					345					350					
Val	Leu	Lys	Glu	Thr	Phe	Thr	Met	Ala	Glu	Asn	Gly	Lys	Thr	Tyr	Val		
	355					360					365						
Trp	Lys	Val	Asp	Lys	Asn	Lys	Val	Lys	Lys	Gln	Glu	Ile	Lys	Thr	Lys		
	370				375						380						
Pro	Phe	Ser	Lys	Gly	Tyr	Val	Glu	Val	Thr	Ser	Gly	Leu	Thr	Met	Gln		
385					390					395					400		
Asp	Lys	Ile	Ala	Gln	Pro	Leu	Pro	Gly	Met	Lys	Asp	Gly	Met	Glu	Val		
			405					410						415			
Gly	Ser	Ile	Val	Lys	Pro												
		420															

<210> SEQ ID NO 137
 <211> LENGTH: 1140
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 137


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atgcgtagag cagaaaaataa caaacacagc cgctattcca ttcgcaaact gagcgttggg      60
gtaacgagta tagcaattgc gagtctcttt ttaggaaagg ttgcctatgc cgtagatggc      120
atccctccaa tctctcttac tcaaaagact acagccacta catcagaaaa ttggcatcat      180
attgataagg atggccttat tccttttaggt ataagcttag aagctgccaa agaggaattt      240
aaaaaagaag tagaagaatc acgtttatct gaagcacaaa aagaaacgta taaacaaaaa      300
attaaaactg caccagacaa agataagcta ttattcacgt atcatagtga gtatatgaca      360
gccgttaagg atcttccagc gtctactgag tctactactc agccagttga ggcacccgtg      420
caggagacac aggcacagc ttcagattcg atggtgacag gtgattcaac atcagttacg      480
actgattctc ctgaggaaac cccatcttcg gaaagtccag tggccccagc tttatctgag      540
gtccagctc aaccagctga gagtgaggaa ccttcagtag cagcatcttc tgaggaaacc      600
ccatctccat caactccagc ggccccagaa actcctgaag aaccagcagc tccatctcca      660
tcacctgaga gtgaggaaac ttcagtagca gtccttctg aggaaacccc atctccagaa      720
actcctgaag aaccagcagc tccatctcaa ccagctgaga gtgaagaatc ttcagtagca      780
gctacgacaa gcccgctctc atcaactcca gctgaatcag agactcagac gccaccagct      840
gttactaaag actctgataa gccatcttca gcagctgaaa aaccagcagc ctcttcactt      900
gtttcagaac aaaccgttca acaaccaact tcaaagagat cttctgataa aaaagaagag      960
caagaacagt cttactctcc aaatcgctca ttgtcaagac aggttagggc ccatgagtca     1020
ggtaagtact tgccttcaac aggtgaaaaa gcacagccac tctttatagc tactatgact     1080
ttgatgtctc tatttggcag tcttttagtc acaaaacgcc aaaaagaaac taaaaaatag     1140

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<210> SEQ ID NO 138

<211> LENGTH: 379

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 138

```

Met Arg Arg Ala Glu Asn Asn Lys His Ser Arg Tyr Ser Ile Arg Lys
1          5          10          15
Leu Ser Val Gly Val Thr Ser Ile Ala Ile Ala Ser Leu Phe Leu Gly
20          25          30
Lys Val Ala Tyr Ala Val Asp Gly Ile Pro Pro Ile Ser Leu Thr Gln
35          40          45
Lys Thr Thr Ala Thr Thr Ser Glu Asn Trp His His Ile Asp Lys Asp
50          55          60
Gly Leu Ile Pro Leu Gly Ile Ser Leu Glu Ala Ala Lys Glu Glu Phe
65          70          75          80
Lys Lys Glu Val Glu Glu Ser Arg Leu Ser Glu Ala Gln Lys Glu Thr
85          90          95
Tyr Lys Gln Lys Ile Lys Thr Ala Pro Asp Lys Asp Lys Leu Leu Phe
100         105         110
Thr Tyr His Ser Glu Tyr Met Thr Ala Val Lys Asp Leu Pro Ala Ser
115         120         125
Thr Glu Ser Thr Thr Gln Pro Val Glu Ala Pro Val Gln Glu Thr Gln
130         135         140
Ala Ser Ala Ser Asp Ser Met Val Thr Gly Asp Ser Thr Ser Val Thr
145         150         155         160
Thr Asp Ser Pro Glu Glu Thr Pro Ser Ser Glu Ser Pro Val Ala Pro
165         170         175
Ala Leu Ser Glu Ala Pro Ala Gln Pro Ala Glu Ser Glu Glu Pro Ser
180         185         190
Val Ala Ala Ser Ser Glu Glu Thr Pro Ser Pro Ser Thr Pro Ala Ala
195         200         205
Pro Glu Thr Pro Glu Glu Pro Ala Ala Pro Ser Pro Ser Pro Glu Ser
210         215         220
Glu Glu Pro Ser Val Ala Ala Pro Ser Glu Glu Thr Pro Ser Pro Glu
225         230         235         240
Thr Pro Glu Glu Pro Ala Ala Pro Ser Gln Pro Ala Glu Ser Glu Glu
245         250         255

```

Ser	Ser	Val	Ala	Ala	Thr	Thr	Ser	Pro	Ser	Pro	Ser	Thr	Pro	Ala	Glu
			260					265					270		
Ser	Glu	Thr	Gln	Thr	Pro	Pro	Ala	Val	Thr	Lys	Asp	Ser	Asp	Lys	Pro
		275					280					285			
Ser	Ser	Ala	Ala	Glu	Lys	Pro	Ala	Ala	Ser	Ser	Leu	Val	Ser	Glu	Gln
	290					295					300				
Thr	Val	Gln	Gln	Pro	Thr	Ser	Lys	Arg	Ser	Ser	Asp	Lys	Lys	Glu	Glu
305					310					315					320
Gln	Glu	Gln	Ser	Tyr	Ser	Pro	Asn	Arg	Ser	Leu	Ser	Arg	Gln	Val	Arg
			325						330					335	
Ala	His	Glu	Ser	Gly	Lys	Tyr	Leu	Pro	Ser	Thr	Gly	Glu	Lys	Ala	Gln
		340						345					350		
Pro	Leu	Phe	Ile	Ala	Thr	Met	Thr	Leu	Met	Ser	Leu	Phe	Gly	Ser	Leu
	355						360					365			
Leu	Val	Thr	Lys	Arg	Gln	Lys	Glu	Thr	Lys	Lys					
	370					375									

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<210> SEQ ID NO 139
<211> LENGTH: 1635
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 139
ttgattgtgt caaaatacct aaaatacttc tctattatca cggtattttt gactgggctt      60
attttagttg catgtcaaca acaaaagcct caaacaaaag aacgtcagcg caaacaacgt      120
ccaaaagacg aacttgtcgt ttctatgggg gcaaagctcc ctcattgaatt cgatccaaag      180
gaccggttat gagtccacaa tgaagggaat atcactcata gcactctatt gaaacggttct      240
cctgaactag atataaaaag agagcttgct aaacataacc atctctctga agatgggctg      300
acttggtcgt ttgacttgca tgatgatttt aaattctcaa atggtgagcc tgttactgct      360
gatgatgtta agtttactta tgatatgttg aaagcagatg gaaaggcttg ggatctaacc      420
ttcattaaga acgttgaagt agttgggaaa aatcaggtca atatccattt gactgaggcg      480
cattcgacat ttacagcaca gttgactgaa atcccaatcg tccctaaaaa acattacaat      540
gataagtata agagcaatcc tatcggttca ggaccttaca tggtaaaaaga atataaggct      600
ggagaacaag ctatttttgt tcgtaaccct tattggcatg ggaaaaaacc atactttaaa      660
aaatggactt ggggtcttact tgatgaaaac acagcactag cagctttaga atctgggtgat      720
gttgatatga tctacgcaac gccagaactt gctgataaaa aagtcaaagg caccgccttc      780
cttgatatcc catcaaatga tgtgcgcggc ttatcattac cttatgtgaa aaagggcgtc      840
atcactgatt ctctgatgg ttatcctgta ggaaatgatg tcactagtga tccagcaatc      900
cgaaaagcct tgactattgg tttaaataag caaaaagtgc tcgatacggg tttaaagtgt      960
tatggtaaac cagcttattc aattattgat aaacacccat tttggaatcc aaaaacagcc     1020
attaaagata ataaagtagc taaagctaag caattattga caaaagcggg atggaaagaa     1080
caagcagacg gtagccgtaa aaaaggtgac cttgatgcag cgtttgatct gtactaccct     1140
actaatgatc aattgcgagc gaacttagcc gttgaagtag cagagcaagc caaggcccta     1200
gggattacta ttaaaactca agctagtaac tgggatgaaa tggcaacgaa gtcacatgac     1260
tcagccttac tttatgccgg aggacgtcat cacgcgcagc aattttatga atcgcatcat     1320
ccaagcctag cagggaaggg ttggaccaat attacgtttt ataacaatcc taccgtgact     1380
aagtaccttg acaaagcaat gacatcttct gaccttgata aagctaacga atattggaag     1440
ttagcgcagt gggatggcaa aacaggtgct tctactcttg gagatttgcc aaatgtatgg     1500
ttgggtgagcc ttaaccatac ttatattggg gataaacgta tcaatgtagg taaacaaggc     1560
gtccacagtc atggtcatga ttggtcatta ttgactaaca ttgccgagtg gacttgggat     1620
gaatcaacta agtaa                                     1635

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<210> SEQ ID NO 140
<211> LENGTH: 544
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 140
Met Ile Val Ser Lys Tyr Leu Lys Tyr Phe Ser Ile Ile Thr Leu Phe

```

1				5					10					15			
Leu	Thr	Gly	Leu	Ile	Leu	Val	Ala	Cys	Gln	Gln	Gln	Lys	Pro	Gln	Thr		
			20					25					30				
Lys	Glu	Arg	Gln	Arg	Lys	Gln	Arg	Pro	Lys	Asp	Glu	Leu	Val	Val	Ser		
		35					40					45					
Met	Gly	Ala	Lys	Leu	Pro	His	Glu	Phe	Asp	Pro	Lys	Asp	Arg	Tyr	Gly		
	50					55					60						
Val	His	Asn	Glu	Gly	Asn	Ile	Thr	His	Ser	Thr	Leu	Leu	Lys	Arg	Ser		
65					70					75					80		
Pro	Glu	Leu	Asp	Ile	Lys	Gly	Glu	Leu	Ala	Lys	Thr	Tyr	His	Leu	Ser		
				85					90					95			
Glu	Asp	Gly	Leu	Thr	Trp	Ser	Phe	Asp	Leu	His	Asp	Asp	Phe	Lys	Phe		
			100					105					110				
Ser	Asn	Gly	Glu	Pro	Val	Thr	Ala	Asp	Asp	Val	Lys	Phe	Thr	Tyr	Asp		
		115					120					125					
Met	Leu	Lys	Ala	Asp	Gly	Lys	Ala	Trp	Asp	Leu	Thr	Phe	Ile	Lys	Asn		
	130				135						140						
Val	Glu	Val	Val	Gly	Lys	Asn	Gln	Val	Asn	Ile	His	Leu	Thr	Glu	Ala		
145				150						155				160			
His	Ser	Thr	Phe	Thr	Ala	Gln	Leu	Thr	Glu	Ile	Pro	Ile	Val	Pro	Lys		
			165						170					175			
Lys	His	Tyr	Asn	Asp	Lys	Tyr	Lys	Ser	Asn	Pro	Ile	Gly	Ser	Gly	Pro		
			180					185					190				
Tyr	Met	Val	Lys	Glu	Tyr	Lys	Ala	Gly	Glu	Gln	Ala	Ile	Phe	Val	Arg		
	195						200					205					
Asn	Pro	Tyr	Trp	His	Gly	Lys	Lys	Pro	Tyr	Phe	Lys	Lys	Trp	Thr	Trp		
	210				215						220						
Val	Leu	Leu	Asp	Glu	Asn	Thr	Ala	Leu	Ala	Ala	Leu	Glu	Ser	Gly	Asp		
225				230					235					240			
Val	Asp	Met	Ile	Tyr	Ala	Thr	Pro	Glu	Leu	Ala	Asp	Lys	Lys	Val	Lys		
			245					250					255				
Gly	Thr	Arg	Leu	Leu	Asp	Ile	Pro	Ser	Asn	Asp	Val	Arg	Gly	Leu	Ser		
			260					265					270				
Leu	Pro	Tyr	Val	Lys	Lys	Gly	Val	Ile	Thr	Asp	Ser	Pro	Asp	Gly	Tyr		
	275					280						285					
Pro	Val	Gly	Asn	Asp	Val	Thr	Ser	Asp	Pro	Ala	Ile	Arg	Lys	Ala	Leu		
	290				295						300						
Thr	Ile	Gly	Leu	Asn	Arg	Gln	Lys	Val	Leu	Asp	Thr	Val	Leu	Asn	Gly		
305				310						315				320			
Tyr	Gly	Lys	Pro	Ala	Tyr	Ser	Ile	Ile	Asp	Lys	Thr	Pro	Phe	Trp	Asn		
			325					330					335				
Pro	Lys	Thr	Ala	Ile	Lys	Asp	Asn	Lys	Val	Ala	Lys	Ala	Lys	Gln	Leu		
			340				345					350					
Leu	Thr	Lys	Ala	Gly	Trp	Lys	Glu	Gln	Ala	Asp	Gly	Ser	Arg	Lys	Lys		
	355					360					365						
Gly	Asp	Leu	Asp	Ala	Ala	Phe	Asp	Leu	Tyr	Tyr	Pro	Thr	Asn	Asp	Gln		
	370				375						380						
Leu	Arg	Ala	Asn	Leu	Ala	Val	Glu	Val	Ala	Glu	Gln	Ala	Lys	Ala	Leu		
385				390					395					400			
Gly	Ile	Thr	Ile	Lys	Leu	Lys	Ala	Ser	Asn	Trp	Asp	Glu	Met	Ala	Thr		
			405					410					415				
Lys	Ser	His	Asp	Ser	Ala	Leu	Leu	Tyr	Ala	Gly	Gly	Arg	His	His	Ala		
			420					425				430					
Gln	Gln	Phe	Tyr	Glu	Ser	His	His	Pro	Ser	Leu	Ala	Gly	Lys	Gly	Trp		
		435				440					445						
Thr	Asn	Ile	Thr	Phe	Tyr	Asn	Asn	Pro	Thr	Val	Thr	Lys	Tyr	Leu	Asp		
	450					455					460						

Lys	Ala	Met	Thr	Ser	Ser	Asp	Leu	Asp	Lys	Ala	Asn	Glu	Tyr	Trp	Lys
465					470					475					480
Leu	Ala	Gln	Trp	Asp	Gly	Lys	Thr	Gly	Ala	Ser	Thr	Leu	Gly	Asp	Leu
				485					490					495	
Pro	Asn	Val	Trp	Leu	Val	Ser	Leu	Asn	His	Thr	Tyr	Ile	Gly	Asp	Lys
			500					505					510		
Arg	Ile	Asn	Val	Gly	Lys	Gln	Gly	Val	His	Ser	His	Gly	His	Asp	Trp
	515					520						525			
Ser	Leu	Leu	Thr	Asn	Ile	Ala	Glu	Trp	Thr	Trp	Asp	Glu	Ser	Thr	Lys
	530					535					540				

<210> SEQ ID NO 141
 <211> LENGTH: 1047
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 141

atgttgacat	caaagcacca	taatctcaac	aaactagtct	ggcgctacgg	gctaacctca	60
gccgctgccg	tccttctagc	ctttggaggc	ggggcaagca	gcgttaaggc	tgaggtttct	120
tctacgacta	tgacgtcgag	tcaaagagag	tcaaaaataa	aagagatcga	agaaagtctt	180
aaaaaatatc	cagaagtgtc	caatgagaaa	ttttgggaaa	gaaagtggta	tggaacctat	240
tttaaagaag	aagattttca	aaaggagcta	aaagatttta	ctgagaagag	gcttaaggag	300
attctagatt	taattggtaa	atctggaatc	aaggagagacc	gtggtgagac	tggtcctgct	360
ggcccagccg	gaccacaagg	taaaactggg	gagagggggc	cccaagggtcc	taaagggtgac	420
cgcggtgagc	aaggaatcca	aggtaaaagc	ggtgaaaaag	gtgagcgcgg	tgaaaaaggc	480
gacaaaagggtg	aaaccgggtga	acgcggtgaa	aaaggcgaa	ctggaatcca	aggcccacaa	540
ggtgaagctg	gtaaagatgg	cgctccaggt	aaagatggag	ctccaggcga	aaagggtgaa	600
aaagggtgacc	gcggtgaaac	cggagctcag	ggtccagtag	gcccacaagg	tgaaaaaggt	660
gaaacggggc	cccaaggccc	agcaggccca	caaggtgagg	caggcaaacc	aggtgagcaa	720
ggcccagcag	gcccacaagg	tgaagcaggc	caaccaggcg	aaaaagctcc	agaaaagagc	780
ccagaaggcg	aagcaggcca	accaggcgaa	aaagctccag	aaaagagcaa	agaggttaact	840
ccagctgcag	aaaaacctgc	tgacaaaagaa	gctaaccaaa	cgccagaacg	ccgcaatggc	900
aatatggcta	agacacctgt	agccaacaac	cacagacgtc	taccagcaac	tggtgagcaa	960
gccaacccat	tctttacagc	agcagcagta	gcagtgatga	caacagctgg	tgtcctagcc	1020
gttacaaaac	gcaaagaaaa	caactaa				1047

<210> SEQ ID NO 142
 <211> LENGTH: 348
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 142

Met	Leu	Thr	Ser	Lys	His	His	Asn	Leu	Asn	Lys	Leu	Val	Trp	Arg	Tyr
1				5					10					15	
Gly	Leu	Thr	Ser	Ala	Ala	Ala	Val	Leu	Leu	Ala	Phe	Gly	Gly	Gly	Ala
			20					25					30		
Ser	Ser	Val	Lys	Ala	Glu	Val	Ser	Ser	Thr	Thr	Met	Thr	Ser	Ser	Gln
		35					40					45			
Arg	Glu	Ser	Lys	Ile	Lys	Glu	Ile	Glu	Glu	Ser	Leu	Lys	Lys	Tyr	Pro
	50					55					60				
Glu	Val	Ser	Asn	Glu	Lys	Phe	Trp	Glu	Arg	Lys	Trp	Tyr	Gly	Thr	Tyr
65					70					75					80
Phe	Lys	Glu	Glu	Asp	Phe	Gln	Lys	Glu	Leu	Lys	Asp	Phe	Thr	Glu	Lys
				85					90					95	
Arg	Leu	Lys	Glu	Ile	Leu	Asp	Leu	Ile	Gly	Lys	Ser	Gly	Ile	Lys	Gly
			100					105					110		
Asp	Arg	Gly	Glu	Thr	Gly	Pro	Ala	Gly	Pro	Ala	Gly	Pro	Gln	Gly	Lys
	115						120					125			
Thr	Gly	Glu	Arg	Gly	Ala	Gln	Gly	Pro	Lys	Gly	Asp	Arg	Gly	Glu	Gln

130		135		140
Gly Ile Gln Gly Lys Ala Gly Glu Lys Gly Glu Arg Gly Glu Lys Gly				
145		150		155
Asp Lys Gly Glu Thr Gly Glu Arg Gly Glu Lys Gly Glu Ala Gly Ile				
	165		170	175
Gln Gly Pro Gln Gly Glu Ala Gly Lys Asp Gly Ala Pro Gly Lys Asp				
	180		185	190
Gly Ala Pro Gly Glu Lys Gly Glu Lys Gly Asp Arg Gly Glu Thr Gly				
	195		200	205
Ala Gln Gly Pro Val Gly Pro Gln Gly Glu Lys Gly Glu Thr Gly Ala				
	210		215	220
Gln Gly Pro Ala Gly Pro Gln Gly Glu Ala Gly Lys Pro Gly Glu Gln				
225		230		235
Gly Pro Ala Gly Pro Gln Gly Glu Ala Gly Gln Pro Gly Glu Lys Ala				
	245		250	255
Pro Glu Lys Ser Pro Glu Gly Glu Ala Gly Gln Pro Gly Glu Lys Ala				
	260		265	270
Pro Glu Lys Ser Lys Glu Val Thr Pro Ala Ala Glu Lys Pro Ala Asp				
	275		280	285
Lys Glu Ala Asn Gln Thr Pro Glu Arg Arg Asn Gly Asn Met Ala Lys				
	290		295	300
Thr Pro Val Ala Asn Asn His Arg Arg Leu Pro Ala Thr Gly Glu Gln				
305		310		315
Ala Asn Pro Phe Phe Thr Ala Ala Ala Val Ala Val Met Thr Thr Ala				
	325		330	335
Gly Val Leu Ala Val Thr Lys Arg Lys Glu Asn Asn				
	340		345	

<210> SEQ ID NO 143

<211> LENGTH: 1371

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 143

ttgatttcac	gcataaaaag	ctttaaaaaac	gctttaaatt	atgataaaat	gaactgtatc	60
gaaattatttt	taaggagaaa	tgacttaatg	tctacatcat	ttgaaaacaa	agctacaaat	120
cgtggcggtga	ttacattttac	aatcagtgcaa	gataaaataa	aaccagctct	tgataaagct	180
tttaataaaaa	tcaaaaaaga	cttgaatgca	ccagggtttcc	gtaaaggaca	catgcctcgt	240
ccagtcttca	acccaaaaatt	tggtgaagaa	gttctttatg	aagatgcttt	gaatattgta	300
ttgccagaag	cttatgaagc	agctgtgacg	gaacttggtc	ttgatgtggt	tgacacaacca	360
aaaatcgatg	ttgtgtcaat	ggaaaaaggg	aaagagtggg	cactttctgc	tgaagttgtg	420
acaaaacctg	aagtgaacct	tggtgattac	aaaaacctag	ttgtagaagt	tgatgcttca	480
aaagaagttt	cagatgaaga	cgtggatgct	aaaattgagc	gcgaacgtca	aaaccttgcg	540
gaactcatta	ttaaagacgg	tgaagcagct	caagggtgaca	ctggttgatg	tgactttggt	600
ggttcagttg	atggtgttga	gtttgatggc	ggtaaaggag	ataacttctc	tcttgaactt	660
ggttcaggac	aatttatccc	aggttttgaa	gatcaactag	ttggtgctaa	agctggcgat	720
gaagtagaag	ttaatgtcac	attcccagaa	tcttaccag	cagaagatct	tgacaggtaaa	780
gccgctaaat	ttatgacaac	tattcacgaa	gtcaaaacaa	aagaagtacc	agagcttgat	840
gatgagcttg	caaaagatat	tgatgaagat	gttgacacac	ttgaagactt	aaaagtaaaa	900
tatcgtaaaag	aacttgaagc	agctcaagaa	actgcttatg	atgatgctgt	tgaaggagct	960
gcgattgaat	tagcagttgc	aaatgctgaa	attggtgatt	taccgaaga	aatgattcat	1020
gaagaagtca	accgttcagt	gaatgaattt	atgggcaaca	tgcaacgtca	aggaatctca	1080
cctgaaatgt	acttccaatt	gactggtaca	actcaagaag	attacataa	ccaatattca	1140
gctgaagctg	acaaacgtgt	taaaacacac	cttgttattg	aagcaattgc	taaagcagaa	1200
ggtttttgaag	caacagatag	tgaaattgaa	caagaaatta	atgaccttgc	aacagaatat	1260
aacatgccag	ctgaccaagt	tcgttctctt	ctttcagcag	atatgttgaa	acatgatatt	1320
gcaatgaaaa	aagcagttga	agtgattaca	agcacagcaa	gcgttaagta	a	1371

<210> SEQ ID NO 144
 <211> LENGTH: 456
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 144

Met	Ile	Ser	Arg	Ile	Lys	Ser	Phe	Lys	Asn	Ala	Leu	Asn	Tyr	Asp	Lys	1	5	10	15
Met	Asn	Cys	Ile	Glu	Ile	Ile	Leu	Arg	Arg	Asn	Asp	Leu	Met	Ser	Thr	20	25	30	
Ser	Phe	Glu	Asn	Lys	Ala	Thr	Asn	Arg	Gly	Val	Ile	Thr	Phe	Thr	Ile	35	40	45	
Ser	Gln	Asp	Lys	Ile	Lys	Pro	Ala	Leu	Asp	Lys	Ala	Phe	Asn	Lys	Ile	50	55	60	
Lys	Lys	Asp	Leu	Asn	Ala	Pro	Gly	Phe	Arg	Lys	Gly	His	Met	Pro	Arg	65	70	75	80
Pro	Val	Phe	Asn	Gln	Lys	Phe	Gly	Glu	Glu	Val	Leu	Tyr	Glu	Asp	Ala	85	90	95	
Leu	Asn	Ile	Val	Leu	Pro	Glu	Ala	Tyr	Glu	Ala	Ala	Val	Thr	Glu	Leu	100	105	110	
Gly	Leu	Asp	Val	Val	Ala	Gln	Pro	Lys	Ile	Asp	Val	Val	Ser	Met	Glu	115	120	125	
Lys	Gly	Lys	Glu	Trp	Thr	Leu	Ser	Ala	Glu	Val	Val	Thr	Lys	Pro	Glu	130	135	140	
Val	Lys	Leu	Gly	Asp	Tyr	Lys	Asn	Leu	Val	Val	Glu	Val	Asp	Ala	Ser	145	150	155	160
Lys	Glu	Val	Ser	Asp	Glu	Asp	Val	Asp	Ala	Lys	Ile	Glu	Arg	Glu	Arg	165	170	175	
Gln	Asn	Leu	Ala	Glu	Leu	Ile	Ile	Lys	Asp	Gly	Glu	Ala	Ala	Gln	Gly	180	185	190	
Asp	Thr	Val	Val	Ile	Asp	Phe	Val	Gly	Ser	Val	Asp	Gly	Val	Glu	Phe	195	200	205	
Asp	Gly	Lys	Gly	Asp	Asn	Phe	Ser	Leu	Glu	Leu	Gly	Ser	Gly	Gln		210	215	220	
Phe	Ile	Pro	Gly	Phe	Glu	Asp	Gln	Leu	Val	Gly	Ala	Lys	Ala	Gly	Asp	225	230	235	240
Glu	Val	Glu	Val	Asn	Val	Thr	Phe	Pro	Glu	Ser	Tyr	Gln	Ala	Glu	Asp	245	250	255	
Leu	Ala	Gly	Lys	Ala	Ala	Lys	Phe	Met	Thr	Thr	Ile	His	Glu	Val	Lys	260	265	270	
Thr	Lys	Glu	Val	Pro	Glu	Leu	Asp	Asp	Glu	Leu	Ala	Lys	Asp	Ile	Asp	275	280	285	
Glu	Asp	Val	Asp	Thr	Leu	Glu	Asp	Leu	Lys	Val	Lys	Tyr	Arg	Lys	Glu	290	295	300	
Leu	Glu	Ala	Ala	Gln	Glu	Thr	Ala	Tyr	Asp	Asp	Ala	Val	Glu	Gly	Ala	305	310	315	320
Ala	Ile	Glu	Leu	Ala	Val	Ala	Asn	Ala	Glu	Ile	Val	Asp	Leu	Pro	Glu	325	330	335	
Glu	Met	Ile	His	Glu	Glu	Val	Asn	Arg	Ser	Val	Asn	Glu	Phe	Met	Gly	340	345	350	
Asn	Met	Gln	Arg	Gln	Gly	Ile	Ser	Pro	Glu	Met	Tyr	Phe	Gln	Leu	Thr	355	360	365	
Gly	Thr	Thr	Gln	Glu	Asp	Leu	His	Asn	Gln	Tyr	Ser	Ala	Glu	Ala	Asp	370	375	380	
Lys	Arg	Val	Lys	Thr	His	Leu	Val	Ile	Glu	Ala	Ile	Ala	Lys	Ala	Glu	385	390	395	400
Gly	Phe	Glu	Ala	Thr	Asp	Ser	Glu	Ile	Glu	Gln	Glu	Ile	Asn	Asp	Leu	405	410	415	

Ala Thr Glu Tyr Asn Met Pro Ala Asp Gln Val Arg Ser Leu Leu Ser
420 425 430
Ala Asp Met Leu Lys His Asp Ile Ala Met Lys Lys Ala Val Glu Val
435 440 445
Ile Thr Ser Thr Ala Ser Val Lys
450 455

<210> SEQ ID NO 145
<211> LENGTH: 927
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 145

atgaaaacta	ttcgaatagc	aaagtatttta	ggaattctat	tccttttgat	aactcttatt	60
agcgtagggtg	ctagtttttta	tttcttttcat	ggtgcacaaa	taagagaaga	gaaatcgttt	120
attaataata	agaaacggag	tacaaataat	ccattatacc	cagctgaaca	gtcttttgac	180
gcttttacctt	acgaaaaaacg	tcaactaaca	aatcgtgggt	taaaacaagt	ggggtggtac	240
ttaccagctg	ctcaaaaaaac	aaaaaagaca	gctattgttg	ttcatgggtt	tacgaatgac	300
aaagaagata	tgaagccata	tgccatgctt	tttcatgatt	tgggctataa	tgtcttaatg	360
ccagacaatg	aggcccatgg	ggaaaagtga	gggaacttga	ttgggttatg	ctggaatgac	420
cgccttaatg	tcatggcttg	gacagaccaa	ctgattaagg	aaaaccctga	aagccaaatc	480
acactctttg	gcttatctat	gggtgctgca	acagtaatga	tggcaagtgg	tgagcgattg	540
cctgcgcaag	tcacctccct	catcgaagat	tgcggttatg	ccagtgtttg	ggacgaattg	600
aagtttcagg	ccaaggctat	gtacaacttg	cctgcctttc	ctttactcta	tgaagtctct	660
gccttatcta	agattcgagc	aggttttagt	tacggagaag	cgagctcagt	gaaacagctg	720
gctaaaaata	aacgtccaac	tttatattatc	cacggtgata	aggatgattt	tgttcctaca	780
aaaatggttt	atgacaatta	taaggccacg	aaaggtccta	aggaaatctt	gattgttaaa	840
ggggcaaaac	acgccaaatc	ctttgaaaca	aaccagaac	aataccagaa	aaaaattgcc	900
gcttttttga	aaaaagttga	gaaataa				927

<210> SEQ ID NO 146
<211> LENGTH: 308
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 146

Met	Lys	Thr	Ile	Arg	Ile	Ala	Lys	Tyr	Leu	Gly	Ile	Leu	Phe	Leu	Leu
1				5					10					15	
Ile	Thr	Leu	Ile	Ser	Val	Gly	Ala	Ser	Phe	Tyr	Phe	Phe	His	Val	Ala
			20					25					30		
Gln	Ile	Arg	Glu	Glu	Lys	Ser	Phe	Ile	Asn	Asn	Lys	Lys	Arg	Ser	Thr
		35				40					45				
Asn	Asn	Pro	Leu	Tyr	Pro	Ala	Glu	Gln	Ser	Phe	Asp	Ala	Leu	Pro	Tyr
	50				55					60					
Glu	Lys	Arg	Gln	Leu	Thr	Asn	Arg	Gly	Leu	Lys	Gln	Val	Gly	Trp	Tyr
65				70				75						80	
Leu	Pro	Ala	Ala	Gln	Lys	Thr	Lys	Lys	Thr	Ala	Ile	Val	Val	His	Gly
			85					90					95		
Phe	Thr	Asn	Asp	Lys	Glu	Asp	Met	Lys	Pro	Tyr	Ala	Met	Leu	Phe	His
		100					105					110			
Asp	Leu	Gly	Tyr	Asn	Val	Leu	Met	Pro	Asp	Asn	Glu	Ala	His	Gly	Glu
	115					120					125				
Ser	Glu	Gly	Asn	Leu	Ile	Gly	Tyr	Gly	Trp	Asn	Asp	Arg	Leu	Asn	Val
	130					135				140					
Met	Ala	Trp	Thr	Asp	Gln	Leu	Ile	Lys	Glu	Asn	Pro	Glu	Ser	Gln	Ile
145				150					155					160	
Thr	Leu	Phe	Gly	Leu	Ser	Met	Gly	Ala	Ala	Thr	Val	Met	Met	Ala	Ser
			165				170							175	
Gly	Glu	Arg	Leu	Pro	Ala	Gln	Val	Thr	Ser	Leu	Ile	Glu	Asp	Cys	Gly

			180					185				190					
Tyr	Ala	Ser	Val	Trp	Asp	Glu	Leu	Lys	Phe	Gln	Ala	Lys	Ala	Met	Tyr		
			195					200					205				
Asn	Leu	Pro	Ala	Phe	Pro	Leu	Leu	Tyr	Glu	Val	Ser	Ala	Leu	Ser	Lys		
			210					215					220				
Ile	Arg	Ala	Gly	Phe	Ser	Tyr	Gly	Glu	Ala	Ser	Ser	Val	Lys	Gln	Leu		
						230					235				240		
Ala	Lys	Asn	Lys	Arg	Pro	Thr	Leu	Phe	Ile	His	Gly	Asp	Lys	Asp	Asp		
				245					250					255			
Phe	Val	Pro	Thr	Lys	Met	Val	Tyr	Asp	Asn	Tyr	Lys	Ala	Thr	Lys	Gly		
			260					265					270				
Pro	Lys	Glu	Ile	Leu	Ile	Val	Lys	Gly	Ala	Lys	His	Ala	Lys	Ser	Phe		
		275						280					285				
Glu	Thr	Asn	Pro	Glu	Gln	Tyr	Gln	Lys	Lys	Ile	Ala	Ala	Phe	Leu	Lys		
		290					295					300					
Lys	Val	Glu	Lys														
																	305

<210> SEQ ID NO 147

<211> LENGTH: 855

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 147

atgaaatcca	aaaaagttgt	tagtggtata	tcacttacct	tatccctttt	tttggtgaca	60
ggttgtgcta	aagttgataa	caacaaatca	gttaatctta	agcctgctac	taaacaaacc	120
tataatagct	atagtgatga	ccaattaaga	tcgcgtgaaa	ataccatgtc	tgttttatgg	180
taccagcgag	ctgcggaaac	tcaagcgctt	tatttacagg	ggtatcagtt	agcaacggat	240
cgttaaaaag	aacaactcaa	taaaccaacg	gataaacctt	attcaattgt	attagatatt	300
gacgaaacag	ttcttgataa	tagcccttat	caagctaaaa	atgttttgga	aggaacagga	360
tttacacctg	aaagctggga	ttattgggta	caaaaagaaag	aagcaaaacc	ggttgctggt	420
gctaaagact	ttttgcaatt	tgcagaccaa	aatgggtgttc	aaatttacta	catttcagac	480
agatcaacta	ctcaagtaga	tgctacaatg	gaaaatctcc	aaaaagaagg	tattccagta	540
caaggtcgtg	atcatcttct	attcttagaa	aaaggcgtaa	aatcaaagga	gagtcgtcgt	600
caaaagggtca	aagaaacaac	taatgtaacg	atgctatttg	gtgataatct	tctagatttt	660
gctgattttt	caaaaaaatc	tcaagaagat	agaacagctt	tattatcaga	tttacaagaa	720
gagtttgga	gacgctttat	cattttccct	aatcctatgt	atggttcatg	ggaaggtgcc	780
atttataaag	gtgaaaagct	ggatgtgctt	aagcaactag	aggaacgccg	taaaagttta	840
aaaagcttta	aataa					855

<210> SEQ ID NO 148

<211> LENGTH: 284

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 148

Met	Lys	Ser	Lys	Lys	Val	Val	Ser	Val	Ile	Ser	Leu	Thr	Leu	Ser	Leu
1			5						10				15		
Phe	Leu	Val	Thr	Gly	Cys	Ala	Lys	Val	Asp	Asn	Asn	Lys	Ser	Val	Asn
			20					25				30			
Leu	Lys	Pro	Ala	Thr	Lys	Gln	Thr	Tyr	Asn	Ser	Tyr	Ser	Asp	Asp	Gln
		35				40					45				
Leu	Arg	Ser	Arg	Glu	Asn	Thr	Met	Ser	Val	Leu	Trp	Tyr	Gln	Arg	Ala
	50				55					60					
Ala	Glu	Thr	Gln	Ala	Leu	Tyr	Leu	Gln	Gly	Tyr	Gln	Leu	Ala	Thr	Asp
65				70					75				80		
Arg	Leu	Lys	Glu	Gln	Leu	Asn	Lys	Pro	Thr	Asp	Lys	Pro	Tyr	Ser	Ile
			85					90					95		
Val	Leu	Asp	Ile	Asp	Glu	Thr	Val	Leu	Asp	Asn	Ser	Pro	Tyr	Gln	Ala

			100					105					110				
Lys	Asn	Val	Leu	Glu	Gly	Thr	Gly	Phe	Thr	Pro	Glu	Ser	Trp	Asp	Tyr		
		115					120					125					
Trp	Val	Gln	Lys	Lys	Glu	Ala	Lys	Pro	Val	Ala	Gly	Ala	Lys	Asp	Phe		
	130					135					140						
Leu	Gln	Phe	Ala	Asp	Gln	Asn	Gly	Val	Gln	Ile	Tyr	Tyr	Ile	Ser	Asp		
145					150					155					160		
Arg	Ser	Thr	Thr	Gln	Val	Asp	Ala	Thr	Met	Glu	Asn	Leu	Gln	Lys	Glu		
			165					170						175			
Gly	Ile	Pro	Val	Gln	Gly	Arg	Asp	His	Leu	Leu	Phe	Leu	Glu	Lys	Gly		
		180					185						190				
Val	Lys	Ser	Lys	Glu	Ser	Arg	Arg	Gln	Lys	Val	Lys	Glu	Thr	Thr	Asn		
	195						200					205					
Val	Thr	Met	Leu	Phe	Gly	Asp	Asn	Leu	Leu	Asp	Phe	Ala	Asp	Phe	Ser		
	210				215						220						
Lys	Lys	Ser	Gln	Glu	Asp	Arg	Thr	Ala	Leu	Leu	Ser	Asp	Leu	Gln	Glu		
225				230						235					240		
Glu	Phe	Gly	Arg	Arg	Phe	Ile	Ile	Phe	Pro	Asn	Pro	Met	Tyr	Gly	Ser		
			245					250						255			
Trp	Glu	Gly	Ala	Ile	Tyr	Lys	Gly	Glu	Lys	Leu	Asp	Val	Leu	Lys	Gln		
		260					265						270				
Leu	Glu	Glu	Arg	Arg	Lys	Ser	Leu	Lys	Ser	Phe	Lys						
		275					280										

<210> SEQ ID NO 149
 <211> LENGTH: 918
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 149

ttgctgtatg	ggtttgaaaa	aagaggaaaa	aaaatgataa	aacgatgtaa	aggaattggt	60
ctagccttaa	tggccttctt	tttggtagct	tgtgtgaatc	agcaccctaa	aacggctaaa	120
gagactgaac	agcagagaat	tgtagccact	tcggttgctg	tggttgatat	ctgtgaccgt	180
ttaaatttag	acctcgttgg	ggtttgtgat	agtaaattat	atacccttcc	taaacgctat	240
gatgctgtta	agcgtgtggg	tttaccatg	aatcctgata	tagagttgat	tgcttctttg	300
aaaccaactt	ggattttgag	tccaatttct	ttacaagaag	atttgggaacc	caagtatcaa	360
aaattggata	ctgagtatgg	ttttttgaac	ttacgaagtg	ttgagggcat	gtaccagtcc	420
attgatgatt	tagggaaacct	tttccaacgt	caacaagaag	caaaagaatt	gcgccagcaa	480
taccaggact	attatcgtgc	tttccaagct	aaacgtaagg	ggaagaaaaa	gcctaaagtg	540
cttattctta	tgggcttgcc	aggtagttat	ttggtggcga	cgaaccaatc	ttatgtaggg	600
aatcttttgg	acttggcagg	tggtgagaat	gtttatcagt	cagatgagaa	agaatttcta	660
tcagctaata	ctgaagacat	gctggctaag	gagcctgact	tgatttttacg	aacagctcat	720
gccattccag	acaaggtaaa	agtgatgttt	gacaaagaat	ttgctgaaaa	tgatatttgg	780
aaacatttta	cggcagtcaa	ggaagggaaa	gtctatgatt	tggacaatac	cctgtttggc	840
atgagtgcta	aattgaacta	cccagaagcc	ttggacacct	taacacagct	ttttgaccac	900
gtgggagatc	atccgtaa					918

<210> SEQ ID NO 150
 <211> LENGTH: 305
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 150

Met	Leu	Tyr	Gly	Phe	Gly	Lys	Arg	Gly	Lys	Lys	Met	Ile	Lys	Arg	Cys
1			5					10					15		
Lys	Gly	Ile	Gly	Leu	Ala	Leu	Met	Ala	Phe	Phe	Leu	Val	Ala	Cys	Val
		20					25				30				
Asn	Gln	His	Pro	Lys	Thr	Ala	Lys	Glu	Thr	Glu	Gln	Gln	Arg	Ile	Val
		35					40						45		

Ala	Thr	Ser	Val	Ala	Val	Val	Asp	Ile	Cys	Asp	Arg	Leu	Asn	Leu	Asp
50						55					60				
Leu	Val	Gly	Val	Cys	Asp	Ser	Lys	Leu	Tyr	Thr	Leu	Pro	Lys	Arg	Tyr
65				70					75					80	
Asp	Ala	Val	Lys	Arg	Val	Gly	Leu	Pro	Met	Asn	Pro	Asp	Ile	Glu	Leu
			85					90					95		
Ile	Ala	Ser	Leu	Lys	Pro	Thr	Trp	Ile	Leu	Ser	Pro	Asn	Ser	Leu	Gln
			100					105				110			
Glu	Asp	Leu	Glu	Pro	Lys	Tyr	Gln	Lys	Leu	Asp	Thr	Glu	Tyr	Gly	Phe
		115					120					125			
Leu	Asn	Leu	Arg	Ser	Val	Glu	Gly	Met	Tyr	Gln	Ser	Ile	Asp	Asp	Leu
	130					135					140				
Gly	Asn	Leu	Phe	Gln	Arg	Gln	Gln	Glu	Ala	Lys	Glu	Leu	Arg	Gln	Gln
145				150						155				160	
Tyr	Gln	Asp	Tyr	Tyr	Arg	Ala	Phe	Gln	Ala	Lys	Arg	Lys	Gly	Lys	Lys
			165					170					175		
Lys	Pro	Lys	Val	Leu	Ile	Leu	Met	Gly	Leu	Pro	Gly	Ser	Tyr	Leu	Val
			180					185					190		
Ala	Thr	Asn	Gln	Ser	Tyr	Val	Gly	Asn	Leu	Leu	Asp	Leu	Ala	Gly	Gly
	195						200					205			
Glu	Asn	Val	Tyr	Gln	Ser	Asp	Glu	Lys	Glu	Phe	Leu	Ser	Ala	Asn	Pro
	210					215					220				
Glu	Asp	Met	Leu	Ala	Lys	Glu	Pro	Asp	Leu	Ile	Leu	Arg	Thr	Ala	His
225				230						235				240	
Ala	Ile	Pro	Asp	Lys	Val	Lys	Val	Met	Phe	Asp	Lys	Glu	Phe	Ala	Glu
			245					250						255	
Asn	Asp	Ile	Trp	Lys	His	Phe	Thr	Ala	Val	Lys	Glu	Gly	Lys	Val	Tyr
		260					265						270		
Asp	Leu	Asp	Asn	Thr	Leu	Phe	Gly	Met	Ser	Ala	Lys	Leu	Asn	Tyr	Pro
	275					280					285				
Glu	Ala	Leu	Asp	Thr	Leu	Thr	Gln	Leu	Phe	Asp	His	Val	Gly	Asp	His
	290					295					300				
Pro															
305															

<210> SEQ ID NO 151

<211> LENGTH: 1143

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 151

atgaaaaagt	ggcaaaaaat	cgtgtgtgtg	actggaactg	tgcttgcaac	gtctagttta	60
gcagcctgcg	aaagcaagtc	agcatcaaaa	gatagtgatg	tcaaattatt	gatgtaccaa	120
gttggtgaca	aacctgataa	cttcgatgaa	ttgatgacaa	ttgctaacaa	gcgcatcaaa	180
gaaaaaacag	gtgcaacggt	tgaccttcaa	tacatcgggt	ggggggactg	ggatgataaa	240
atgagtacca	tcattgcctc	tggtgaaaac	tacgacattg	cttttgccaa	taattatgtg	300
gtcaatgcac	aaaaaggtgc	ttttgctgat	ttgacaacgt	taatgccaaa	atacgctaag	360
aaaacgtata	aaaacttaga	cccagcctat	attaaaggaa	atactattga	cggtaaactc	420
tatgccttcc	cagtagatgc	caacgtttat	gcccacacaga	tgctttcttt	caataaagaa	480
ctagtggaca	aatatggcct	tgacatttca	aacattaagt	cctatgcaga	tgctgaaaat	540
gtcttgaaac	aattccacga	aaaagaacca	aatacagcag	cttttgctat	tggtcaagtc	600
tttagtatgt	cagggtgacta	tgactaccca	ttaacacaaa	cccaaccctt	tgctgtgaaa	660
attgatgaag	gcaagccaac	catcattaat	cagtatgaag	atgagtcctt	taaaaacaat	720
ctccgcttga	tgacacaaatg	gtataaagaa	ggtttgattc	caacagatgc	agcgaccaat	780
acagaagggt	atcccccttga	aggaaacact	tggtttatgc	gtgaagaaac	ccaaggtcct	840
atggactatg	cgatactat	cttgaccaat	gctgcaggaa	aagacatcgt	gtctcgtcca	900
ttgactaaac	gcctaataaac	cacatcacaa	gcacaaatgg	caaactttgt	ggatcaagc	960
gtatctaaaa	acaaagaaaa	agcagttgaa	gtcctttctc	ttcttaatag	cgatcccgaa	1020

ttgttaaagt	ggcttggtta	tggtgtcgaa	ggcaaagctt	gggaaaaaat	tggcgacaag	1080
aaaatcaaac	tgctcgatgg	ctatcaacct	aaaaatgcac	atgggtgctt	ggaatactgg	1140
taa						1143

<210> SEQ ID NO 152

<211> LENGTH: 380

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 152

Met	Lys	Lys	Trp	Gln	Lys	Ile	Val	Cys	Val	Thr	Gly	Thr	Val	Leu	Ala
1			5						10					15	
Thr	Ser	Ser	Leu	Ala	Ala	Cys	Glu	Ser	Lys	Ser	Ala	Ser	Lys	Asp	Ser
			20					25					30		
Asp	Val	Lys	Leu	Leu	Met	Tyr	Gln	Val	Gly	Asp	Lys	Pro	Asp	Asn	Phe
		35					40					45			
Asp	Glu	Leu	Met	Thr	Ile	Ala	Asn	Lys	Arg	Ile	Lys	Glu	Lys	Thr	Gly
	50					55					60				
Ala	Thr	Val	Asp	Leu	Gln	Tyr	Ile	Gly	Trp	Gly	Asp	Trp	Asp	Asp	Lys
65					70					75					80
Met	Ser	Thr	Ile	Ile	Ala	Ser	Gly	Glu	Asn	Tyr	Asp	Ile	Ala	Phe	Ala
				85					90					95	
Asn	Asn	Tyr	Val	Val	Asn	Ala	Gln	Lys	Gly	Ala	Phe	Ala	Asp	Leu	Thr
			100					105					110		
Thr	Leu	Met	Pro	Lys	Tyr	Ala	Lys	Lys	Thr	Tyr	Lys	Asn	Leu	Asp	Pro
		115					120					125			
Ala	Tyr	Ile	Lys	Gly	Asn	Thr	Ile	Asp	Gly	Lys	Leu	Tyr	Ala	Phe	Pro
	130					135					140				
Val	Asp	Ala	Asn	Val	Tyr	Ala	Gln	Gln	Met	Leu	Ser	Phe	Asn	Lys	Glu
145					150					155					160
Leu	Val	Asp	Lys	Tyr	Gly	Leu	Asp	Ile	Ser	Asn	Ile	Lys	Ser	Tyr	Ala
			165					170						175	
Asp	Ala	Glu	Asn	Val	Leu	Lys	Gln	Phe	His	Glu	Lys	Glu	Pro	Asn	Thr
			180					185					190		
Ala	Ala	Phe	Ala	Ile	Gly	Gln	Val	Phe	Ser	Met	Ser	Gly	Asp	Tyr	Asp
		195					200						205		
Tyr	Pro	Leu	Thr	Lys	Thr	Gln	Pro	Phe	Ala	Val	Lys	Ile	Asp	Glu	Gly
	210					215						220			
Lys	Pro	Thr	Ile	Ile	Asn	Gln	Tyr	Glu	Asp	Glu	Ser	Phe	Lys	Asn	Asn
225					230					235					240
Leu	Arg	Leu	Met	His	Lys	Trp	Tyr	Lys	Glu	Gly	Leu	Ile	Pro	Thr	Asp
				245					250					255	
Ala	Ala	Thr	Asn	Thr	Glu	Gly	Tyr	Pro	Leu	Glu	Gly	Asn	Thr	Trp	Phe
			260					265					270		
Met	Arg	Glu	Glu	Thr	Gln	Gly	Pro	Met	Asp	Tyr	Gly	Asp	Thr	Ile	Leu
		275				280						285			
Thr	Asn	Ala	Ala	Gly	Lys	Asp	Ile	Val	Ser	Arg	Pro	Leu	Thr	Lys	Pro
	290					295					300				
Leu	Lys	Thr	Thr	Ser	Gln	Ala	Gln	Met	Ala	Asn	Phe	Val	Val	Ser	Ser
305					310					315					320
Val	Ser	Lys	Asn	Lys	Glu	Lys	Ala	Val	Glu	Val	Leu	Ser	Leu	Leu	Asn
			325						330					335	
Ser	Asp	Pro	Glu	Leu	Leu	Asn	Gly	Leu	Val	Tyr	Gly	Val	Glu	Gly	Lys
		340						345					350		
Ala	Trp	Glu	Lys	Ile	Gly	Asp	Lys	Lys	Ile	Lys	Leu	Leu	Asp	Gly	Tyr
		355					360					365			
Gln	Pro	Lys	Asn	Ala	His	Gly	Cys	Leu	Glu	Tyr	Trp				
	370					375					380				

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<210> SEQ ID NO 153
<211> LENGTH: 624
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 153
atgaaaaaag gactattagt aacaactggt ttggcttgct tcgggctact aactgcttgc      60
tcaacccaag acaatatggc taaaaaggaa ataactcagg acaagatgag catggcagct      120
aaaaagaaaag ataagatgct aacatcaaag gacaagtcca tgatggcaga taaatcatct      180
gataagaaaa tgaccaatga tggtcctatg gcgcctgatt tcgaactcaa aggcacatgat      240
ggtaagacct atcgcttatc agagttcaaa ggtaaaaaaag tttatttgaa attttgggcc      300
tcttggtggt caatctgtct atcaaccttg gcagataccg aagacctggc taaaatgtca      360
gataaagact atgtggtcct aacagttgct tcgccaggtc atcaagggga aaaatcagaa      420
gcagacttta aaaaatgggt ccaaggaaca gactataagg acttaccagt cttgttagat      480
ccggatggca agctattgga agcttacggt gtcagatctt acccaacaga agttttcatt      540
ggaagtgatg gtgttcttgc taaaaaacac attggttatg ccaaaaaatc agacatcaaa      600
aagaccctta aaggtataca ttag                                     624

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<210> SEQ ID NO 154
<211> LENGTH: 207
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 154
Met Lys Lys Gly Leu Leu Val Thr Thr Gly Leu Ala Cys Leu Gly Leu
1          5          10          15
Leu Thr Ala Cys Ser Thr Gln Asp Asn Met Ala Lys Lys Glu Ile Thr
20          25          30
Gln Asp Lys Met Ser Met Ala Ala Lys Lys Lys Asp Lys Met Ser Thr
35          40          45
Ser Lys Asp Lys Ser Met Met Ala Asp Lys Ser Ser Asp Lys Lys Met
50          55          60
Thr Asn Asp Gly Pro Met Ala Pro Asp Phe Glu Leu Lys Gly Ile Asp
65          70          75          80
Gly Lys Thr Tyr Arg Leu Ser Glu Phe Lys Gly Lys Lys Val Tyr Leu
85          90          95
Lys Phe Trp Ala Ser Trp Cys Ser Ile Cys Leu Ser Thr Leu Ala Asp
100         105         110
Thr Glu Asp Leu Ala Lys Met Ser Asp Lys Asp Tyr Val Val Leu Thr
115         120         125
Val Val Ser Pro Gly His Gln Gly Glu Lys Ser Glu Ala Asp Phe Lys
130         135         140
Lys Trp Phe Gln Gly Thr Asp Tyr Lys Asp Leu Pro Val Leu Leu Asp
145         150         155         160
Pro Asp Gly Lys Leu Leu Glu Ala Tyr Gly Val Arg Ser Tyr Pro Thr
165         170         175
Glu Val Phe Ile Gly Ser Asp Gly Val Leu Ala Lys Lys His Ile Gly
180         185         190
Tyr Ala Lys Lys Ser Asp Ile Lys Lys Thr Leu Lys Gly Ile His
195         200         205

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<210> SEQ ID NO 155
<211> LENGTH: 228
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 155
gtgttaagaa agaagaaaac taccattgta gggattatgt taggaatgat gatagtgacc      60
ttacttgctg gctgtttgac tggtaaaaag aaaggctttc ctcctaaagc aggtgagcgg      120

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cagcaaacgg	ctgacttaaa	aatgaaaaaa	agattagaaa	aactgttcaa	aaaccgttac	180
ctgaaaaaatc	taaagaggct	aagcaagctg	ttatggatgc	agatttag		228

<210> SEQ ID NO 156
 <211> LENGTH: 75
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 156

Met	Leu	Arg	Lys	Lys	Lys	Thr	Thr	Ile	Val	Gly	Ile	Ile	Leu	Gly	Met
1			5						10				15		
Met	Ile	Val	Thr	Leu	Leu	Val	Gly	Cys	Leu	Thr	Gly	Lys	Lys	Lys	Gly
			20					25					30		
Phe	Pro	Pro	Lys	Ala	Gly	Glu	Arg	Gln	Gln	Thr	Ala	Asp	Leu	Lys	Met
		35					40					45			
Lys	Lys	Arg	Leu	Glu	Lys	Leu	Phe	Lys	Asn	Arg	Tyr	Leu	Lys	Asn	Leu
	50					55					60				
Lys	Arg	Leu	Ser	Lys	Leu	Leu	Trp	Met	Gln	Ile					
65					70					75					

<210> SEQ ID NO 157
 <211> LENGTH: 1032
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 157

atgaaaacga	aaaaagttat	tatttttagtt	ggtctattgt	tatcatctca	gttgactttg	60
atagcttgtc	aatcacgagg	taatggtaca	tatcccatta	aaacgaaaca	atcacgtaag	120
ggaatgacgt	caaacaaaat	taaaccgatt	aaaaaaagca	aaaagacaaa	caagactcac	180
aaaggtgtgg	cgggtgtcga	ttttcctaca	gatgatgggt	ttattttaac	caaagactca	240
aaaatcttat	caaaaacaga	tcagggaatc	gttggtgacc	atgatggtca	ttcgcatttt	300
attttttatg	ccgatttaaa	gggaagtcca	tttgaatacc	ttattccaaa	aggagcaagt	360
ttagctaagc	cagctgttgc	tcagcgagca	gctagtcaag	ggacttctaa	agtagcagat	420
cctcatcacc	attatgaatt	taaccagcg	gatattgtgg	ctgaagatgc	tttaggctac	480
acggttcgcc	acgatgatca	cttccattat	attttgaagt	caagcttatc	aggtcagaca	540
caggcacaa	ctaaacaggt	tgctactcgc	ttgccacaaa	ccagtagcct	tgtttcaaca	600
gctacagcta	atggtattcc	aggcttgcat	ttcccaacct	cagatggttt	tcaatttaac	660
ggtcaaggta	ttggtgggg	aacaaaagac	agtattttag	tggaccacga	tggtcactta	720
catcctat	cttttgcgga	ccttcgctcag	ggtggctggg	cacatgtggc	agatcaatac	780
gatcccgcta	aaaaagcaga	aaagccagca	gaaacccatc	agacaccaga	gctatctgaa	840
cgtgaaaagg	aataccaaga	aaaattagct	tatttggcag	aaaaattggg	gattgatcca	900
tcaactatta	aacgtgtgga	aacacaagac	ggtaaaacttg	gtttggaata	ccctcaccat	960
gaccacgcac	acgtattgat	gttatctgaa	attgaaatcg	ggaaaagaca	ttccagatcc	1020
acatgctatt	ga					1032

<210> SEQ ID NO 158
 <211> LENGTH: 343
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 158

Met	Lys	Thr	Lys	Lys	Val	Ile	Ile	Leu	Val	Gly	Leu	Leu	Leu	Ser	Ser
1			5						10				15		
Gln	Leu	Thr	Leu	Ile	Ala	Cys	Gln	Ser	Arg	Gly	Asn	Gly	Thr	Tyr	Pro
			20					25					30		
Ile	Lys	Thr	Lys	Gln	Ser	Arg	Lys	Gly	Met	Thr	Ser	Asn	Lys	Ile	Lys
		35					40					45			
Pro	Ile	Lys	Lys	Ser	Lys	Lys	Thr	Asn	Lys	Thr	His	Lys	Gly	Val	Ala
	50					55					60				
Gly	Val	Asp	Phe	Pro	Thr	Asp	Asp	Gly	Phe	Ile	Leu	Thr	Lys	Asp	Ser

65					70					75					80
Lys	Ile	Leu	Ser	Lys	Thr	Asp	Gln	Gly	Ile	Val	Val	Asp	His	Asp	Gly
				85					90					95	
His	Ser	His	Phe	Ile	Phe	Tyr	Ala	Asp	Leu	Lys	Gly	Ser	Pro	Phe	Glu
			100					105					110		
Tyr	Leu	Ile	Pro	Lys	Gly	Ala	Ser	Leu	Ala	Lys	Pro	Ala	Val	Ala	Gln
		115					120					125			
Arg	Ala	Ala	Ser	Gln	Gly	Thr	Ser	Lys	Val	Ala	Asp	Pro	His	His	His
	130					135					140				
Tyr	Glu	Phe	Asn	Pro	Ala	Asp	Ile	Val	Ala	Glu	Asp	Ala	Leu	Gly	Tyr
145				150						155					160
Thr	Val	Arg	His	Asp	Asp	His	Phe	His	Tyr	Ile	Leu	Lys	Ser	Ser	Leu
			165						170					175	
Ser	Gly	Gln	Thr	Gln	Ala	Gln	Ala	Lys	Gln	Val	Ala	Thr	Arg	Leu	Pro
			180					185					190		
Gln	Thr	Ser	Ser	Leu	Val	Ser	Thr	Ala	Thr	Ala	Asn	Gly	Ile	Pro	Gly
		195					200					205			
Leu	His	Phe	Pro	Thr	Ser	Asp	Gly	Phe	Gln	Phe	Asn	Gly	Gln	Gly	Ile
	210					215					220				
Val	Gly	Val	Thr	Lys	Asp	Ser	Ile	Leu	Val	Asp	His	Asp	Gly	His	Leu
225				230						235					240
His	Pro	Ile	Ser	Phe	Ala	Asp	Leu	Arg	Gln	Gly	Gly	Trp	Ala	His	Val
			245						250					255	
Ala	Asp	Gln	Tyr	Asp	Pro	Ala	Lys	Lys	Ala	Glu	Lys	Pro	Ala	Glu	Thr
			260				265						270		
His	Gln	Thr	Pro	Glu	Leu	Ser	Glu	Arg	Glu	Lys	Glu	Tyr	Gln	Glu	Lys
		275					280					285			
Leu	Ala	Tyr	Leu	Ala	Glu	Lys	Leu	Gly	Ile	Asp	Pro	Ser	Thr	Ile	Lys
	290					295					300				
Arg	Val	Glu	Thr	Gln	Asp	Gly	Lys	Leu	Gly	Leu	Glu	Tyr	Pro	His	His
305				310						315					320
Asp	His	Ala	His	Val	Leu	Met	Leu	Ser	Glu	Ile	Glu	Ile	Gly	Lys	Arg
			325						330					335	
His	Ser	Arg	Ser	Thr	Cys	Tyr									
			340												

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<210> SEQ ID NO 159
<211> LENGTH: 300
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 159
atgtcatgga attggaaaaa aacatctgtg cttggaactt tacccttagc ttcagtgcta      60
cccctaactg cttgcgtaag tgggtggtggt aaaggcgta aggaacaga cggaaagact      120
attgtagtct ctgttgatga gggatatggt gattacatta agagtattaa gggtagagttt      180
gaaaaagaac ataaagtcac cgtaaagtc aaaaaagaag gtatgatgga tactcttgat      240
aagctatcaa cggatgggtcc aacaggagct tcaccagatg tcttttttagc acctttttga      300

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<210> SEQ ID NO 160
<211> LENGTH: 99
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 160
Met Ser Trp Asn Trp Lys Lys Thr Ser Val Leu Gly Thr Leu Ser Leu
1          5          10          15
Ala Ser Val Leu Pro Leu Thr Ala Cys Val Ser Gly Gly Gly Lys Gly
20          25          30
Val Lys Glu Thr Asp Gly Lys Thr Ile Val Val Ser Val Asp Glu Gly

```

	35						40					45					
Tyr	Val	Asp	Tyr	Ile	Lys	Ser	Ile	Lys	Gly	Glu	Phe	Glu	Lys	Glu	His		
	50					55					60						
Lys	Val	Thr	Val	Lys	Val	Lys	Lys	Glu	Gly	Met	Met	Asp	Thr	Leu	Asp		
65					70					75					80		
Lys	Leu	Ser	Thr	Asp	Gly	Pro	Thr	Gly	Ala	Ser	Pro	Asp	Val	Phe	Leu		
				85					90						95		
Ala	Pro	Phe															

<210> SEQ ID NO 161

<211> LENGTH: 621

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 161

atgacaaaaa	aacacttact	aacacttctt	ctcatctctt	tttttactag	cttttttgta	60
gcttggttcaa	caacgaaaga	taaagagcct	caaccgtctg	attcagaaat	cattactccc	120
cgactacacc	aagccgctca	tcaagataaa	cgcgctaaact	ttgaaaaaat	taaacttgcg	180
actggttgatt	cctcatttac	aggagggaca	agccttgaag	aacttatctt	actctttgga	240
gagcctagcc	aacatgatcc	aaaaacagca	ggcgaagtaa	caatcgacgc	ttatacttgg	300
cagtttgatc	aagttactct	cactgttaat	ctttatcaaa	atagtagtat	tggtaaaacc	360
atctctaatt	ttacctttgc	aagagagtta	ggcttatcgc	aaaaggaata	ccaacaatta	420
caaaaaggaa	tgtcttatga	agacgttaaa	aagatcttaa	cagaacctga	taattatagc	480
caagcgtcat	ctagtgatca	tcaaactttg	caagcgattt	gggttagtgg	cttaaagaca	540
gatacaagcg	gagctaatat	ttctctcgtt	tttgaaaata	atcagttaac	agaaatgtct	600
caggtaggac	ttgaagaata	a				621

<210> SEQ ID NO 162

<211> LENGTH: 206

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 162

Met	Thr	Lys	Lys	His	Leu	Leu	Thr	Leu	Leu	Ile	Ser	Phe	Phe	Thr
1				5					10				15	
Ser	Phe	Leu	Val	Ala	Cys	Ser	Thr	Thr	Lys	Asp	Lys	Glu	Pro	Gln
			20					25				30		
Ser	Asp	Ser	Glu	Ile	Ile	Thr	Pro	Arg	Leu	His	Gln	Ala	Ala	His
			35				40				45			
Asp	Lys	Arg	Ala	Asn	Phe	Glu	Lys	Ile	Lys	Leu	Ala	Thr	Val	Asp
	50					55				60				
Ser	Phe	Thr	Gly	Gly	Thr	Ser	Leu	Glu	Glu	Leu	Ile	Ser	Leu	Phe
65				70					75					80
Glu	Pro	Ser	Gln	His	Asp	Pro	Lys	Thr	Ala	Gly	Glu	Val	Thr	Ile
				85				90					95	
Ala	Tyr	Thr	Trp	Gln	Phe	Asp	Gln	Val	Thr	Leu	Thr	Val	Asn	Leu
			100				105					110		
Gln	Asn	Ser	Ser	Ile	Val	Lys	Thr	Ile	Ser	Asn	Phe	Thr	Phe	Ala
		115				120					125			
Glu	Leu	Gly	Leu	Ser	Gln	Lys	Glu	Tyr	Gln	Gln	Leu	Gln	Lys	Gly
	130					135				140				
Ser	Tyr	Glu	Asp	Val	Lys	Lys	Ile	Leu	Thr	Glu	Pro	Asp	Asn	Tyr
145					150					155				160
Gln	Ala	Ser	Ser	Ser	Asp	His	Gln	Thr	Leu	Gln	Ala	Ile	Trp	Val
				165				170					175	
Gly	Leu	Lys	Thr	Asp	Thr	Ser	Gly	Ala	Asn	Ile	Ser	Leu	Val	Phe
			180				185					190		
Asn	Asn	Gln	Leu	Thr	Glu	Met	Ser	Gln	Val	Gly	Leu	Glu	Glu	
		195					200					205		

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<210> SEQ ID NO 163
<211> LENGTH: 867
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 163
  atgaaaatga aaaaaaaatt ctttttggtta agtcttttgg ccctatcaac tttcttttta    60
  tccgcatggt ctagctggat tgataaagggt gagtcaataa ccgctgtagg atcaacagca    120
  ctacaaccct tagtagaagc agtagctgat gaatttggaa gcagtaatct aggcaagact    180
  gtcaatgttc aaggtggtgg ttcaggtaca gggttgtctc aagttcaatc aggagctgtc    240
  caaattggaa atagtgatgt ctttgcgga gaaaaagatg gtattgatgc ttctaaatta    300
  gttgatcatc aagtagctgt tgcaggactt gcagttattg ccaatcctaa agtcaagggt    360
  tccaatctca gtagtcagca gttgcaaaag attttttcag gagaatatac caattggaaa    420
  caagttggag gagaagatct tgcgatttca gtgatcaacc gagcagcaag ttctgggtca    480
  cgagcaacct ttgacagtgt tatcatgaaa ggggtcaacg ctaaacaaaag tcaagagcaa    540
  gactccaatg ggatgggttaa atcgattggt tcacaaacac caggtgccat ttcttacctt    600
  tcctttgcct acgttgattc atctgttaaa tctttgcaat taaatggggt taaggcaaat    660
  gctaagaacg tggctacaaa tgattggcca atctggtcct acgaacacat gtataccaaa    720
  gataaaccaa cagggttgac caaggaattt cttgattata tgttttcaga tgaagtacaa    780
  cagaacattg ttacacatat gggatatatt tcgataaatg atatggaagt ggtcaaactc    840
  catgatggaa aagtaacaaa aaggttaa                                867

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<210> SEQ ID NO 164
<211> LENGTH: 288
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 164
  Met Lys Met Lys Lys Lys Phe Phe Leu Leu Ser Leu Leu Ala Leu Ser
  1      5      10      15
  Thr Phe Phe Leu Ser Ala Cys Ser Ser Trp Ile Asp Lys Gly Glu Ser
  20     25     30
  Ile Thr Ala Val Gly Ser Thr Ala Leu Gln Pro Leu Val Glu Ala Val
  35     40     45
  Ala Asp Glu Phe Gly Ser Ser Asn Leu Gly Lys Thr Val Asn Val Gln
  50     55     60
  Gly Gly Gly Ser Gly Thr Gly Leu Ser Gln Val Gln Ser Gly Ala Val
  65     70     75     80
  Gln Ile Gly Asn Ser Asp Val Phe Ala Glu Glu Lys Asp Gly Ile Asp
  85     90     95
  Ala Ser Lys Leu Val Asp His Gln Val Ala Val Ala Gly Leu Ala Val
  100    105    110
  Ile Ala Asn Pro Lys Val Lys Val Ser Asn Leu Ser Ser Gln Gln Leu
  115    120    125
  Gln Lys Ile Phe Ser Gly Glu Tyr Thr Asn Trp Lys Gln Val Gly Gly
  130    135    140
  Glu Asp Leu Ala Ile Ser Val Ile Asn Arg Ala Ala Ser Ser Gly Ser
  145    150    155    160
  Arg Ala Thr Phe Asp Ser Val Ile Met Lys Gly Val Asn Ala Lys Gln
  165    170    175
  Ser Gln Glu Gln Asp Ser Asn Gly Met Val Lys Ser Ile Val Ser Gln
  180    185    190
  Thr Pro Gly Ala Ile Ser Tyr Leu Ser Phe Ala Tyr Val Asp Ser Ser
  195    200    205
  Val Lys Ser Leu Gln Leu Asn Gly Phe Lys Ala Asn Ala Lys Asn Val
  210    215    220
  Ala Thr Asn Asp Trp Pro Ile Trp Ser Tyr Glu His Met Tyr Thr Lys
  225    230    235    240

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Asp	Lys	Pro	Thr	Gly	Leu	Thr	Lys	Glu	Phe	Leu	Asp	Tyr	Met	Phe	Ser
				245					250					255	
Asp	Glu	Val	Gln	Gln	Asn	Ile	Val	Thr	His	Met	Gly	Tyr	Ile	Ser	Ile
			260					265					270		
Asn	Asp	Met	Glu	Val	Val	Lys	Ser	His	Asp	Gly	Lys	Val	Thr	Lys	Arg
		275					280						285		

<210> SEQ ID NO 165
 <211> LENGTH: 1053
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 165

atgaacaaga	aattttattgg	tcttggttta	gcgtcagtg	ctgtgctgag	tttagctgct	60
tgtggtaatc	gtggtgcttc	taaaggtggg	gcatcaggaa	aaactgattt	aaaagttgca	120
atgggtaccg	atactggtgg	tgtagatgac	aaatcattca	accaatcagc	atgggaaggc	180
ctgcaatcct	ggggtaaaga	aatgggcctt	caaaaaggaa	caggtttcga	ttattttcaa	240
tctacaagtg	aatctgagta	tgcaactaat	ctcgatacag	cagtttcagg	agggtatcaa	300
ctgatttatg	gtatcggtct	tgcattgaaa	gatgctattg	ctaaagcagc	tggagataat	360
gaaggagtta	agtttggtat	tatcgatgat	attatcgaag	gaaaagataa	tgtagccagt	420
gttacctttg	ccgaccatga	agctgcttat	cttgcaggaa	ttgcagctgc	aaaaacaaca	480
aaaacaaaaa	cagttgggtt	cgtgggcggt	atggaaggaa	ctgtcataac	tcgatttgaa	540
aaaggttttg	aagcaggagt	taagtctggt	gacgatacaa	tccaagttaa	agttgattat	600
gctggatcat	ttggtgacgc	tgcaaaaagga	aaaacaatcg	cagcagctca	gtatgcagca	660
ggtgctgatg	ttattttacca	ggcagcagga	ggcactggag	caggtgtatt	taatgaagca	720
aaagctatta	atgaaaaacg	tagtgaagct	gataaagttt	gggttattgg	tgttgaccgt	780
gatcaaaaag	acgaaggaaa	atacacttct	aaagatggca	aagaagcaaa	ctttgtactt	840
gcatcatcaa	tcaaagaagt	cggtaaaagct	gttcagttaa	tcaacaagca	agtagcagat	900
aaaaaattcc	ctggaggaaa	aacaactgtc	tatgggtctaa	aagatggcgg	tgttgaaatc	960
gcaactacaa	atgtttcaaa	agaagctgtt	aaagctatta	aagaagcgaa	agcaaaaatt	1020
aaatctggtg	acattaaagt	tcctgaaaaa	tag			1053

<210> SEQ ID NO 166
 <211> LENGTH: 350
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 166

Met	Asn	Lys	Lys	Phe	Ile	Gly	Leu	Gly	Leu	Ala	Ser	Val	Ala	Val	Leu
1				5					10					15	
Ser	Leu	Ala	Ala	Cys	Gly	Asn	Arg	Gly	Ala	Ser	Lys	Gly	Gly	Ala	Ser
			20					25					30		
Gly	Lys	Thr	Asp	Leu	Lys	Val	Ala	Met	Val	Thr	Asp	Thr	Gly	Gly	Val
		35				40					45				
Asp	Asp	Lys	Ser	Phe	Asn	Gln	Ser	Ala	Trp	Glu	Gly	Leu	Gln	Ser	Trp
	50				55					60					
Gly	Lys	Glu	Met	Gly	Leu	Gln	Lys	Gly	Thr	Gly	Phe	Asp	Tyr	Phe	Gln
65					70				75					80	
Ser	Thr	Ser	Glu	Ser	Glu	Tyr	Ala	Thr	Asn	Leu	Asp	Thr	Ala	Val	Ser
			85					90					95		
Gly	Gly	Tyr	Gln	Leu	Ile	Tyr	Gly	Ile	Gly	Phe	Ala	Leu	Lys	Asp	Ala
		100					105						110		
Ile	Ala	Lys	Ala	Ala	Gly	Asp	Asn	Glu	Gly	Val	Lys	Phe	Val	Ile	Ile
		115				120						125			
Asp	Asp	Ile	Ile	Glu	Gly	Lys	Asp	Asn	Val	Ala	Ser	Val	Thr	Phe	Ala
	130					135					140				
Asp	His	Glu	Ala	Ala	Tyr	Leu	Ala	Gly	Ile	Ala	Ala	Ala	Lys	Thr	Thr
145					150				155					160	
Lys	Thr	Lys	Thr	Val	Gly	Phe	Val	Gly	Gly	Met	Glu	Gly	Thr	Val	Ile

				165					170					175			
Thr	Arg	Phe	Glu	Lys	Gly	Phe	Glu	Ala	Gly	Val	Lys	Ser	Val	Asp	Asp		
			180					185					190				
Thr	Ile	Gln	Val	Lys	Val	Asp	Tyr	Ala	Gly	Ser	Phe	Gly	Asp	Ala	Ala		
		195					200					205					
Lys	Gly	Lys	Thr	Ile	Ala	Ala	Ala	Gln	Tyr	Ala	Ala	Gly	Ala	Asp	Val		
	210					215					220						
Ile	Tyr	Gln	Ala	Ala	Gly	Gly	Thr	Gly	Ala	Gly	Val	Phe	Asn	Glu	Ala		
225					230					235				240			
Lys	Ala	Ile	Asn	Glu	Lys	Arg	Ser	Glu	Ala	Asp	Lys	Val	Trp	Val	Ile		
			245					250					255				
Gly	Val	Asp	Arg	Asp	Gln	Lys	Asp	Glu	Gly	Lys	Tyr	Thr	Ser	Lys	Asp		
		260						265				270					
Gly	Lys	Glu	Ala	Asn	Phe	Val	Leu	Ala	Ser	Ser	Ile	Lys	Glu	Val	Gly		
	275					280					285						
Lys	Ala	Val	Gln	Leu	Ile	Asn	Lys	Gln	Val	Ala	Asp	Lys	Lys	Phe	Pro		
	290					295				300							
Gly	Gly	Lys	Thr	Thr	Val	Tyr	Gly	Leu	Lys	Asp	Gly	Gly	Val	Glu	Ile		
305					310					315				320			
Ala	Thr	Thr	Asn	Val	Ser	Lys	Glu	Ala	Val	Lys	Ala	Ile	Lys	Glu	Ala		
			325					330				335					
Lys	Ala	Lys	Ile	Lys	Ser	Gly	Asp	Ile	Lys	Val	Pro	Glu	Lys				
		340						345				350					

<210> SEQ ID NO 167

<211> LENGTH: 708

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 167

atgacaaaaa	agaaaggtaa	gcttgacttt	atcagtccttt	ttgttctagc	agcttggttta	60
ggagcttata	gtgcaatgag	acaatctcat	aaaacttcaa	acgtgtcagc	tgagactatc	120
gccagttcct	caacccgaca	ttttattgat	gaaattggtc	caactgctag	tactattggt	180
caagaacgtg	atctttatgc	gtctgttatg	atagcacaag	cgattttaga	atcaagtaat	240
ggtaaatcaa	gtctaagtca	agcaccttat	tataattttt	tcggtattaa	gggtgcctat	300
aacggttcct	ctgtgacgat	gtcaacttgg	gaagatgatg	gtaatggcaa	tacctatacg	360
attgatcaag	cctttagagc	ttatccaagt	attgcagact	cccttaatga	ctacgcggac	420
ttgctaagtt	ctagcactta	tataggtgct	agaaaatcaa	acacgctatc	gtatcaagat	480
gctacagcag	ctctaactgg	cttatacgct	acagacacca	gttataactt	aaaactaaat	540
aatattattg	caacctatgg	tttgacggct	tatgatgttg	ctaatagctc	agctcaagaa	600
actggtctag	caacttcggg	ttatgtttgg	aatgaatata	gtcgtaatga	cactgatgcg	660
gagaccctag	cagttgatga	ggcttgggct	aaacgcata	cttattaa		708

<210> SEQ ID NO 168

<211> LENGTH: 235

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 168

Met	Thr	Lys	Lys	Lys	Gly	Lys	Leu	Val	Leu	Ile	Ser	Leu	Phe	Val	Leu
1			5					10					15		
Ala	Ala	Cys	Leu	Gly	Ala	Tyr	Ser	Ala	Met	Arg	Gln	Ser	His	Lys	Thr
		20					25					30			
Ser	Asn	Val	Ser	Ala	Glu	Thr	Ile	Ala	Ser	Ser	Ser	Thr	Arg	His	Phe
	35					40					45				
Ile	Asp	Glu	Ile	Gly	Pro	Thr	Ala	Ser	Thr	Ile	Gly	Gln	Glu	Arg	Asp
	50				55				60						
Leu	Tyr	Ala	Ser	Val	Met	Ile	Ala	Gln	Ala	Ile	Leu	Glu	Ser	Ser	Asn
65				70					75					80	

Gly	Lys	Ser	Ser	Leu	Ser	Gln	Ala	Pro	Tyr	Tyr	Asn	Phe	Phe	Gly	Ile
				85					90					95	
Lys	Gly	Ala	Tyr	Asn	Gly	Ser	Ser	Val	Thr	Met	Ser	Thr	Trp	Glu	Asp
			100					105					110		
Asp	Gly	Asn	Gly	Asn	Thr	Tyr	Thr	Ile	Asp	Gln	Ala	Phe	Arg	Ala	Tyr
		115					120					125			
Pro	Ser	Ile	Ala	Asp	Ser	Leu	Asn	Asp	Tyr	Ala	Asp	Leu	Leu	Ser	Ser
		130				135					140				
Ser	Thr	Tyr	Ile	Gly	Ala	Arg	Lys	Ser	Asn	Thr	Leu	Ser	Tyr	Gln	Asp
145					150					155					160
Ala	Thr	Ala	Ala	Leu	Thr	Gly	Leu	Tyr	Ala	Thr	Asp	Thr	Ser	Tyr	Asn
				165					170					175	
Leu	Lys	Leu	Asn	Asn	Ile	Ile	Ala	Thr	Tyr	Gly	Leu	Thr	Ala	Tyr	Asp
			180					185					190		
Val	Ala	Asn	Ser	Ser	Ala	Gln	Glu	Thr	Gly	Leu	Ala	Thr	Ser	Gly	Tyr
		195					200					205			
Val	Trp	Asn	Glu	Tyr	Arg	Arg	Asn	Tyr	Thr	Asp	Ala	Glu	Thr	Leu	Ala
	210					215					220				
Val	Asp	Glu	Ala	Trp	Ala	Lys	Arg	Met	Thr	Tyr					
225					230					235					

<210> SEQ ID NO 169
 <211> LENGTH: 549
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 169

atgaaaaaat	taactctact	attaacactc	tgtttgacaa	ctattacctt	aatcgctgt	60
ggtaatcaag	caactaatca	ttctaacacc	gcctcaaaaa	gtttatcgcc	tatgcctcaa	120
attgctggtg	tgacttatta	cggagatatt	cctaaacagc	ctaagcgagt	agtcagtctg	180
gcttcaactt	acactgggta	cctcaaaaaa	ttagatatga	atctagtcgg	ggttacttct	240
tatgacaaga	aaaaccccat	cctagcaaag	actgtaaaaa	aagcaaagca	agttgctgca	300
actgatttag	aagccgttac	aacgccttaag	cctgacctca	ttgttggttg	ctctacagaa	360
gaaaatatta	aacaattggc	agaaattgcg	cctgttatct	cgattgaata	ccgcaaacgt	420
gattatttac	aagtgttatc	tgacttcggc	cgcattctta	acaaagaaga	caaagccaag	480
aagtgggtaa	aagattggaa	aactaaaaca	gcagcttatg	aaaaagaaag	tcaaggccgt	540
tacaggtga						549

<210> SEQ ID NO 170
 <211> LENGTH: 182
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 170

Met	Lys	Lys	Leu	Thr	Leu	Leu	Leu	Thr	Leu	Cys	Leu	Thr	Thr	Ile	Thr
1				5					10					15	
Leu	Ile	Ala	Cys	Gly	Asn	Gln	Ala	Thr	Asn	His	Ser	Asn	Thr	Ala	Ser
			20					25					30		
Lys	Ser	Leu	Ser	Pro	Met	Pro	Gln	Ile	Ala	Gly	Val	Thr	Tyr	Tyr	Gly
		35				40					45				
Asp	Ile	Pro	Lys	Gln	Pro	Lys	Arg	Val	Val	Ser	Leu	Ala	Ser	Thr	Tyr
	50					55				60					
Thr	Gly	Tyr	Leu	Lys	Lys	Leu	Asp	Met	Asn	Leu	Val	Gly	Val	Thr	Ser
65					70					75					80
Tyr	Asp	Lys	Lys	Asn	Pro	Ile	Leu	Ala	Lys	Thr	Val	Lys	Lys	Ala	Lys
			85						90					95	
Gln	Val	Ala	Ala	Thr	Asp	Leu	Glu	Ala	Val	Thr	Thr	Leu	Lys	Pro	Asp
			100					105					110		
Leu	Ile	Val	Val	Gly	Ser	Thr	Glu	Glu	Asn	Ile	Lys	Gln	Leu	Ala	Glu

	115						120					125					
Ile	Ala	Pro	Val	Ile	Ser	Ile	Glu	Tyr	Arg	Lys	Arg	Asp	Tyr	Leu	Gln		
	130						135					140					
Val	Leu	Ser	Asp	Phe	Gly	Arg	Ile	Phe	Asn	Lys	Glu	Asp	Lys	Ala	Lys		
145					150					155					160		
Lys	Trp	Leu	Lys	Asp	Trp	Lys	Thr	Lys	Thr	Ala	Ala	Tyr	Glu	Lys	Glu		
				165					170					175			
Ser	Gln	Gly	Arg	Tyr	Arg												
				180													

<210> SEQ ID NO 171
 <211> LENGTH: 924
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 171

ttgaaactaa	cattaaatcg	catcctcttt	tcaggactag	cactgtcaat	tctactcacc	60
ttgacaggct	gtgtgggaag	agacgctcac	ggaaatccca	aaggtatgat	ttgggaattt	120
cttggaatac	ccatgtcata	ctttatcgat	tactttgcaa	acaatgctgg	actaggttat	180
ggactggcta	tcatcatcgt	aaccattatt	gttagaacac	ttatcttacc	actagggtta	240
tatcaatctt	ggaaagcaag	ttatcaatct	gagaaaaatg	ccttcttgaa	acctgttttt	300
gaaccaatca	acaaacgtat	caaacaggca	aatagtcagg	aagaaaaaat	ggctgcccac	360
acagaattaa	tggctgctca	gcgtgctcat	gggattaacc	ctcttggagg	tattggatgt	420
ctacctcttc	tcatccagat	gccattcttt	tctgccatgt	atcttgccgc	tcaatacact	480
aaaggagtat	caacaagcac	ctttatgggt	attgatcttg	gtagccgtag	tttagtggtta	540
acagcaatta	tcgctgctct	ttacttcttc	caatcatggt	tatcaatgat	ggccgtttca	600
gaagaacaac	gtgagcaaag	gaagacgatg	atgtacacca	tgcctatcat	gatgatcttc	660
atgtccttct	cactccctgc	tgggtgttgg	ctttactggc	tagttggtgg	tttctttagt	720
attattcaac	agttaatcac	aacctacctc	ttaaaacctc	gattgcataa	gcaaattaaa	780
gaagaatacg	ctaaaaaccc	gcctaaagca	taccaatcaa	cttcttctcg	taaggacgtt	840
acgccttcac	aaaacatgga	acaggctaac	ttgcctaaaa	aaataaaaatc	caatcgtaat	900
gctggaaaac	agcgaaagcg	ttaa				924

<210> SEQ ID NO 172
 <211> LENGTH: 307
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 172

Met	Lys	Leu	Thr	Leu	Asn	Arg	Ile	Leu	Phe	Ser	Gly	Leu	Ala	Leu	Ser
1				5					10					15	
Ile	Leu	Leu	Thr	Leu	Thr	Gly	Cys	Val	Gly	Arg	Asp	Ala	His	Gly	Asn
			20					25					30		
Pro	Lys	Gly	Met	Ile	Trp	Glu	Phe	Leu	Gly	Lys	Pro	Met	Ser	Tyr	Phe
		35					40					45			
Ile	Asp	Tyr	Phe	Ala	Asn	Asn	Ala	Gly	Leu	Gly	Tyr	Gly	Leu	Ala	Ile
	50					55				60					
Ile	Ile	Val	Thr	Ile	Ile	Val	Arg	Thr	Leu	Ile	Leu	Pro	Leu	Gly	Leu
65					70					75				80	
Tyr	Gln	Ser	Trp	Lys	Ala	Ser	Tyr	Gln	Ser	Glu	Lys	Met	Ala	Phe	Leu
				85					90					95	
Lys	Pro	Val	Phe	Glu	Pro	Ile	Asn	Lys	Arg	Ile	Lys	Gln	Ala	Asn	Ser
			100						105				110		
Gln	Glu	Glu	Lys	Met	Ala	Ala	Gln	Thr	Glu	Leu	Met	Ala	Ala	Gln	Arg
		115					120					125			
Ala	His	Gly	Ile	Asn	Pro	Leu	Gly	Gly	Ile	Gly	Cys	Leu	Pro	Leu	Leu
	130					135					140				
Ile	Gln	Met	Pro	Phe	Phe	Ser	Ala	Met	Tyr	Phe	Ala	Ala	Gln	Tyr	Thr
145					150					155					160

Phe	Lys	Lys	Thr	Glu	Trp	Ser	Ser	Ile	Phe	Thr	Gly	Leu	Asp	Ser	Gly	
				85					90					95		
Lys	Tyr	Gln	Met	Gly	Gly	Asn	Asn	Ile	Ser	Phe	Thr	Lys	Glu	Arg	Ser	
			100					105					110			
Ala	Lys	Tyr	Leu	Phe	Ser	Tyr	Pro	Ile	Gly	Ser	Thr	Pro	Ser	Val	Leu	
			115				120					125				
Val	Val	Pro	Lys	Asp	Ser	Asp	Ile	Lys	Ser	Phe	Asp	Asp	Ile	Gln	Gly	
			130			135					140					
His	Thr	Thr	Gln	Val	Val	Gln	Gly	Thr	Thr	Ser	Val	Ala	Gln	Leu	Glu	
					150					155					160	
Asp	Phe	Asn	Lys	Lys	His	Ser	Asp	Asn	Pro	Val	Thr	Leu	Lys	Phe	Thr	
				165					170					175		
Asn	Glu	Asn	Ile	Thr	Gln	Met	Leu	Thr	Asn	Leu	Ser	Glu	Gly	Lys	Ala	
			180					185					190			
Asp	Phe	Lys	Ile	Phe	Asp	Ala	Pro	Thr	Val	Asn	Ala	Ile	Ile	Lys	Asn	
			195			200						205				
Gln	Gly	Leu	Asp	Asn	Leu	Lys	Thr	Ile	Glu	Leu	Thr	Ser	Thr	Glu	Gln	
			210			215						220				
Pro	Phe	Ile	Tyr	Phe	Ile	Phe	Ser	Gln	Asp	Gln	Glu	Lys	Leu	Gln	Ser	
					230				235						240	
Phe	Val	Asn	Lys	Arg	Ile	Lys	Glu	Leu	Thr	Ala	Asp	Gly	Thr	Leu	Ser	
				245					250					255		
Lys	Leu	Ala	Lys	Glu	His	Leu	Gly	Gly	Asp	Tyr	Val	Pro	Ser	Asp	Lys	
			260				265						270			
Glu	Leu	Lys	Leu	Pro	Thr	Ala	Asn									
			275				280									

<210> SEQ ID NO 175

<211> LENGTH: 828

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 175

ttgagaaagg	ttttgagagt	gaagaaaaac	attaaaattg	caagaatagt	ccccttagtt	60
ctattattag	tggcctgtgg	tcgtggtgag	gtaacggcac	aatcatctag	tggttgggac	120
cagttggttt	acttatttgc	cagagcaatt	caatggcttt	cctttgatgg	ttcaattggg	180
gttggcatta	ttctttttac	ccttactatc	cgtctcatgc	tcatgccttt	gtttaacatg	240
caaatcaaat	caagccagaa	gatgcaagac	atccaacctg	agcttagaga	attgcaaagg	300
aaatacgctg	gtaaagacac	acaaacgcgg	atgaagttgg	ctgaagaaag	tcaagccctt	360
tacaaaaaat	atgggggttaa	cccttatgct	agtctcttac	ccctcttaat	tcagatgcca	420
gttatgattg	ccttattcca	agccttgaca	cgggtatctt	tcttaaaaac	agggactttc	480
ttgtgggtgg	aattggcaca	acatgatcat	ttgtaccttt	taccagtttt	ggcagctgtc	540
ttcactttct	tgtccacttg	gttgaccaat	ctagcggcta	aagaaaaaaa	tgtcatgatg	600
actgttatga	tttatgtgat	gccgctaata	atctttttca	tgggctttta	cttggctagt	660
ggagtagtgc	tctattggac	ggtctccaat	gcctttcaag	tggtacaact	actgttatta	720
aacaatcctt	ttaagattat	tgcggaaaga	caacgtcttg	ccaatgaaga	aaaagaacgc	780
cgtcttcgtg	aacgtcgtgc	tcgtaaaaaa	gcaatgaaga	gaaaatag		828

<210> SEQ ID NO 176

<211> LENGTH: 275

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 176

Met	Arg	Lys	Val	Leu	Arg	Val	Lys	Lys	Asn	Ile	Lys	Ile	Ala	Arg	Ile	
1			5						10				15			
Val	Pro	Leu	Val	Leu	Leu	Val	Ala	Cys	Gly	Arg	Gly	Glu	Val	Thr		
			20				25					30				
Ala	Gln	Ser	Ser	Ser	Gly	Trp	Asp	Gln	Leu	Val	Tyr	Leu	Phe	Ala	Arg	

actcttagta tttcatttgc tagtaggaac tag

1233

<210> SEQ ID NO 178

<211> LENGTH: 410

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 178

Met	Gly	Val	Met	Met	Lys	Gln	Lys	Ile	Lys	Ile	Leu	Thr	Val	Ile	Gly
1				5					10					15	
Leu	Met	Thr	Val	Gly	Met	Ser	Ala	Cys	His	Asn	Thr	Ser	Lys	Pro	Ser
			20					25					30		
Asn	Thr	Asp	Ser	Val	Phe	Ser	Leu	Thr	Gly	Lys	Lys	Arg	Gln	Gln	Ile
		35					40					45			
Val	Lys	Gln	Val	Arg	Gln	Arg	Tyr	Tyr	Phe	Gln	Gln	Leu	Ser	Lys	Thr
	50					55					60				
Glu	Gln	Glu	Asn	Tyr	Leu	Thr	Leu	Tyr	Asp	Ser	Leu	Ala	Gln	Phe	Arg
65					70					75					80
Glu	Ile	Ile	Ser	Leu	Thr	Pro	Ala	Ser	Lys	Lys	Ser	Leu	Ile	Lys	Thr
			85						90					95	
Ile	Asp	Ala	Phe	Val	Met	Asp	Asn	Pro	Glu	Phe	Tyr	Trp	Ile	Thr	Ser
			100					105					110		
Ala	Asp	Tyr	Arg	Phe	Glu	Phe	Ser	Asp	Gln	Thr	Val	Phe	Val	Thr	Phe
	115						120					125			
Pro	Ile	Pro	Glu	Asp	Ala	Lys	Asn	Ile	Tyr	Gln	Asp	Leu	Gln	Ala	Ile
	130					135						140			
Gly	Asn	Asp	Ile	Val	Ala	Asn	Thr	Pro	Ser	Lys	Asp	Arg	Tyr	Glu	Gln
145					150					155					160
Val	Lys	Tyr	Phe	Tyr	Glu	Val	Ile	Ile	Arg	Asp	Thr	Asp	Tyr	Asn	Lys
			165						170					175	
Lys	Ala	Phe	Glu	Ala	Tyr	Gln	Ser	Gly	Ser	Gln	Ala	Gln	Val	Ala	Ser
			180					185					190		
Asn	Gln	Asp	Ile	Lys	Ser	Val	Phe	Ile	Asp	His	Leu	Ser	Val	Cys	Asn
		195					200					205			
Gly	Tyr	Ala	Gln	Ala	Phe	Gln	Phe	Leu	Cys	Gln	Lys	Ala	Gly	Ile	Pro
	210					215					220				
Val	Ala	Tyr	Ile	Arg	Gly	Thr	Gly	Thr	Ser	Gln	Gln	Pro	Gln	Gln	Ser
225					230					235					240
Phe	Ala	His	Ala	Trp	Asn	Ala	Val	Gln	Ile	Asn	Asn	Thr	Tyr	Tyr	Gly
			245						250					255	
Val	Asp	Val	Thr	Trp	Gly	Asp	Pro	Val	Phe	Asp	Asn	His	Leu	Ser	His
			260					265					270		
Gln	Lys	Gln	Gly	Thr	Ile	Asn	Tyr	Ser	Phe	Leu	Cys	Leu	Pro	Asp	Tyr
		275				280						285			
Leu	Met	Ala	Leu	Ser	His	Gln	Pro	Ser	Lys	Asp	Ile	Ala	Phe	Asn	Thr
	290					295					300				
Lys	Glu	Arg	Phe	Glu	Asn	Val	Trp	Thr	Ile	Pro	Ser	Cys	Thr	Asp	Asp
305					310					315					320
Ser	Leu	Leu	Tyr	Ser	Lys	Arg	His	Gln	Ser	Tyr	Ile	Ser	Thr	Phe	Asp
			325						330					335	
Ser	Asp	Ala	Ile	Leu	Ala	Ser	Leu	Glu	Asn	Gln	Leu	Leu	Asn	Arg	Gln
			340					345					350		
Glu	Pro	Leu	Ser	Leu	Gln	Phe	Ala	His	Gln	Asp	Asp	Tyr	Gln	Gln	Met
		355				360						365			
Val	Thr	Asp	Leu	Thr	Thr	Asn	Gln	Thr	Gly	Tyr	His	Asn	Leu	Phe	Asn
	370					375					380				
Gln	Tyr	Trp	Asn	Asn	Tyr	Thr	Gly	Phe	Thr	Tyr	Gly	Leu	Leu	Pro	Glu
385					390					395					400

Thr Leu Ser Ile Ser Phe Ala Ser Arg Asn
405 410

<210> SEQ ID NO 179
<211> LENGTH: 1044
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 179

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atgaacaaaa aagtaatgtc acttgggtctt gtttcgactg ccctattcac attaggaggc 60
tgtaccaata actccgctaa acaaacaaact gacaattcat taaaaatcgc tatgattact 120
aatcagacgg gtattgatga caagtcattt aaccagtcag cctgggaagg cttacaagct 180
tggggaaaaa aaaataaaact tgaaaaagga aaaggctatg attattttcca atcagccaat 240
gaatcagagt ttaccacaaa ccttgagtca gcagtaacca atgggtataa tcttgttttt 300
gggattggat ttccattaca tgacgctgta gaaaaagtag ccgcaacaa tcctgacaac 360
cattttgcaa ttgtggatga tgtgattaaa ggtcaaaaaa atggttgcaag tatcaccttt 420
tcagaccatg aagcggcata cctagccggt gttgcagcag ctaaaacgac aaaaaccaag 480
caagttgggt ttgtagggtg tatggaagga gatgttgta agcgctttga aaaaggtttt 540
gaagctgggt tgaaatcagt agatgatacc atcaaagtaa gagttgctta tgcaggctct 600
tttgagatg ctgccaaaagg caagacgatt gcagctgctc aatacgctga aggcgcagat 660
gttattttat atgcagcagg aggcacaggg gcgggtgtct ttagcgaagc taagtctatc 720
aacgaaaaac gtaaagaaga agataagggt tgggttattg gtgttgaccg tgaccaaaagt 780
gaagatggaa aatacactac aaaagatggc aagtcagcta attttgtttt gacctcaagt 840
atcaaggaag tcggaaaagc tttagtaaaa gtagccgtaa aaacctcaga agaccaattc 900
ccaggtgggt aaataaccac ttttggttta aaagaagggt gtgttagcct tacaacggat 960
gctctgacac aagacactaa aaaagctatt gaggctgcta aaaaagcgat tatcgaagga 1020
accatcacag ttcctgaaaa ctaa 1044
```

<210> SEQ ID NO 180
<211> LENGTH: 347
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 180

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Met Asn Lys Lys Val Met Ser Leu Gly Leu Val Ser Thr Ala Leu Phe
1 5 10 15
Thr Leu Gly Gly Cys Thr Asn Asn Ser Ala Lys Gln Thr Thr Asp Asn
20 25 30
Ser Leu Lys Ile Ala Met Ile Thr Asn Gln Thr Gly Ile Asp Asp Lys
35 40 45
Ser Phe Asn Gln Ser Ala Trp Glu Gly Leu Gln Ala Trp Gly Lys Glu
50 55 60
Asn Lys Leu Glu Lys Gly Lys Gly Tyr Asp Tyr Phe Gln Ser Ala Asn
65 70 75 80
Glu Ser Glu Phe Thr Thr Asn Leu Glu Ser Ala Val Thr Asn Gly Tyr
85 90 95
Asn Leu Val Phe Gly Ile Gly Phe Pro Leu His Asp Ala Val Glu Lys
100 105 110
Val Ala Ala Asn Asn Pro Asp Asn His Phe Ala Ile Val Asp Asp Val
115 120 125
Ile Lys Gly Gln Lys Asn Val Ala Ser Ile Thr Phe Ser Asp His Glu
130 135 140
Ala Ala Tyr Leu Ala Gly Val Ala Ala Ala Lys Thr Thr Lys Thr Lys
145 150 155 160
Gln Val Gly Phe Val Gly Gly Met Glu Gly Asp Val Val Lys Arg Phe
165 170 175
Glu Lys Gly Phe Glu Ala Gly Val Lys Ser Val Asp Asp Thr Ile Lys
180 185 190
Val Arg Val Ala Tyr Ala Gly Ser Phe Ala Asp Ala Ala Lys Gly Lys
```


<400> SEQUENCE: 184

```
Met Thr Ser Lys Lys Ala Cys Leu Ser Ser Ile Ile Val Leu Ala Ser
1      5      10      15
Leu Thr Cys Gly Asn Asp Thr Val Ser Ala Asn His Leu Ser Ala Thr
20     25     30
Gly Asp Lys Phe Asp Asp Cys Ser Thr Leu Val Glu Lys Asp Val Ala
35     40     45
Pro Lys Asp Glu Leu Glu Met Leu Ala Trp Ser Ser Ser Gln Thr Thr
50     55     60
Asp Asp Ala Asp Arg Asp Tyr Glu Asp Phe Leu Asp Asp Asp Ser Phe
65     70     75     80
Ile Ser Gln Asn Glu Thr Asp Lys Met Phe Glu Asn Leu Thr Asp Asp
85     90     95
Arg Leu Leu Asn Glu Leu Asp Glu Leu Asp Glu Glu Asn Glu Glu Asp
100    105    110
Glu Glu Asp Thr Ile Glu Pro Glu Gln Asn Val Ile Met Pro Ser Asp
115    120    125
Asp Glu Leu Phe Asp Leu Thr Asp Ala Val Glu Thr Arg Leu Thr Val
130    135    140
Ser Ser Ala Pro His Leu Glu Ala Glu Leu Pro Lys Pro His Leu Arg
145    150    155    160
Ser Leu Ser Asp Thr Ala Leu Arg Ser Gly Glu Ile Arg Gly His Leu
165    170    175
Asp Asn Lys Leu Asp Ala Leu Ser Val Thr Ala Thr Lys Leu Ala Leu
180    185    190
Thr Met Ala Gln Lys Phe Asp Leu Thr Thr His Val Tyr Ser Ile Gly
195    200    205
Glu Ser Phe Ser Glu Val Leu Ala Ala His Tyr Glu Asp Arg Lys Ala
210    215    220
Glu Ser Ala Phe Ser Lys Lys Lys Arg Phe His Leu Pro Ile Ala Thr
225    230    235    240
Pro Asp Val Val Ile Glu Glu Leu Arg Arg Leu Val Ser Ser Ile Gly
245    250    255
Ser Ser Lys Glu Asp Val Ser Val Pro Tyr Ser Arg Lys Leu Gly Met
260    265    270
Ala Val Ala Lys Arg Lys Ile Ala Leu Pro Gln Thr Gly Glu Arg Phe
275    280    285
Ser Tyr Tyr Pro Val Leu Leu Gly Leu Met Ile Leu Gly Leu Thr Pro
290    295    300
Ile Met Ile Pro Lys Lys Ile Asn Asn
305    310
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<210> SEQ ID NO 185

<211> LENGTH: 882

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 185

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ttgctgacct ttggaggtgc aagtgcggtt aaggcggaag aaaatgaaaa agtaagagag      60
caagaaaagc tcatacagca actttctgaa aagctagtgg aaattaatga cttacaaact    120
ttaaatggtg ataaagagag tatacagtct ctcgtagatt atctgactcg aagaggaaaa    180
cttgaagaag aatggatgga atatttgaat tctggtattc aacgcaaact ttttgttggt    240
ccaaaaggac ctgcagggtga aaaaggagaa caaggtccta ctggaaaaca aggcgagcgt    300
ggtgagaccg gccctgcagg tccacgtggt gacaagggcg aaactggtga caaaggagcc    360
cagggctccag taggtcccgc tggcaaggac ggccaaaacg gtaaagatgg tcttccaggt    420
aaagacggca aggacggcca aaacggtaaa gatggtcttc caggtaaaga cggcaaggac    480
ggccaagacg gtaaagatgg cctcccaggt aaagacggta aggatggcca aaatggcaaa    540
gatggtcttc caggtaaaga cggtaacca ggtaaacag ctcctaaaac accagaggtc    600
```

cctcaaaacc	cagatactgc	accacatact	ccaaaaaccc	ctcggatccc	tggtcaatca	660
aaagacgtga	cacctgctcc	tcaaaaccct	tctaatagag	gtctaaacaa	accacaaaca	720
caaggtggta	atcagctcgc	aaaaacaccg	gcagctcacg	acacacacag	acaattgcca	780
gcaacaggcg	aaacaacca	tccattcttt	acagcagctg	ctgtagctat	catgacgaca	840
gctggagtgtg	tagctgttgc	aaaacgtcaa	gaaaacaact	aa		882

<210> SEQ ID NO 186
 <211> LENGTH: 293
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 186

Met	Leu	Thr	Phe	Gly	Gly	Ala	Ser	Ala	Val	Lys	Ala	Glu	Glu	Asn	Glu	
1				5					10					15		
Lys	Val	Arg	Glu	Gln	Glu	Lys	Leu	Ile	Gln	Gln	Leu	Ser	Glu	Lys	Leu	
			20					25					30			
Val	Glu	Ile	Asn	Asp	Leu	Gln	Thr	Leu	Asn	Gly	Asp	Lys	Glu	Ser	Ile	
			35				40					45				
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Pro	Lys	Gly	Pro	Ala	Gly	Glu	Lys	Gly	Glu	Gln	Gly	Pro	Thr	Gly	Lys	
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Gln	Gly	Glu	Arg	Gly	Glu	Thr	Gly	Pro	Ala	Gly	Pro	Arg	Gly	Asp	Lys	
			100					105					110			
Gly	Glu	Thr	Gly	Asp	Lys	Gly	Ala	Gln	Gly	Pro	Val	Gly	Pro	Ala	Gly	
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Lys	Asp	Gly	Gln	Asn	Gly	Lys	Asp	Gly	Leu	Pro	Gly	Lys	Asp	Gly	Lys	
	130					135					140					
Asp	Gly	Gln	Asn	Gly	Lys	Asp	Gly	Leu	Pro	Gly	Lys	Asp	Gly	Lys	Asp	
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Gly	Gln	Asp	Gly	Lys	Asp	Gly	Leu	Pro	Gly	Lys	Asp	Gly	Lys	Asp	Gly	
				165					170					175		
Gln	Asn	Gly	Lys	Asp	Gly	Leu	Pro	Gly	Lys	Asp	Gly	Gln	Pro	Gly	Lys	
			180					185					190			
Pro	Ala	Pro	Lys	Thr	Pro	Glu	Val	Pro	Gln	Asn	Pro	Asp	Thr	Ala	Pro	
			195				200						205			
His	Thr	Pro	Lys	Thr	Pro	Arg	Ile	Pro	Gly	Gln	Ser	Lys	Asp	Val	Thr	
	210					215					220					
Pro	Ala	Pro	Gln	Asn	Pro	Ser	Asn	Arg	Gly	Leu	Asn	Lys	Pro	Gln	Thr	
225				230						235					240	
Gln	Gly	Gly	Asn	Gln	Leu	Ala	Lys	Thr	Pro	Ala	Ala	His	Asp	Thr	His	
			245						250					255		
Arg	Gln	Leu	Pro	Ala	Thr	Gly	Glu	Thr	Thr	Asn	Pro	Phe	Phe	Thr	Ala	
			260					265					270			
Ala	Ala	Val	Ala	Ile	Met	Thr	Thr	Ala	Gly	Val	Val	Ala	Val	Ala	Lys	
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Arg	Gln	Glu	Asn	Asn												
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<210> SEQ ID NO 187
 <211> LENGTH: 3525
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 187

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taccatgcgc	acgcttatcg	acctttgaaa	aaaggttacc	ttcgaatcaa	ctaccacaat	660
caatcgggac	actacgataa	cttagctgtc	tggaccttta	aagatgtcaa	aaccccaacg	720
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acggctaatac	cctctcagca	aaagagtcag	acagagcatc	atcaaaccaa	aacaccagat	3360
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<210> SEQ ID NO 188

<211> LENGTH: 1174

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 188

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Gly	Ser	Lys	Arg	Tyr	Gln	Tyr	Leu	Leu	Lys	Lys	Trp	Gly	Ile	Gly	Phe
		20					25					30			
Val	Ile	Ala	Ala	Thr	Gly	Thr	Val	Val	Leu	Gly	Cys	Thr	Pro	Ser	Ile
	35					40					45				
Leu	Thr	His	Gln	Val	Ala	Ala	Lys	Thr	Ile	Val	Gly	Leu	Ala	Arg	Asp
	50					55				60					
Glu	Ala	Gln	Gln	Gly	Asp	Gly	Asn	Ala	Lys	Ser	Gly	Asp	Gly	Leu	Gln
65				70						75					80
Ser	Ser	Ser	Lys	Glu	Ala	Lys	Pro	Val	Leu	Asp	Ser	Ser	Ser	Ala	Asn
			85						90					95	
Pro	Ala	Ser	Ile	Ala	Glu	His	His	Leu	Arg	Met	His	Phe	Lys	Thr	Leu
			100					105					110		
Pro	Ala	Gly	Glu	Ser	Leu	Gly	Ser	Leu	Gly	Leu	Trp	Val	Trp	Gly	Asp
		115				120						125			
Val	Asp	Gln	Pro	Ser	Lys	Asp	Trp	Pro	Asn	Gly	Ala	Ile	Thr	Met	Thr
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Lys	Ala	Lys	Lys	Asp	Asp	Tyr	Gly	Tyr	Tyr	Leu	Asp	Val	Pro	Leu	Ala
145				150						155					160
Ala	Lys	His	Arg	Gln	Gln	Val	Ser	Tyr	Leu	Ile	Asn	Asn	Lys	Ala	Gly
			165						170					175	
Glu	Asn	Leu	Ser	Lys	Asp	Gln	His	Ile	Ser	Leu	Leu	Thr	Pro	Lys	Met
		180						185					190		
Asn	Glu	Val	Trp	Ile	Asp	Glu	Asn	Tyr	His	Ala	His	Ala	Tyr	Arg	Pro
		195				200						205			
Leu	Lys	Lys	Gly	Tyr	Leu	Arg	Ile	Asn	Tyr	His	Asn	Gln	Ser	Gly	His
	210					215					220				
Tyr	Asp	Asn	Leu	Ala	Val	Trp	Thr	Phe	Lys	Asp	Val	Lys	Thr	Pro	Thr
225				230						235					240
Thr	Asp	Trp	Pro	Asn	Gly	Leu	Asp	Leu	Ser	His	Lys	Gly	His	Tyr	Gly
			245						250					255	
Ala	Tyr	Val	Asp	Val	Pro	Leu	Lys	Glu	Gly	Ala	Asn	Glu	Ile	Gly	Phe
		260						265					270		
Leu	Ile	Leu	Asp	Lys	Ser	Lys	Thr	Gly	Asp	Ala	Ile	Lys	Val	Gln	Pro
	275						280					285			
Lys	Asp	Tyr	Leu	Phe	Lys	Glu	Leu	Asp	Asn	His	Thr	Gln	Val	Phe	Val
	290					295					300				
Lys	Asp	Thr	Asp	Pro	Lys	Val	Tyr	Asn	Asn	Pro	Tyr	Tyr	Ile	Asp	Gln
305				310						315					320
Val	Ser	Leu	Lys	Gly	Ala	Glu	Gln	Thr	Thr	Pro	Asn	Glu	Ile	Lys	Ala
			325						330					335	
Ile	Phe	Thr	Thr	Leu	Asp	Gly	Leu	Asp	Glu	Asp	Ala	Val	Lys	Gln	Asn
		340						345					350		
Ile	Lys	Ile	Thr	Asp	Lys	Ala	Gly	Lys	Thr	Val	Ala	Ile	Asp	Glu	Leu
	355						360					365			
Thr	Leu	Asp	Arg	Asp	Lys	Ser	Val	Met	Thr	Leu	Lys	Gly	Asp	Phe	Lys
	370					375					380				
Ala	Gln	Gly	Ala	Val	Tyr	Thr	Val	Thr	Phe	Gly	Glu	Val	Ser	Gln	Val
385				390						395					400
Ala	Arg	Gln	Ser	Trp	Gln	Leu	Lys	Asp	Lys	Leu	Tyr	Ala	Tyr	Asp	Gly

				405					410				415			
Glu	Leu	Gly	Ala	Thr	Leu	Ala	Lys	Asp	Gly	Ser	Val	Asp	Leu	Ala	Leu	
			420					425					430			
Trp	Ser	Pro	Ser	Ala	Asp	Thr	Val	Lys	Val	Val	Val	Tyr	Asp	Lys	Gln	
		435					440					445				
Asp	Gln	Thr	Arg	Val	Val	Gly	Gln	Ala	Asp	Leu	Thr	Lys	Ser	Asp	Lys	
	450					455					460					
Gly	Val	Trp	Arg	Ala	His	Leu	Thr	Ser	Asp	Ser	Val	Lys	Gly	Ile	Ser	
465				470					475						480	
Asp	Tyr	Thr	Gly	Tyr	Tyr	Tyr	Leu	Tyr	Glu	Ile	Thr	Arg	Gly	Gln	Glu	
			485					490						495		
Lys	Val	Met	Val	Leu	Asp	Pro	Tyr	Ala	Lys	Ser	Leu	Ala	Ala	Trp	Asn	
		500						505					510			
Asp	Ala	Thr	Ala	Thr	Asp	Asp	Ile	Lys	Thr	Ala	Lys	Ala	Ala	Phe	Ile	
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Asn	Phe	Lys	Lys	Arg	Glu	Asp	Ala	Ile	Ile	Tyr	Glu	Ala	His	Val	Arg	
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Asp	Phe	Thr	Ser	Asp	Lys	Ala	Leu	Glu	Gly	Lys	Leu	Thr	His	Pro	Phe	
			565					570						575		
Gly	Thr	Phe	Ser	Ala	Phe	Val	Glu	Gln	Leu	Asp	Tyr	Leu	Lys	Asp	Leu	
		580					585						590			
Gly	Val	Thr	His	Val	Gln	Leu	Leu	Pro	Val	Leu	Ser	Tyr	Phe	Tyr	Ala	
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Lys	Asn	Leu	Val	Asn	Glu	Ile	His	Lys	Arg	Gly	Met	Gly	Val	Ile	Phe	
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	675					680						685				
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	690					695					700					
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705				710						715					720	
Ile	Leu	Val	Asp	Ser	Ile	Thr	Tyr	Leu	Thr	Arg	Glu	Phe	Lys	Val	Asp	
			725					730						735		
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		740					745						750			
Gln	Ala	Phe	Lys	Ala	Ala	Lys	Ala	Ile	Asn	Pro	Asn	Thr	Ile	Met	Ile	
	755					760						765				
Gly	Glu	Gly	Trp	Arg	Thr	Tyr	Gln	Gly	Asp	Glu	Gly	Lys	Lys	Glu	Ile	
	770					775						780				
Ala	Ala	Asp	Gln	Asp	Trp	Met	Lys	Ala	Thr	Asn	Thr	Val	Gly	Val	Phe	
785				790						795					800	
Ser	Asp	Asp	Ile	Arg	Asn	Thr	Leu	Lys	Ser	Gly	Phe	Pro	Asn	Glu	Gly	
			805					810						815		
Thr	Ala	Ala	Phe	Ile	Thr	Gly	Gly	Ala	Lys	Asn	Leu	Glu	Gly	Leu	Phe	
		820					825						830			
Lys	Thr	Ile	Lys	Ala	Gln	Pro	Gly	Asn	Phe	Glu	Ala	Asp	Ala	Pro	Gly	
	835					840						845				
Asp	Val	Val	Gln	Tyr	Ile	Ala	Ala	His	Asp	Asn	Leu	Thr	Leu	His	Asp	
	850					855					860					


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<210> SEQ ID NO 190

<211> LENGTH: 433

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 190

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20          25          30
Ser Phe Ser Met Glu Glu Lys Leu Phe Asn Lys His Phe Val Ala Ile
35          40          45
Thr Val Ile Asn Phe Ile Val Tyr Met Val Tyr Tyr Leu Phe Thr Val
50          55          60
Ile Ile Ala Phe Val Ala Thr Arg Glu Leu Gly Ala Gln Thr Ser Gln
65          70          75          80
Ala Gly Leu Ala Thr Gly Ile Tyr Ile Leu Gly Thr Leu Leu Ala Arg
85          90          95
Leu Ile Phe Gly Lys Gln Leu Glu Val Phe Gly Arg Arg Leu Val Leu
100         105         110
Arg Gly Gly Ala Ile Phe Tyr Leu Leu Thr Thr Leu Ala Tyr Phe Tyr
115         120         125
Met Pro Thr Ile Ser Met Met Tyr Leu Val Arg Phe Leu Asn Gly Phe
130         135         140
Gly Tyr Gly Val Val Ser Thr Ala Thr Asn Thr Ile Val Thr Ala Tyr
145         150         155         160
Ile Pro Ala Arg Lys Arg Gly Glu Gly Ile Asn Phe Tyr Gly Leu Ser
165         170         175
Thr Ser Leu Ala Ala Ala Ile Gly Pro Phe Val Gly Thr Phe Met Leu
180         185         190
Asp Asn Leu His Ile Asp Phe Arg Met Ile Ile Val Leu Cys Ser Val
195         200         205
Leu Ile Gly Cys Val Val Val Gly Ala Phe Ala Phe Pro Val Lys Asn
210         215         220
Met Ser Leu Asn Ala Glu Gln Leu Ala Lys Thr Lys Ser Trp Thr Val
225         230         235         240
Asp Ser Phe Ile Glu Lys Lys Ala Leu Phe Ile Thr Ala Ile Ala Phe
245         250         255
Leu Met Gly Ile Ala Tyr Ala Ser Val Leu Gly Phe Gln Lys Leu Tyr
260         265         270
Thr Ser Glu Ile His Leu Thr Thr Val Gly Ala Tyr Phe Phe Val Val
275         280         285
Tyr Ala Leu Ile Ile Thr Ile Thr Arg Pro Ala Met Gly Arg Leu Met
290         295         300
Asp Ala Lys Gly Asp Lys Trp Val Leu Tyr Pro Ser Tyr Leu Phe Leu

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305		310		315		320									
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		340					345						350		
Cys	Gly	Gln	Ala	Ala	Ser	Ile	Gln	Gly	Val	Asp	Glu	His	Arg	Phe	Asn
		355					360					365			
Thr	Ala	Met	Ser	Thr	Tyr	Met	Ile	Gly	Leu	Asp	Leu	Gly	Leu	Gly	Ala
		370					375					380			
Gly	Pro	Tyr	Leu	Leu	Gly	Leu	Ile	Lys	Asp	Leu	Ala	Leu	Gly	Ser	Gly
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Val	Ala	Ser	Phe	Arg	His	Leu	Phe	Trp	Leu	Ala	Ala	Val	Ile	Pro	Leu
			405						410				415		
Ile	Cys	Thr	Leu	Leu	Tyr	Leu	Leu	Lys	Thr	Lys	Thr	Arg	Gln	Val	Val
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Ser															

<210> SEQ ID NO 191
 <211> LENGTH: 948
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 191

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ggctatggct	taggagttat	gatgccagct	ttgatgtttg	gtaatgtatc	tggaaaccat	300
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acgatttcat	ctcttgataa	tgggtcaaaaa	gacagtcata	aagcctctta	tatcaatggg	540
ttcttaaacg	aatttgtagg	ttcatttggt	cttttctttg	gtgctttggc	tttgactaaa	600
aactactttg	gggtagagtt	agttggtaaa	ttgattgaag	caggctacga	ccaaacaact	660
gcagcaacac	aaatttcacc	atacgtgaca	ggctcattgg	cggttgctca	cattgggtatt	720
ggtttcttag	ttatggtcct	ggttacttca	ttaggtggac	caactgggcc	agcactaaac	780
ccagcgcgtg	attttggggc	tcgtttgtta	caccacttct	taccaaatac	agttcttggg	840
caagccaaaag	gtgattcaaa	atgggtggtat	gcatgggttc	ctgtagttgc	acctatctta	900
gcggcgatag	tagccgtagc	agcgttttaa	tacctttata	tcagataa		948

<210> SEQ ID NO 192
 <211> LENGTH: 315
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 192

Met	Ile	Ile	Leu	Phe	Ile	Ile	Leu	Leu	Pro	Leu	His	Ser	Ser	Ile	Ser
1			5				10							15	
Leu	Leu	Lys	Trp	Tyr	Leu	Leu	Tyr	Phe	Ile	Ile	Trp	Arg	Lys	Pro	Glu
		20					25						30		
Asn	Met	Glu	Met	Thr	Trp	Thr	Val	Lys	Tyr	Ile	Thr	Glu	Phe	Ile	Ala
		35					40					45			
Thr	Ala	Phe	Leu	Ile	Ile	Leu	Gly	Asn	Gly	Ala	Val	Ala	Asn	Val	Asp
		50				55					60				
Leu	Lys	Gly	Thr	Lys	Gly	His	Asn	Ser	Gly	Trp	Leu	Val	Ile	Ala	Phe
		65			70				75					80	
Gly	Tyr	Gly	Leu	Gly	Val	Met	Met	Pro	Ala	Leu	Met	Phe	Gly	Asn	Val
			85				90						95		
Ser	Gly	Asn	His	Ile	Asn	Pro	Ala	Phe	Thr	Val	Gly	Leu	Ala	Val	Ser

			100					105					110				
Gly	Leu	Phe	Pro	Trp	Ala	His	Val	Leu	Gln	Tyr	Val	Val	Ala	Gln	Leu		
		115						120					125				
Leu	Gly	Ala	Ile	Phe	Gly	Gln	Leu	Val	Val	Val	Met	Val	Tyr	Lys	Pro		
	130					135						140					
Tyr	Phe	Met	Lys	Thr	Glu	Asn	Pro	Asn	His	Val	Leu	Gly	Ser	Phe	Ser		
145					150					155					160		
Thr	Ile	Ser	Ser	Leu	Asp	Asn	Gly	Gln	Lys	Asp	Ser	His	Lys	Ala	Ser		
			165						170					175			
Tyr	Ile	Asn	Gly	Phe	Leu	Asn	Glu	Phe	Val	Gly	Ser	Phe	Val	Leu	Phe		
		180						185					190				
Phe	Gly	Ala	Leu	Ala	Leu	Thr	Lys	Asn	Tyr	Phe	Gly	Val	Glu	Leu	Val		
	195						200					205					
Gly	Lys	Leu	Ile	Glu	Ala	Gly	Tyr	Asp	Gln	Thr	Thr	Ala	Ala	Thr	Gln		
	210					215					220						
Ile	Ser	Pro	Tyr	Val	Thr	Gly	Ser	Leu	Ala	Val	Ala	His	Ile	Gly	Ile		
225					230					235					240		
Gly	Phe	Leu	Val	Met	Val	Leu	Val	Thr	Ser	Leu	Gly	Gly	Pro	Thr	Gly		
			245					250						255			
Pro	Ala	Leu	Asn	Pro	Ala	Arg	Asp	Phe	Gly	Pro	Arg	Leu	Leu	His	His		
		260						265					270				
Phe	Leu	Pro	Lys	Ser	Val	Leu	Gly	Gln	Ala	Lys	Gly	Asp	Ser	Lys	Trp		
	275						280					285					
Trp	Tyr	Ala	Trp	Val	Pro	Val	Val	Ala	Pro	Ile	Leu	Ala	Ala	Ile	Val		
	290					295					300						
Ala	Val	Ala	Ala	Phe	Lys	Tyr	Leu	Tyr	Ile	Arg							
305					310					315							

<210> SEQ ID NO 193

<211> LENGTH: 951

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 193

atgggtttacg	aaatgacttt	ggcggtcatt	aaatgtattg	aaaaccatct	tcacaaaaaa	60
gtatacaaaag	gggccagtct	ggctctcttt	caatctggtc	gatggcaaga	ataccatattc	120
ggaacaattg	atggaagacg	accagttgat	gctaacttag	tttatgactt	ggctagtgtt	180
tcaaaagttg	ttggtgtggc	cacaatatgc	aatatattttat	tgaataatgg	tacgttagca	240
ttagatgatac	ccttaaagggt	atattatcct	agtattgctg	atgcgactgt	cactattcga	300
cagttattga	ctcataccag	tggtcttgat	ccttatattc	ctaacagaga	tgttttaaat	360
gcacaacaat	taagaaaagc	acttaatcat	cttactcaaa	aagaaaataa	aaacttttat	420
tacacagatg	tcaatttcct	cttgttaggc	ttcatgttag	aagagctctt	tagtgaatct	480
ttagaccaga	tatttgacaa	gactatcttt	actccctttg	ggatgtatca	tacgtctttt	540
ggccctcgtc	cagaagctgt	accaacatta	aagggtgtga	gtgatggaga	agttcatgat	600
cccaaagcaa	aaatcttaaa	aaaacattct	ggatctgcgg	ggctattttc	aactcttgca	660
gatttagaaa	gttttagcaa	tcattatctt	aatgatccat	tttcagattg	tctgtggcgc	720
aactacagcc	aacaaacaat	tgagcgggtca	ctaggggtgga	atttagatgg	cgattggatt	780
agtcatacag	gttacacagg	gccgtttcta	atgcttaata	aaaaagagca	aacggcagct	840
atTTTTTTTga	ccaaccgtac	ttacgacgag	gatgataaaa	gtaaatgggt	aaaagaacgt	900
cagttgcttt	acaatgcact	aaagcatgat	ctgacaaccc	ccgtatcgta	a	951

<210> SEQ ID NO 194

<211> LENGTH: 316

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 194

Met	Val	Tyr	Glu	Met	Thr	Leu	Ala	Val	Ile	Lys	Cys	Ile	Glu	Asn	His
1					5				10				15		

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 196

Met	Ile	Ser	Tyr	Glu	Lys	Val	Arg	Gln	Ala	Leu	Lys	Thr	Ser	Thr	Ile
1				5					10					15	
Ala	Ile	Ile	Ile	Leu	Asn	Gly	Leu	Gly	Val	Val	Leu	Ser	Leu	Met	Gly
			20					25					30		
Phe	Ala	Gly	Ile	Phe	Tyr	Leu	Gln	Ser	Gln	Leu	Lys	Asn	Glu	Ala	Phe
		35					40					45			
Arg	Ala	Gln	Leu	Thr	Thr	Glu	Gln	Leu	Ala	Gln	Leu	Gln	Ser	Ser	Met
	50					55					60				
Thr	Pro	Phe	Met	Ile	Phe	Leu	Ser	Val	Leu	Asn	Val	Leu	Ala	Ile	Ile
65				70						75				80	
Ala	Ile	Ile	Val	Phe	Cys	Ala	Gln	Asn	Leu	Ser	Lys	Leu	Lys	Gln	Gly
				85				90						95	
Leu	Thr	Val	Ser	Tyr	Ile	Pro	Tyr	Ile	Leu	Gly	Leu	Ile	Leu	Ser	Val
			100					105					110		
Ile	Gly	Leu	Val	Asn	Gln	Phe	Thr	Thr	Thr	Met	Ser	Met	Val	Gly	Thr
		115					120					125			
Ile	Leu	Ile	Leu	Ile	Gln	Ala	Ala	Leu	Tyr	Gly	Phe	Ala	Phe	Tyr	Lys
	130					135					140				
Ala	Lys	Thr	Leu	Asn	Glu	Lys	Gly	Asp	Asp	Thr	Asp	Gln	Ala	Met	Leu
145					150					155					160

<210> SEQ ID NO 197

<211> LENGTH: 2454

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 197

atggaatac	g	tttttac	agg	tactgtt	gat	cgtatc	at	ttt	tg	aaa	acca	ggcta	atttc		60			
tttaaaattc	t	ctctc	ttg	cattg	aggat	acagac	agtg	acattg	acga	ctttg	aaatc				120			
attatcacag	g	aacgat	ggc	tgacatt	att	gaagg	agatg	actacac	ctt	ttggg	gggaa				180			
ttgacccagc	a	ccctaa	aata	tgga	cagcaa	ctcaa	actaa	gccgt	tacca	aaaa	atcaaa				240			
cctagttcat	t	gggtt	gggt	taatt	atttt	tctag	cgacc	atttta	agg	gattg	gtaaa				300			
aaaacagcgg	a	gaaa	atcat	tg	cgtatat	ggtc	ataata	ccattg	acca	tatttt	tagaa				360			
gacccaagca	a	attaga	aaac	tatct	ctggc	ctatc	taagg	cta	atcgt	ca	agc	ctttg	tc		420			
gctaaactaa	a	attga	atta	cggc	acagag	caact	gattg	ctggt	ctcgt	cga	actt	ggc			480			
cttagcaacc	g	ttttg	ccct	tcaag	cgttt	gaaa	agtata	aaga	agagg	tc	ttgac	ctt			540			
gttaaagaaa	a	tc	cctatca	gttag	tcgaa	gat	ctaca	ag	gtttt	gggtt	taaa	atgg	ca		600			
gatgctctcg	ct	gaaa	actt	agg	gattg	aa	gcgact	ctc	cgaaa	cgttt	tcgtg	cagcc			660			
ctccttcaact	gt	ctctt	gga	aga	atccatc	aat	cgagg	ag	ata	cttatgt	cca	agcac	ga		720			
caattattag	a	ctttg	ccat	cac	actcctt	ga	gatgc	ac	gtca	agtaga	atgtg	atcct			780			
gctgctgtgg	ct	gaaca	act	aag	cgagtta	at	catag	agg	gcaaa	atcaa	aa	acagt	gac		840			
accaaactgt	tt	gatg	ctag	c	tttatttt	gctg	aaga	ag	ggattg	ctaa	ca	acat	ctct		900			
cgtctcttag	a	tactc	cttt	aag	tcagtca	tttag	tcatg	at	accatt	ca	a	caacc	atc		960			
caagccggtc	a	aaa	agactt	tg	ccatcacc	tatg	accaag	tg	cagca	aga	ag	cattact			1020			
aaggctttaa	c	cagca	agggt	cttt	ctccta	ac	agg	tggtc	ccgga	acagg	aaaa	acaact			1080			
gttattcgag	gc	atttt	gca	gg	cttac	cg		aac	ctgc	atc	ag	attg	attt	gg	ataaaaaa	1140		
gaccttccta	t	cttg	ttagc	ag	ctcca	aca	ggtc	ggg	ctg	cac	gtc	gcat	ga	atg	agttg	1200		
actggacttc	ct	ag	cgcaac	cat	ccac	agg	cact	tag	ggc	tca	atgg	cga	ca	acg	attac	1260		
caagccatgg	agg	attat	ct	ag	actg	cgac	ctg	ctg	attg	tc	gatga	att	tt	ca	atgg	1320		
gatacctggc	tt	gcca	acca	gtt	gttag	ga	gct	atta	act	ca	aca	actca	ag	t	gattatt	1380		
gtcggagata	gtg	acc	agct	t	cttc	gg	tt	gg	acc	cggtc	aag	tc	ctg	tc	agatctttta	1440		
aaagtcaata	g	ctg	cccca	a	atc	gc	ccttg	c	aaa	agatat	t	tc	gt	caatc	cca	agaatct	1500	
actattgtca	a	ttt	ggcaga	c	cag	atgc	gt	c	g	gaat	ct	t	ag	ctg	ctga	ctttcgtgat	1560	
aaaaaagctg	a	cc	gttctta	t	ttt	ga	agcc	c	ag	gag	cct	t	t	at	ccctga	catgat	1620	
aaaattgtcc	t	at	ctg	ctat	t	aaa	agtggc	a	t	cc	ctg	ctg	agg	aa	attca	aatttttagca	1680	
cctatgtaca	a	agg	aca	agc	t	gg	catcaat	c	at	ct	taatc	a	act	cat	gca	aga	actttctc	1740

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aatcccttgc aaggacaaac agaatttctg ttcaatgata cgcatttttcg taaaggtgat 1800
aaagtccctcc acttagtcaa cgatgctcag ttgaatgtct ttaacggaga tattgggttat 1860
attacagatt tgattcctgc taaatacacc gaatctaagc aagacgaatt aatccttagat 1920
tttgacggta gcgaagtcac gtaccctaga aatgaatggc taaaattaac cctggcctat 1980
gccatgagca ttcataaatc gcaagggagt gagtttcaag tgggtgatttt acctatcaca 2040
cgccaaagcg gccgactctt gcaacgaaat gtgatttaca cggccattac tcggtctaaa 2100
agtaagttaa ttctgttggg agaataatact gcctttgagt atgctattaa acacgaaggc 2160
gataaacgcc aaacctactt gatcgaacgc ttccaagaac aatccgactt agcctcctct 2220
caacctaacc aagagctaaa atcaaaaagag cagacctccc ttttttctaa tacggcaacc 2280
cttgaggacg actctcaaaa atcttcctct caatcaacaa actctaacc cactgagaac 2340
tctcagtcag ataatgatga ttttaggtta acacctgaga attattcgac tatcgattcg 2400
atgatagggc ttacagaatc agatattgcc ctctttttcc agaaaaaatc ctag 2454

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<210> SEQ ID NO 198

<211> LENGTH: 817

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 198

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Met Glu Tyr Val Phe Thr Gly Thr Val Asp Arg Ile Ile Phe Glu Asn
1      5      10     15
Gln Ala Asn Phe Phe Lys Ile Leu Leu Leu Ala Ile Glu Asp Thr Asp
20     25     30
Ser Asp Ile Asp Asp Phe Glu Ile Ile Ile Thr Gly Thr Met Ala Asp
35     40     45
Ile Ile Glu Gly Asp Asp Tyr Thr Phe Trp Gly Glu Leu Thr Gln His
50     55     60
Pro Lys Tyr Gly Gln Gln Leu Lys Leu Ser Arg Tyr Gln Lys Ile Lys
65     70     75     80
Pro Ser Ser Ser Gly Leu Val Asn Tyr Phe Ser Ser Asp His Phe Lys
85     90     95
Gly Ile Gly Lys Lys Thr Ala Glu Lys Ile Ile Ala Leu Tyr Gly His
100    105    110
Asn Thr Ile Asp His Ile Leu Glu Asp Pro Ser Lys Leu Glu Thr Ile
115    120    125
Ser Gly Leu Ser Lys Ala Asn Arg Gln Ala Phe Val Ala Lys Leu Lys
130    135    140
Leu Asn Tyr Gly Thr Glu Gln Leu Ile Ala Gly Leu Val Glu Leu Gly
145    150    155    160
Leu Ser Asn Arg Phe Ala Leu Gln Ala Phe Glu Lys Tyr Lys Glu Glu
165    170    175
Ala Leu Asp Leu Val Lys Glu Asn Pro Tyr Gln Leu Val Glu Asp Leu
180    185    190
Gln Gly Phe Gly Phe Lys Met Ala Asp Ala Leu Ala Glu Asn Leu Gly
195    200    205
Ile Glu Ser Asp Ser Pro Lys Arg Phe Arg Ala Ala Leu Leu His Cys
210    215    220
Leu Leu Glu Glu Ser Ile Asn Arg Gly Asp Thr Tyr Val Gln Ala Arg
225    230    235    240
Gln Leu Leu Asp Phe Ala Ile Thr Leu Leu Glu Asp Ala Arg Gln Val
245    250    255
Glu Cys Asp Pro Ala Ala Val Ala Glu Gln Leu Ser Glu Leu Ile Ile
260    265    270
Glu Gly Lys Ile Lys Asn Ser Asp Thr Lys Leu Phe Asp Ala Ser Leu
275    280    285
Tyr Phe Ala Glu Glu Gly Ile Ala Asn Asn Ile Ser Arg Leu Leu Asp
290    295    300
Thr Pro Leu Ser Gln Ser Phe Ser His Asp Thr Ile Gln Thr Thr Ile

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305					310					315				320
Gln	Ala	Val	Gln	Lys	Asp	Phe	Ala	Ile	Thr	Tyr	Asp	Gln	Val	Gln
				325					330					335
Glu	Ala	Ile	Thr	Lys	Ala	Leu	Thr	Ser	Lys	Val	Phe	Leu	Leu	Thr
			340					345					350	
Gly	Pro	Gly	Thr	Gly	Lys	Thr	Thr	Val	Ile	Arg	Gly	Ile	Leu	Gln
		355					360				365			
Tyr	Ala	Asn	Leu	His	Gln	Ile	Asp	Leu	Asp	Lys	Lys	Asp	Leu	Pro
	370					375				380				
Leu	Leu	Ala	Ala	Pro	Thr	Gly	Arg	Ala	Ala	Arg	Arg	Met	Asn	Glu
385				390						395				400
Thr	Gly	Leu	Pro	Ser	Ala	Thr	Ile	His	Arg	His	Leu	Gly	Leu	Asn
				405					410					415
Asp	Asn	Asp	Tyr	Gln	Ala	Met	Glu	Asp	Tyr	Leu	Asp	Cys	Asp	Leu
			420					425				430		
Ile	Val	Asp	Glu	Phe	Ser	Met	Val	Asp	Thr	Trp	Leu	Ala	Asn	Gln
		435					440					445		
Leu	Gly	Ala	Ile	Asn	Ser	Thr	Thr	Gln	Val	Ile	Ile	Val	Gly	Asp
	450					455				460				
Asp	Gln	Leu	Pro	Ser	Val	Gly	Pro	Gly	Gln	Val	Leu	Ser	Asp	Leu
465				470					475					480
Lys	Val	Asn	Ser	Leu	Pro	Gln	Ile	Ala	Leu	Gln	Lys	Ile	Phe	Arg
				485					490					495
Ser	Gln	Glu	Ser	Thr	Ile	Val	Asn	Leu	Ala	Asp	Gln	Met	Arg	Arg
			500					505				510		
Ile	Leu	Ala	Ala	Asp	Phe	Arg	Asp	Lys	Lys	Ala	Asp	Arg	Ser	Tyr
		515					520					525		
Glu	Ala	Gln	Ala	Ala	Phe	Ile	Pro	Asp	Met	Ile	Gln	Lys	Ile	Val
	530					535					540			
Ser	Ala	Ile	Lys	Ser	Gly	Ile	Pro	Ala	Glu	Glu	Ile	Gln	Ile	Leu
545				550					555					560
Pro	Met	Tyr	Lys	Gly	Gln	Ala	Gly	Ile	Asn	His	Leu	Asn	Gln	Leu
				565					570					575
Gln	Glu	Leu	Leu	Asn	Pro	Leu	Gln	Gly	Gln	Thr	Glu	Phe	Leu	Phe
			580				585						590	
Asp	Thr	His	Phe	Arg	Lys	Gly	Asp	Lys	Val	Leu	His	Leu	Val	Asn
		595					600					605		
Ala	Gln	Leu	Asn	Val	Phe	Asn	Gly	Asp	Ile	Gly	Tyr	Ile	Thr	Asp
	610					615					620			
Ile	Pro	Ala	Lys	Tyr	Thr	Glu	Ser	Lys	Gln	Asp	Glu	Leu	Ile	Leu
625				630					635					640
Phe	Asp	Gly	Ser	Glu	Val	Thr	Tyr	Pro	Arg	Asn	Glu	Trp	Leu	Lys
				645					650					655
Thr	Leu	Ala	Tyr	Ala	Met	Ser	Ile	His	Lys	Ser	Gln	Gly	Ser	Glu
			660				665						670	
Gln	Val	Val	Ile	Leu	Pro	Ile	Thr	Arg	Gln	Ser	Gly	Arg	Leu	Leu
		675					680					685		
Arg	Asn	Val	Ile	Tyr	Thr	Ala	Ile	Thr	Arg	Ser	Lys	Ser	Lys	Leu
	690					695					700			
Leu	Leu	Gly	Glu	Tyr	Thr	Ala	Phe	Glu	Tyr	Ala	Ile	Lys	His	Glu
705				710					715					720
Asp	Lys	Arg	Gln	Thr	Tyr	Leu	Ile	Glu	Arg	Phe	Gln	Glu	Gln	Ser
				725					730					735
Leu	Ala	Ser	Ser	Gln	Pro	Asn	Gln	Glu	Leu	Lys	Ser	Lys	Glu	Gln
			740					745					750	
Ser	Leu	Phe	Ser	Asn	Thr	Ala	Thr	Leu	Glu	Asp	Asp	Ser	Gln	Lys
		755					760							

Ser	Ser	Gln	Ser	Thr	Asn	Ser	Asn	Pro	Thr	Glu	Asn	Ser	Gln	Ser	Asp
770						775					780				
Asn	Asp	Asp	Phe	Arg	Leu	Thr	Pro	Glu	Asn	Tyr	Ser	Thr	Ile	Asp	Ser
785					790					795					800
Met	Ile	Gly	Leu	Thr	Glu	Ser	Asp	Ile	Ala	Leu	Phe	Phe	Gln	Lys	Lys
				805					810					815	
Ser															

<210> SEQ ID NO 199

<211> LENGTH: 660

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 199

gtgctaaact	tcacttcgcc	aacactcaca	aagcgcaagc	gcttctcact	aaataaaaagg	60
aatcatatga	aacagtttat	taaagaatgg	ggcccattca	ctctcttttt	aattctcttt	120
gggtctatctc	gtcttttttt	gtggcaggct	gttaaagtag	acggccattc	tatggaccca	180
actctagctc	atggcgaaacg	ccttatcggt	tttaatcaag	ctagaattga	tcgctttgat	240
attgtagttg	ctcaggaaga	agaaaacgga	caaaagaaaag	aaatcgtaaa	aagagttatt	300
ggattgccag	gcgataccat	ttcttataat	gatgacacac	tttatattaa	tggtaaaaaaa	360
acagttgagc	cgtatttggc	tgagtatcta	aaacaattta	aaaacgataa	actccaaaaa	420
acttacgcct	ataataccct	attccaacag	ttagcagaaa	catctgatgc	ttttacaact	480
aattctgagg	gacaaacacg	ctttgagatg	agtgttccaa	aaggagaata	ccttcttctt	540
gggtgatgatc	gtattgtttc	cagggatagt	cgcgaagtgt	gtagtttcaa	aaaagaaaac	600
cttatcggtg	aagtgaaagc	tcgttttttg	ccactcaata	aaatgaccgt	ttttaattag	660

<210> SEQ ID NO 200

<211> LENGTH: 219

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 200

Met	Leu	Asn	Phe	Thr	Ser	Pro	Thr	Leu	Thr	Lys	Arg	Lys	Arg	Phe	Ser
1			5						10					15	
Leu	Asn	Lys	Arg	Asn	His	Met	Lys	Gln	Phe	Ile	Lys	Glu	Trp	Gly	Pro
		20						25					30		
Phe	Thr	Leu	Phe	Leu	Ile	Leu	Phe	Gly	Leu	Ser	Arg	Leu	Phe	Leu	Trp
		35					40					45			
Gln	Ala	Val	Lys	Val	Asp	Gly	His	Ser	Met	Asp	Pro	Thr	Leu	Ala	His
	50					55				60					
Gly	Glu	Arg	Leu	Ile	Val	Phe	Asn	Gln	Ala	Arg	Ile	Asp	Arg	Phe	Asp
65				70					75					80	
Ile	Val	Val	Ala	Gln	Glu	Glu	Glu	Asn	Gly	Gln	Lys	Lys	Glu	Ile	Val
			85					90					95		
Lys	Arg	Val	Ile	Gly	Leu	Pro	Gly	Asp	Thr	Ile	Ser	Tyr	Asn	Asp	Asp
		100					105					110			
Thr	Leu	Tyr	Ile	Asn	Gly	Lys	Lys	Thr	Val	Glu	Pro	Tyr	Leu	Ala	Glu
	115					120						125			
Tyr	Leu	Lys	Gln	Phe	Lys	Asn	Asp	Lys	Leu	Gln	Lys	Thr	Tyr	Ala	Tyr
	130				135						140				
Asn	Thr	Leu	Phe	Gln	Gln	Leu	Ala	Glu	Thr	Ser	Asp	Ala	Phe	Thr	Thr
145					150					155					160
Asn	Ser	Glu	Gly	Gln	Thr	Arg	Phe	Glu	Met	Ser	Val	Pro	Lys	Gly	Glu
			165					170					175		
Tyr	Leu	Leu	Leu	Gly	Asp	Asp	Arg	Ile	Val	Ser	Arg	Asp	Ser	Arg	Glu
		180					185					190			
Val	Gly	Ser	Phe	Lys	Lys	Glu	Asn	Leu	Ile	Gly	Glu	Val	Lys	Ala	Arg
	195					200						205			
Phe	Trp	Pro	Leu	Asn	Lys	Met	Thr	Val	Phe	Asn					

210

215

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<210> SEQ ID NO 201
<211> LENGTH: 504
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 201
atgatggaat catatgaaca cttttatgcc aaactatctc aaccttttag aaaaacccca      60
cagttaataa ttcttttaaa tgttttacta aaaataatca caggagtgat gtacatactt      120
tatccatctt ttctgatatt tacgctttgg caagggatga catttcaatt atgggtaagg      180
ttattaatta ttctgctgtg tggctttata gctttgtctt acattaggaa acgctttgat      240
tttccacgac cgtatgaaaa atggaatatt aaacctttaa ttgataagga tacaaaggga      300
agggtcaatgc ctacgagaca tgttttttca gctacgatga ttagtatgtg tttgttacga      360
tattatgttt actttggaat agttttgttta atattatcgg ctttattggc aatttgccgt      420
gtgatagcag gtattcacta tcctaaggat gttattgtag gttaccttat tggcttgatg      480
ttagggcttt gtttattgat ttag

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<210> SEQ ID NO 202
<211> LENGTH: 167
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 202
Met Met Glu Ser Tyr Glu His Phe Tyr Ala Lys Leu Ser Gln Pro Phe
1          5          10          15
Arg Lys Thr Pro Gln Leu Ile Ile Leu Leu Asn Val Leu Leu Lys Ile
20          25          30
Ile Thr Gly Val Met Tyr Ile Leu Tyr Pro Ser Phe Leu Ile Phe Thr
35          40          45
Leu Trp Gln Gly Met Thr Phe Gln Leu Trp Leu Arg Leu Leu Ile Ile
50          55          60
Pro Ala Val Gly Phe Ile Ala Leu Ser Tyr Ile Arg Lys Arg Phe Asp
65          70          75          80
Phe Pro Arg Pro Tyr Glu Lys Trp Asn Ile Lys Pro Leu Ile Asp Lys
85          90          95
Asp Thr Lys Gly Arg Ser Met Pro Ser Arg His Val Phe Ser Ala Thr
100         105         110
Met Ile Ser Met Cys Leu Leu Arg Tyr Tyr Val Tyr Phe Gly Ile Val
115         120         125
Cys Leu Ile Leu Ser Ala Leu Leu Ala Ile Cys Arg Val Ile Ala Gly
130         135         140
Ile His Tyr Pro Lys Asp Val Ile Val Gly Tyr Leu Ile Gly Leu Met
145         150         155         160
Leu Gly Leu Cys Leu Leu Ile
165

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<210> SEQ ID NO 203
<211> LENGTH: 1884
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<220> FEATURE:
<221> NAME/KEY: Unsure
<222> LOCATION: (1700)..(1700)
<223> OTHER INFORMATION: unsure
<400> SEQUENCE: 203
atggataatc gtcagattgc agctgaagtg attgaggctt taggtggccg agaaaatgtg      60
agaagtgttg cccactgtgc aactcgcctt cgcgtgatgg tttatgatga aggaaagatt      120
gataaggaaa aagcagaagc tattgacaag gttaaaggag ctttctttta ctctgggtcaa      180

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tatcagatga	tttttggaac	tggtagcggt	aataacattt	atgacgaagt	tgttgctctt	240
ggtttaccca	cgatcatcaac	cagttagcaa	aaggcagaag	caggcaaaca	tggaatatc	300
ttccaacggg	cgattcgtac	gtttggagat	gtctttgttc	ccattattcc	agctattgta	360
gcaacgggtc	tctttatggg	ggttcgtggg	ttggtagacc	agccagctat	tatggattta	420
tttgggggtc	atgagtacgg	ggaaaatttt	ctcatgtaca	ctcgtattct	aacggataca	480
gcctttgtct	acttgccagc	tttggtaggt	tggtagcgct	ttaggggtctt	tgggggtaat	540
cctattatcg	gtattgtttt	aggattgatg	ctggtttcca	atgagttgcc	taatgcttgg	600
gtagttgcct	ctggtaggag	tgtagagccg	ctaaccctct	ttggatttgt	tcctgttggt	660
ggttatcaag	gtaccgtttt	acccgccttc	tttgttggtc	tggtaggagc	taagttggag	720
aaatggttgc	acaaaaaggt	tccagaagct	ttggacttat	tggtagacac	gtttttaacg	780
tttgctatta	tgagtacctt	gggactattt	gtgattggac	cagttttcca	ttctcttgaa	840
aaccttggtc	tggctgggac	acaggccgtc	ttgcatttgc	cgtttggtcat	tgagggttg	900
attgttgggg	gaatccaaca	attaatcgta	gtgactggta	ttcaccatat	ctttaacttc	960
ctagaagcgc	agctgattgc	caataccgga	aaagatcctt	tcaatgctta	cctaacagca	1020
gcaacagctg	ctcaagctgg	agctacctta	gctgttgctg	ttaaaaccaa	atcaacaaaa	1080
ctaaaagggtc	tggcctttcc	atcaaccttg	tcagctcttt	tagggattac	tgaaccagct	1140
atttttgggg	tcaacctccg	ttatccaaaa	gtctttgttt	cagggtcttat	tggtagtgcc	1200
ttaggtaggt	gggtcgctgg	gctctttggc	attgcaggaa	ctggttttgg	gattaccgtc	1260
ttaccaggaa	ctctccttta	cttgaatggc	caattattac	aataccttgt	gactatgctt	1320
gtcgggtctg	gggtagcctt	tgcaattgct	tatacttggg	gttatcaaga	tagagaaacc	1380
cttcggttac	cagctgtcga	agttgatcaa	acggctgac	agccagcctt	agcagaggaa	1440
actttatata	gtcctttgaa	tggaaacagt	gtagacttat	ctgcggtttc	agaccctgtt	1500
ttttcatcag	gtgctatggg	tcaaggctta	gcaattaagc	cagaagataa	taccctatac	1560
tcaccagttg	atggtaaagt	tgaaattgtc	tttgaaacag	gtcatgccta	tgctataacg	1620
tcaagtcaag	gagcagaagt	gttacttcat	attggtattg	ataccgagtc	gatggcagga	1680
gatgggtttg	aatctcttgn	agcagtagga	caggcggtta	aaaacggtga	tcttctaggc	1740
tgctttgatc	ctagcaagat	tgtagaagct	gcactagatg	acaccgcccgt	gatgattgtg	1800
accaatagca	ctgactatca	aagcgtggac	attcgtgctc	aaggacatgt	tttgagtggg	1860
gatcaagtgg	cacttatcaa	ataa				1884

<210> SEQ ID NO 204

<211> LENGTH: 627

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<220> FEATURE:

<221> NAME/KEY: UNSURE

<222> LOCATION: (567)..(567)

<223> OTHER INFORMATION: unsure

<400> SEQUENCE: 204

Met	Asp	Asn	Arg	Gln	Ile	Ala	Ala	Glu	Val	Ile	Glu	Ala	Leu	Gly	Gly
1				5				10						15	
Arg	Glu	Asn	Val	Arg	Ser	Val	Ala	His	Cys	Ala	Thr	Arg	Leu	Arg	Val
			20					25					30		
Met	Val	Tyr	Asp	Glu	Gly	Lys	Ile	Asp	Lys	Glu	Lys	Ala	Glu	Ala	Ile
		35				40						45			
Asp	Lys	Val	Lys	Gly	Ala	Phe	Phe	Asn	Ser	Gly	Gln	Tyr	Gln	Met	Ile
	50				55					60					
Phe	Gly	Thr	Gly	Thr	Val	Asn	Asn	Ile	Tyr	Asp	Glu	Val	Val	Ala	Leu
65				70					75					80	
Gly	Leu	Pro	Thr	Ser	Ser	Thr	Ser	Glu	Gln	Lys	Ala	Glu	Ala	Gly	Lys
			85					90						95	
His	Gly	Asn	Ile	Phe	Gln	Arg	Ala	Ile	Arg	Thr	Phe	Gly	Asp	Val	Phe
		100						105					110		
Val	Pro	Ile	Ile	Pro	Ala	Ile	Val	Ala	Thr	Gly	Leu	Phe	Met	Gly	Val
	115					120					125				
Arg	Gly	Leu	Val	Thr	Gln	Pro	Ala	Ile	Met	Asp	Leu	Phe	Gly	Val	His
	130					135					140				

Glu	Tyr	Gly	Glu	Asn	Phe	Leu	Met	Tyr	Thr	Arg	Ile	Leu	Thr	Asp	Thr
145					150					155					160
Ala	Phe	Val	Tyr	Leu	Pro	Ala	Leu	Val	Ala	Trp	Ser	Ala	Phe	Arg	Val
				165					170					175	
Phe	Gly	Gly	Asn	Pro	Ile	Ile	Gly	Ile	Val	Leu	Gly	Leu	Met	Leu	Val
			180					185					190		
Ser	Asn	Glu	Leu	Pro	Asn	Ala	Trp	Val	Val	Ala	Ser	Gly	Gly	Asp	Val
		195					200					205			
Lys	Pro	Leu	Thr	Phe	Phe	Gly	Phe	Val	Pro	Val	Val	Gly	Tyr	Gln	Gly
	210					215					220				
Thr	Val	Leu	Pro	Ala	Phe	Phe	Val	Gly	Leu	Val	Gly	Ala	Lys	Leu	Glu
225					230					235					240
Lys	Trp	Leu	His	Lys	Lys	Val	Pro	Glu	Ala	Leu	Asp	Leu	Leu	Val	Thr
				245					250					255	
Pro	Phe	Leu	Thr	Phe	Ala	Ile	Met	Ser	Thr	Leu	Gly	Leu	Phe	Val	Ile
			260					265						270	
Gly	Pro	Val	Phe	His	Ser	Leu	Glu	Asn	Leu	Val	Leu	Ala	Gly	Thr	Gln
		275					280					285			
Ala	Val	Leu	His	Leu	Pro	Phe	Gly	Ile	Ala	Gly	Leu	Ile	Val	Gly	Gly
	290					295					300				
Ile	Gln	Gln	Leu	Ile	Val	Val	Thr	Gly	Ile	His	His	Ile	Phe	Asn	Phe
305					310					315					320
Leu	Glu	Ala	Gln	Leu	Ile	Ala	Asn	Thr	Gly	Lys	Asp	Pro	Phe	Asn	Ala
				325					330					335	
Tyr	Leu	Thr	Ala	Ala	Thr	Ala	Ala	Gln	Ala	Gly	Ala	Thr	Leu	Ala	Val
			340					345					350		
Ala	Val	Lys	Thr	Lys	Ser	Thr	Lys	Leu	Lys	Gly	Leu	Ala	Phe	Pro	Ser
		355					360					365			
Thr	Leu	Ser	Ala	Leu	Leu	Gly	Ile	Thr	Glu	Pro	Ala	Ile	Phe	Gly	Val
	370					375					380				
Asn	Leu	Arg	Tyr	Pro	Lys	Val	Phe	Val	Ser	Gly	Leu	Ile	Gly	Gly	Ala
385					390					395					400
Leu	Gly	Gly	Trp	Val	Ala	Gly	Leu	Phe	Gly	Ile	Ala	Gly	Thr	Gly	Phe
				405					410					415	
Gly	Ile	Thr	Val	Leu	Pro	Gly	Thr	Leu	Leu	Tyr	Leu	Asn	Gly	Gln	Leu
			420					425					430		
Leu	Gln	Tyr	Leu	Val	Thr	Met	Leu	Val	Gly	Leu	Gly	Val	Ala	Phe	Ala
		435					440					445			
Ile	Ala	Tyr	Thr	Trp	Gly	Tyr	Gln	Asp	Arg	Glu	Thr	Leu	Pro	Leu	Pro
	450					455					460				
Ala	Val	Glu	Val	Asp	Gln	Thr	Ala	Asp	Gln	Pro	Ala	Leu	Ala	Glu	Glu
465					470					475					480
Thr	Leu	Tyr	Ser	Pro	Leu	Asn	Gly	Thr	Val	Val	Asp	Leu	Ser	Ala	Val
				485					490					495	
Ser	Asp	Pro	Val	Phe	Ser	Ser	Gly	Ala	Met	Gly	Gln	Gly	Leu	Ala	Ile
			500					505					510		
Lys	Pro	Glu	Asp	Asn	Thr	Leu	Tyr	Ser	Pro	Val	Asp	Gly	Lys	Val	Glu
		515					520					525			
Ile	Val	Phe	Glu	Thr	Gly	His	Ala	Tyr	Ala	Ile	Thr	Ser	Ser	Gln	Gly
	530					535					540				
Ala	Glu	Val	Leu	Leu	His	Ile	Gly	Ile	Asp	Thr	Glu	Ser	Met	Ala	Gly
545					550					555					560
Asp	Gly	Phe	Glu	Ser	Leu	Xaa	Ala	Val	Gly	Gln	Ala	Val	Lys	Asn	Gly
				565					570					575	
Asp	Leu	Leu	Gly	Cys	Phe	Asp	Pro	Ser	Lys	Ile	Ala	Glu	Ala	Ala	Leu
			580					585					590		
Asp	Asp	Thr	Ala	Val	Met	Ile	Val	Thr	Asn	Ser	Thr	Asp	Tyr	Gln	Ser

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<210> SEQ ID NO 205
<211> LENGTH: 996
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 205
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<210> SEQ ID NO 206
<211> LENGTH: 331
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 206
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Met	Gln	Leu	Ser	Arg	Leu	Met	Leu	Met	Val	Met	Val	Leu	Ser	Arg	Cys
1				5					10					15	
Gln	Lys	His	Ser	Tyr	Leu	Gln	Val	Asp	Gly	Tyr	Cys	Val	Ser	Asn	Leu
			20					25					30		
Asp	Glu	Ala	Leu	Gln	Leu	Arg	Gln	Ala	Gly	Ile	Asp	Lys	Glu	Ile	Leu
		35					40					45			
Ile	Leu	Gly	Val	Leu	Leu	Pro	Asn	Glu	Leu	Glu	Leu	Ala	Val	Ala	Asn
	50					55					60				
Ala	Ile	Thr	Val	Thr	Ile	Ala	Ser	Leu	Asp	Trp	Ile	Ala	Leu	Ala	Arg
65				70					75					80	
Leu	Glu	Lys	Lys	Glu	Cys	Gln	Gly	Leu	Lys	Val	His	Val	Lys	Val	Asp
			85						90				95		
Ser	Gly	Met	Gly	Arg	Ile	Gly	Leu	Arg	Ser	Ser	Lys	Glu	Val	Asn	Leu
			100					105					110		
Leu	Ile	Asp	Ser	Leu	Lys	Glu	Leu	Gly	Ala	Asp	Val	Glu	Gly	Ile	Phe
		115					120					125			
Thr	His	Phe	Ala	Thr	Ala	Asp	Glu	Ala	Asp	Asp	Thr	Lys	Phe	Asn	Gln
	130					135					140				
Gln	Leu	Gln	Phe	Phe	Lys	Lys	Leu	Ile	Ala	Gly	Leu	Glu	Asp	Lys	Pro
145				150						155				160	
Arg	Leu	Val	His	Ala	Ser	Asn	Ser	Ala	Thr	Ser	Ile	Trp	His	Ser	Asp
			165						170				175		
Thr	Ile	Phe	Asn	Ala	Val	Arg	Leu	Gly	Ile	Val	Ser	Tyr	Gly	Leu	Asn

			180					185				190					
Pro	Ser	Gly	Ser	Asp	Leu	Ser	Leu	Pro	Phe	Pro	Leu	Gln	Glu	Ala	Leu		
		195					200					205					
Ser	Leu	Glu	Ser	Ser	Leu	Val	His	Val	Lys	Met	Ile	Ser	Ala	Gly	Asp		
	210					215					220						
Thr	Val	Gly	Tyr	Gly	Ala	Thr	Tyr	Thr	Ala	Lys	Lys	Ser	Glu	Tyr	Val		
225					230					235					240		
Gly	Thr	Val	Pro	Ile	Gly	Tyr	Ala	Asp	Gly	Trp	Thr	Arg	Asn	Met	Gln		
				245					250					255			
Gly	Phe	Ser	Val	Leu	Val	Asp	Gly	Gln	Phe	Cys	Glu	Ile	Ile	Gly	Arg		
		260					265						270				
Val	Ser	Met	Asp	Gln	Leu	Thr	Ile	Arg	Leu	Pro	Lys	Ala	Tyr	Pro	Leu		
		275					280					285					
Gly	Thr	Lys	Val	Thr	Leu	Ile	Gly	Ser	Asn	Gln	Gln	Lys	Asn	Ile	Ser		
	290					295					300						
Thr	Thr	Asp	Ile	Ala	Asn	Tyr	Arg	Asn	Thr	Ile	Asn	Tyr	Glu	Val	Leu		
305					310					315					320		
Cys	Leu	Leu	Ser	Asp	Arg	Ile	Pro	Arg	Ile	Tyr							
				325					330								

<210> SEQ ID NO 207
 <211> LENGTH: 1512
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 207

atgaataaaa	acaaactatt	aagagttgcc	atgctactaa	gtctcttagc	cccgacagca	60
gaaagcatga	cagtgtctggc	tcaagatgta	atgcttgaga	cgcataaagc	aactacaaat	120
gaaaccagtg	attcttcttc	aaaagaggaa	aataataaaa	atgcagcacc	tacaacatca	180
gataaaactg	accaaggtcc	ccttgatgct	tctgcagaaa	caaactctaa	tagtcttggt	240
aacgcggatg	ataaaaaaag	aagcgattct	agtcagtctg	ctataggctc	ttcggacaac	300
aaggcagaag	cagaaaacca	ggtagatgat	aaatcaactg	atcattcgaa	atcaactgat	360
cattcgaaac	caactgacca	gcccaaacca	tcaccatcta	aagttgatac	ggcacctgct	420
tcttcattgt	cgaacaact	gccagaggca	agaactccta	ttcagtcgtt	gtccccttac	480
gtatcagatt	tagatttgag	tgagatagat	atcccttctg	tcaacacata	cgcggcatat	540
gtagagcatt	ggagtggtaa	aaatgcctat	accacccatc	ttttatctcg	ccgttatggg	600
attaaagctg	accagattga	tagttactta	aaatcaacag	gcattgccta	tgacagcaca	660
cgtattaatg	gtgagaagct	attgcaatgg	gaaaagaaaa	gtgggctgga	tgttcgagct	720
atcgtagcta	ttgcgatgtc	tgagagttct	ttaggaactc	aagggattgc	aactttgctt	780
ggagctaata	tgtttggtta	tgagagttct	gatctagatc	cgactcaagc	aagtaagttt	840
aatgatgata	gtgctattgt	caaaatgaca	caagacacca	ttattaaaaa	caaaaatagc	900
aattttgcac	ttcaagattt	aaaagcggct	aagttttcac	gaggtcaatt	aaactttgca	960
agtgcagggg	gtgtttat	tactgatact	actggtagtg	gtaaacgtcg	cgcacaaatt	1020
atggaagacc	tggataagtg	gattgatgac	catggtggca	caccagccat	tccagccgaa	1080
ttgaaagtg	agtcatcagc	tagttttgca	tctgtgccag	caggttataa	gctctctaag	1140
agttatgatg	tcttgggtta	tcaagcttcg	agttatgctt	ggggacaatg	cacttggtat	1200
gtgtataatc	gcgccaaaaga	attgggttac	caatttgatc	cttttatggg	aaatgggtgga	1260
gattggaagt	ataaagtagg	gtatgccctt	tcaaagactc	caaaagtagg	ttatgctatt	1320
tcatttgcac	cagggcaagc	gggcgctgat	ggcacttatg	gccacgtatc	aattgtagaa	1380
gatgtagtaa	aagatgggtc	tattcttatt	tcagagtcta	actgtatcgg	cttaggtaag	1440
atttcttatc	gtacctttac	agctcagcag	gctgaacagc	taacatatgt	tattggcaag	1500
agtaaaaaact	aa					1512

<210> SEQ ID NO 208
 <211> LENGTH: 503
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 208

Met	Asn	Lys	Asn	Lys	Leu	Leu	Arg	Val	Ala	Met	Leu	Leu	Ser	Leu	Leu		
1				5					10					15			
Ala	Pro	Thr	Ala	Glu	Ser	Met	Thr	Val	Leu	Ala	Gln	Asp	Val	Met	Leu		
			20					25					30				
Glu	Thr	His	Lys	Ala	Thr	Thr	Asn	Glu	Thr	Ser	Asp	Ser	Ser	Ser	Lys		
		35					40					45					
Glu	Glu	Asn	Asn	Lys	Asn	Ala	Ala	Pro	Thr	Thr	Ser	Asp	Lys	Thr	Asp		
	50					55					60						
Gln	Gly	Pro	Leu	Asp	Ala	Ser	Ala	Glu	Thr	Asn	Ser	Asn	Ser	Leu	Val		
65					70					75					80		
Asn	Ala	Asp	Asp	Lys	Lys	Arg	Ser	Asp	Ser	Ser	Gln	Ser	Ala	Ile	Gly		
				85					90					95			
Ser	Ser	Asp	Asn	Lys	Ala	Glu	Ala	Glu	Asn	Gln	Val	Asp	Asp	Lys	Ser		
			100					105					110				
Thr	Asp	His	Ser	Lys	Ser	Thr	Asp	His	Ser	Lys	Pro	Thr	Asp	Gln	Pro		
		115					120					125					
Lys	Pro	Ser	Pro	Ser	Lys	Val	Asp	Thr	Ala	Pro	Ala	Ser	Ser	Leu	Ser		
	130					135					140						
Lys	Gln	Leu	Pro	Glu	Ala	Arg	Thr	Pro	Ile	Gln	Ser	Leu	Ser	Pro	Tyr		
145				150						155					160		
Val	Ser	Asp	Leu	Asp	Leu	Ser	Glu	Ile	Asp	Ile	Pro	Ser	Val	Asn	Thr		
				165					170					175			
Tyr	Ala	Ala	Tyr	Val	Glu	His	Trp	Ser	Gly	Lys	Asn	Ala	Tyr	Thr	His		
			180					185					190				
His	Leu	Leu	Ser	Arg	Arg	Tyr	Gly	Ile	Lys	Ala	Asp	Gln	Ile	Asp	Ser		
	195						200					205					
Tyr	Leu	Lys	Ser	Thr	Gly	Ile	Ala	Tyr	Asp	Ser	Thr	Arg	Ile	Asn	Gly		
	210				215						220						
Glu	Lys	Leu	Leu	Gln	Trp	Glu	Lys	Lys	Ser	Gly	Leu	Asp	Val	Arg	Ala		
225				230						235					240		
Ile	Val	Ala	Ile	Ala	Met	Ser	Glu	Ser	Ser	Leu	Gly	Thr	Gln	Gly	Ile		
				245					250					255			
Ala	Thr	Leu	Leu	Gly	Ala	Asn	Met	Phe	Gly	Tyr	Ala	Ala	Phe	Asp	Leu		
			260					265					270				
Asp	Pro	Thr	Gln	Ala	Ser	Lys	Phe	Asn	Asp	Asp	Ser	Ala	Ile	Val	Lys		
		275					280					285					
Met	Thr	Gln	Asp	Thr	Ile	Ile	Lys	Asn	Lys	Asn	Ser	Asn	Phe	Ala	Leu		
	290					295					300						
Gln	Asp	Leu	Lys	Ala	Ala	Lys	Phe	Ser	Arg	Gly	Gln	Leu	Asn	Phe	Ala		
305				310						315					320		
Ser	Asp	Gly	Gly	Val	Tyr	Phe	Thr	Asp	Thr	Thr	Gly	Ser	Gly	Lys	Arg		
				325					330					335			
Arg	Ala	Gln	Ile	Met	Glu	Asp	Leu	Asp	Lys	Trp	Ile	Asp	Asp	His	Gly		
			340					345					350				
Gly	Thr	Pro	Ala	Ile	Pro	Ala	Glu	Leu	Lys	Val	Gln	Ser	Ser	Ala	Ser		
		355					360					365					
Phe	Ala	Ser	Val	Pro	Ala	Gly	Tyr	Lys	Leu	Ser	Lys	Ser	Tyr	Asp	Val		
	370					375					380						
Leu	Gly	Tyr	Gln	Ala	Ser	Ser	Tyr	Ala	Trp	Gly	Gln	Cys	Thr	Trp	Tyr		
385				390						395					400		
Val	Tyr	Asn	Arg	Ala	Lys	Glu	Leu	Gly	Tyr	Gln	Phe	Asp	Pro	Phe	Met		
				405					410					415			
Gly	Asn	Gly	Gly	Asp	Trp	Lys	Tyr	Lys	Val	Gly	Tyr	Ala	Leu	Ser	Lys		
			420					425					430				
Thr	Pro	Lys	Val	Gly	Tyr	Ala	Ile	Ser	Phe	Ala	Pro	Gly	Gln	Ala	Gly		
		435					440					445					
Ala	Asp	Gly	Thr	Tyr	Gly	His	Val	Ser	Ile	Val	Glu	Asp	Val	Arg	Lys		

	450					455					460					
Asp	Gly	Ser	Ile	Leu	Ile	Ser	Glu	Ser	Asn	Cys	Ile	Gly	Leu	Gly	Lys	
465						470					475					480
Ile	Ser	Tyr	Arg	Thr	Phe	Thr	Ala	Gln	Gln	Ala	Glu	Gln	Leu	Thr	Tyr	
	485										490					495
Val	Ile	Gly	Lys	Ser	Lys	Asn										
	500															

atgacaaagg	tagtaataaa	gcaattgttg	caggtaaatg	tagtgttcat	gataagttta	60
tcgacaatga	caaatcttgt	gtatgcagat	aaagggtcaaa	tttatggatg	tattattcaa	120
agaaattatc	gtcatccgat	atctgggcag	atagaagata	gcggagggga	gcattccttt	180
gatattggtc	aagggtatggt	tgaaggaact	gtctatagt	atgccatgct	agaagtatct	240
gatgctggaa	agatcgttct	tacttttcgt	atgagcttag	ctgattattc	gggcaattat	300
cagttctgga	tacaacctgg	aggaactgga	agctttcagg	cagttgatta	caatatcacc	360
caaaaaggta	ctgataccaa	tgggacaaca	ctagatattg	ctattagttt	gcctactgta	420
aatagtatca	ttcgaggcag	catgtttggt	gaacctatgg	gcagagaagt	ggtcttttac	480
ctgtcagctt	cagagttaat	acaaaagtat	tcaggtaata	tgttggccca	gcttgttact	540
gaaacagaca	attctcaaaa	tcaagaagta	aaagacagtc	aaaagcctgt	tgatacaaaa	600
ctaggagaaa	gtcaagatga	gtctcacaca	ggtgctatga	taactcagaa	taagcctaaa	660
gccactcat	caaataacaa	gagtcataca	gataaaaaaa	ttcttccttc	taagatgggc	720
ttaacgactt	cttttagagt	aaaaaaaagaa	gataagtttc	gggtcaaaaa	agacttatca	780
atcatgattt	actactttcc	aacttttttt	ctgatgttag	gagggtttgc	tgatgggtt	840
tggaaaaaaga	ggaaaaaaa	tgataaaacg	atgtaa			876

```
<210> SEQ ID NO 210
<211> LENGTH: 291
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 210
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Met	Thr	Lys	Val	Val	Ile	Lys	Gln	Leu	Leu	Gln	Val	Ile	Val	Val	Phe
1				5					10					15	
Met	Ile	Ser	Leu	Ser	Thr	Met	Thr	Asn	Leu	Val	Tyr	Ala	Asp	Lys	Gly
			20					25					30		
Gln	Ile	Tyr	Gly	Cys	Ile	Ile	Gln	Arg	Asn	Tyr	Arg	His	Pro	Ile	Ser
		35					40					45			
Gly	Gln	Ile	Glu	Asp	Ser	Gly	Gly	Glu	His	Ser	Phe	Asp	Ile	Gly	Gln
	50					55					60				
Gly	Met	Val	Glu	Gly	Thr	Val	Tyr	Ser	Asp	Ala	Met	Leu	Glu	Val	Ser
65					70					75					80
Asp	Ala	Gly	Lys	Ile	Val	Leu	Thr	Phe	Arg	Met	Ser	Leu	Ala	Asp	Tyr
				85					90					95	
Ser	Gly	Asn	Tyr	Gln	Phe	Trp	Ile	Gln	Pro	Gly	Gly	Thr	Gly	Ser	Phe
			100					105					110		
Gln	Ala	Val	Asp	Tyr	Asn	Ile	Thr	Gln	Lys	Gly	Thr	Asp	Thr	Asn	Gly
		115					120					125			
Thr	Thr	Leu	Asp	Ile	Ala	Ile	Ser	Leu	Pro	Thr	Val	Asn	Ser	Ile	Ile
	130					135					140				
Arg	Gly	Ser	Met	Phe	Val	Glu	Pro	Met	Gly	Arg	Glu	Val	Val	Phe	Tyr
145					150					155					160
Leu	Ser	Ala	Ser	Glu	Leu	Ile	Gln	Lys	Tyr	Ser	Gly	Asn	Met	Leu	Ala
				165					170					175	
Gln	Leu	Val	Thr	Glu	Thr	Asp	Asn	Ser	Gln	Asn	Gln	Glu	Val	Lys	Asp

			180					185					190				
Ser	Gln	Lys	Pro	Val	Asp	Thr	Lys	Leu	Gly	Glu	Ser	Gln	Asp	Glu	Ser		
		195					200					205					
His	Thr	Gly	Ala	Met	Ile	Thr	Gln	Asn	Lys	Pro	Lys	Ala	Asn	Ser	Ser		
	210					215					220						
Asn	Asn	Lys	Ser	Leu	Ser	Asp	Lys	Lys	Ile	Leu	Pro	Ser	Lys	Met	Gly		
225					230					235					240		
Leu	Thr	Thr	Ser	Leu	Glu	Leu	Lys	Lys	Glu	Asp	Lys	Phe	Arg	Ser	Lys		
			245						250					255			
Lys	Asp	Leu	Ser	Ile	Met	Ile	Tyr	Tyr	Phe	Pro	Thr	Phe	Phe	Leu	Met		
		260					265						270				
Leu	Gly	Gly	Phe	Ala	Val	Trp	Val	Trp	Lys	Lys	Arg	Lys	Lys	Asn	Asp		
	275						280					285					
Lys	Thr	Met															
	290																

```

<210> SEQ ID NO 211
<211> LENGTH: 1050
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 211
ttgaccacgt gggagatcat ccgtaacatg acagcatcag atttacaaag ggatcaatcc      60
ctactggcta aaaaacgttt cagaagtggc ctttatctag ttcttttaat tctcagcctc    120
ctatTTTTtg cggttattgc cttatccctt ggtggtttgg cggtttctta tggggcaatt    180
gtcaagggac tgtttgtggc ttatgacccc caagtggctt tgatttatga tttgcgtttt    240
ccaagaattg tcattgcttt attagcagga gcagggatag ctgtttcggt agttcttttt    300
caagcagtgt tgaaaaatcc tatttcagac cctgctatta tagggatttg tagtggtgct    360
agttttatgg ttttagtctc tagtttactt ctgccgcagt tgctgctgta tgggtccaatc    420
gtatcctttt taggaggcgg agtgtctttc ctgctgattt atggtttagc atggaagaaa    480
gggcttaatc ctattcggct tattctaaca gggattgcta ttaatgcttt atttatgggg    540
ttatcaactg ctttaaccag ctttttcacc tcagctagtc ccatgggtcaa tgctctttta    600
gcaggtcata ttagtcaaaa aacatgggct gatgtagggg ttttattccc ttatacatc    660
attggcttgt tactagcttt gttattgtca aaaacttgta accttcttct tttagatgat    720
caggtgattc gtcatttagg aatcgatgct acagcggtac ggttggaat ttccttggtt    780
gctgttttat tggcttcggg agccacttcg atcgttgagg tggtttcttt cctaggcttg    840
attgtccctc atatgagccg cttgctgggt ggaagtaagc accaaatctt aattcctttt    900
tcagctttgc ttggagcctt tgtctttttg ctagccgata ctttaggaag aagtcttgct    960
taccattggg aaattagccc tgcgattata atgagtattg taggcgggcc ttactttatt   1020
tacctgctaa ggaggtctga tattatatga                               1050

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<210> SEQ ID NO 212
<211> LENGTH: 349
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 212
Met Thr Thr Trp Glu Ile Ile Arg Asn Met Thr Ala Ser Asp Leu Gln
1          5          10          15
Arg Asp Gln Ser Leu Leu Ala Lys Lys Arg Phe Arg Ser Gly Leu Tyr
20          25          30
Leu Val Leu Leu Ile Leu Ser Leu Leu Phe Leu Ala Val Ile Ala Leu
35          40          45
Ser Leu Gly Gly Leu Ala Val Ser Tyr Gly Ala Ile Val Lys Gly Leu
50          55          60
Phe Val Ala Tyr Asp Pro Gln Val Ala Leu Ile Tyr Asp Leu Arg Phe
65          70          75          80
Pro Arg Ile Val Ile Ala Leu Leu Ala Gly Ala Gly Ile Ala Val Ser
85          90          95

```


caaggaaaaa	caagtctagc	tcaactcctc	ttgaaacgcc	agtctgcaac	gactggggcat	1200
attttatttg	acggtttaga	cagtgacaat	ttgtcgcaag	aaactatcaa	ccagcaggtt	1260
ctttatgtat	cggaccaatc	taccttattg	aaccgtagca	tttacgataa	tttaaggtta	1320
gcagcaaadc	tctctaaaaa	agaaatctta	gattggatag	atcaacatgg	tttggttaagc	1380
ttcatcaact	ggctaccaga	tggctcttgac	acaatagtgtg	gtgaaaatgg	taacctgtta	1440
tcaccaggcc	aaaagcaaca	ggtgatttgc	gcaagagctc	tattaagtaa	gaggtctctt	1500
tatatctttg	atgaggcaac	atctagtcta	gatgcagaaa	atgaacgtat	tattgacaat	1560
ttaataacga	gattagctaa	gacagcaata	gttattgtga	ttactcataa	gatgtctcga	1620
ctgaaaggag	ctaaccaagt	actcttttta	aacacagggc	agcctgcttg	tttaggcaaa	1680
ccttgcgacc	tttatcgga	ccaaccaact	tatcgtcacc	tagttgatac	tcaagcaaga	1740
ctggaggcaa	gtatttatgg	ctaa				1764

<210> SEQ ID NO 214

<211> LENGTH: 587

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 214

Met	Met	Glu	Thr	Glu	Asp	Thr	Ile	Ser	Arg	Gly	Lys	Arg	Lys	Arg	Leu
1				5					10					15	
Leu	Lys	Arg	Leu	Arg	Glu	Arg	Ile	Ala	Pro	Lys	Arg	Tyr	Leu	Leu	Tyr
			20					25					30		
Val	Ser	Ala	Phe	Leu	Ser	Trp	Leu	Gln	Phe	Val	Met	Arg	Met	Ile	Ser
			35				40					45			
Phe	Tyr	Leu	Ile	Ala	Lys	Thr	Phe	Ser	Thr	Phe	Ile	Leu	Gly	His	Ala
			50			55					60				
Ile	Ala	Leu	Gly	Arg	Leu	Ala	Gly	Leu	Leu	Leu	Leu	Leu	Asn	Val	Val
65					70				75					80	
Gly	Phe	Val	Leu	Ala	Ile	Leu	Gly	Lys	Gln	Leu	Gln	Gly	Ile	Ala	Ser
				85				90					95		
Gln	Phe	Ala	Arg	Asp	Ser	Leu	Lys	Gln	Ser	Phe	Phe	Glu	Ala	Phe	Ile
			100					105					110		
Asp	Leu	Asp	Gly	Gln	Phe	Asp	Ala	His	Ala	Ser	Asp	Ala	Asp	Ile	Leu
			115				120					125			
Thr	Leu	Ala	Ser	Gln	Gly	Ile	Asp	Ser	Leu	Asp	Thr	Tyr	Tyr	Gly	Tyr
			130			135					140				
Tyr	Leu	Ser	Leu	Ser	Met	Arg	Thr	Lys	Trp	Asn	Cys	Thr	Thr	Ile	Met
145					150					155				160	
Ile	Leu	Val	Phe	Leu	Ile	Tyr	Pro	Leu	Ala	Gly	Leu	Val	Phe	Leu	Gly
			165					170						175	
Val	Leu	Pro	Leu	Ile	Pro	Leu	Ser	Ile	Val	Ala	Met	Gln	Lys	Arg	Ser
			180					185					190		
Gln	Pro	Asn	Met	Ser	His	Tyr	Trp	Ser	Ser	Tyr	Met	Asp	Val	Gly	Asn
			195				200					205			
Leu	Phe	Met	Asp	Asp	Leu	Lys	Gly	Leu	Asn	Thr	Leu	Tyr	Ser	Tyr	Gln
			210			215					220				
Ala	Thr	Glu	Arg	Tyr	Glu	Gln	Glu	Phe	Ser	Gly	Lys	Ala	Glu	Gln	Phe
225					230					235				240	
Arg	Lys	Ala	Thr	Met	Ser	Leu	Leu	Gly	Phe	Gln	Leu	Gln	Ala	Val	Gly
			245					250						255	
Tyr	Met	Asp	Ala	Val	Met	Tyr	Leu	Gly	Ile	Gly	Leu	Ser	Gly	Phe	Leu
			260				265						270		
Ala	Val	Gln	Ala	Leu	Ala	Thr	Gly	Gln	Leu	Ser	Phe	Phe	Asn	Phe	Leu
			275				280					285			
Phe	Phe	Leu	Leu	Ile	Ala	Thr	Glu	Phe	Phe	Thr	Pro	Ile	Arg	Glu	Gln
			290			295					300				
Gly	Tyr	Gly	Met	His	Leu	Val	Met	Met	Asn	Thr	Lys	Met	Ala	Asp	Arg
305					310					315				320	


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acaaaacaaa tagatcgttt aaggagtgtt tcttttgagg acctcagttt tgcttatcca 1080
aagcgccaag agctggtttt taaggattta acagttacct ttcaagaaaa ggggattatt 1140
ggcattaaag gcgaatcagg atctggtaaa tcaactttgg tgaaattaat tatgaaatgg 1200
tataattgga agacaggaga tatttttctt aatgatagga atagttgctt actaaatgct 1260
gctaaattac aagatactat tgcttatgtg ccacaaacag cgcagctttt ccaacagtct 1320
atccgtgaaa atcttatctt tggccgtcaa gatatttcag atgagtccat ttggaattta 1380
gctgaggctt gtggtatgaa agacagactg ttagcttgta aggaagggtt ggatacgatt 1440
atcaagagtc cttctgactt ttcagctgga gaaggtaaac gtttagagtt gatgcgagct 1500
ttattgaaag atgcgagttg ctatatTTTT gatgaaccca cgtcaaattt agattctcta 1560
aatgaagcta tcttgcttga ttttaattaaa acacattgtc aaggattggt cttcttaatt 1620
tctcacaggc catcaaccct agcttgtgtt gatcatctat tttgcgtaaa aaatgggtcc 1680
ctaaaagagg tgaataaaaa atga 1704

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<210> SEQ ID NO 216

<211> LENGTH: 567

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 216

```

Met Ile Leu Lys Gln Asp Trp Arg Gln Val Phe Met Ala Lys Pro Asn
1           5           10           15
Arg Ser Thr Leu Ser Leu Val Trp Arg Leu Leu Thr Leu Met Lys Thr
20          25          30
Leu Leu Pro Trp Ile Ile Leu Ala Val Gly Phe Ala Val Met Gly Phe
35          40          45
Val Ile Thr Val Ser Ile Pro Thr Gly Ile Ala Tyr Leu Gly Leu Leu
50          55          60
Ala Ile Arg Gln Glu Val Ile Pro Ile Leu Ala Leu Tyr Leu Leu Ile
65          70          75          80
Ala Leu Ala Phe Leu Arg Gly Phe Val Arg Tyr Gly Glu His Tyr Phe
85          90          95
Gly His Phe Val Ala Phe His Ser Leu Ala Ala Phe Arg Asn Leu Ile
100         105         110
Phe Lys Lys Leu Arg Ala Leu Ser Pro Ala Cys Leu Asp Ser Gln Asp
115         120         125
Ser Gly Tyr Leu Leu Lys Met Ile Gly Glu Asp Ile Glu Ala Leu Glu
130         135         140
Val Phe Phe Ala His Thr Ile Ala Pro Ile Cys Thr Ala Ile Leu Ser
145         150         155         160
Ala Gly Leu Met Phe Trp Tyr Phe Cys Gln Ser Ser Trp Gln Leu Ala
165         170         175
Leu Leu Ala Leu Ala Thr Tyr Ala Cys Leu Ala Ile Val Ile Pro Ile
180         185         190
Tyr Phe Ala Asn Ile Leu Gln Val Leu Leu Lys Ser Gln Asn Glu Gly
195         200         205
Arg Lys Asp Tyr Leu Ser Tyr Phe Leu Glu Ser Leu Arg Ser Val Lys
210         215         220
Asp Leu Leu Gln Phe Gln Val Leu Asp Glu Gln Phe Glu Arg Leu Ile
225         230         235         240
Lys Lys Ser Asn His Val Asn Ala Leu Asp Arg Asn Val Ala Gln Ala
245         250         255
Gln Phe Leu Gln Met Ala Leu Thr Phe Phe Trp Leu Gly Leu Met Ile
260         265         270
Leu Ala Phe Ser Tyr Met Val Phe Asp Gly Ile Cys His Asp Ser Leu
275         280         285
Ser Phe Asp Lys Gly Leu Leu Thr Phe Ile Ala Phe Thr Ala Ser Phe
290         295         300
Ser Pro Phe Leu Glu Leu Gly Arg Leu Pro Leu Gly Phe Lys Arg Ala

```

305		310		315		320									
Met	Asn	Ala	Ala	Arg	Asn	Ile	Phe	Asp	Leu	Leu	Asp	Glu	Asn	Val	Ile
				325					330					335	
Val	Asp	Glu	Gly	Thr	Lys	Gln	Ile	Asp	Arg	Leu	Arg	Ser	Val	Ser	Phe
			340					345					350		
Glu	Asp	Leu	Ser	Phe	Ala	Tyr	Pro	Lys	Arg	Gln	Glu	Leu	Val	Phe	Lys
	355						360				365				
Asp	Leu	Thr	Val	Thr	Phe	Gln	Glu	Lys	Gly	Ile	Ile	Gly	Ile	Lys	Gly
	370					375					380				
Glu	Ser	Gly	Ser	Gly	Lys	Ser	Thr	Leu	Val	Lys	Leu	Ile	Met	Lys	Trp
385					390					395					400
Tyr	Asn	Trp	Lys	Thr	Gly	Asp	Ile	Phe	Leu	Asn	Asp	Arg	Asn	Ser	Cys
			405						410					415	
Leu	Leu	Asn	Ala	Ala	Lys	Leu	Gln	Asp	Thr	Ile	Ala	Tyr	Val	Pro	Gln
		420						425					430		
Thr	Ala	Gln	Leu	Phe	Gln	Gln	Ser	Ile	Arg	Glu	Asn	Leu	Ile	Phe	Gly
	435						440					445			
Arg	Gln	Asp	Ile	Ser	Asp	Glu	Ser	Ile	Trp	Asn	Leu	Ala	Glu	Ala	Cys
	450				455					460					
Gly	Met	Lys	Asp	Arg	Leu	Leu	Ala	Cys	Lys	Glu	Gly	Leu	Asp	Thr	Ile
465					470				475						480
Ile	Lys	Ser	Pro	Ser	Asp	Phe	Ser	Ala	Gly	Glu	Gly	Gln	Arg	Leu	Glu
			485					490					495		
Leu	Met	Arg	Ala	Leu	Leu	Lys	Asp	Ala	Ser	Cys	Tyr	Ile	Phe	Asp	Glu
		500						505				510			
Pro	Thr	Ser	Asn	Leu	Asp	Ser	Leu	Asn	Glu	Ala	Ile	Leu	Leu	Asp	Leu
	515					520						525			
Ile	Lys	Thr	His	Cys	Gln	Gly	Leu	Val	Phe	Leu	Ile	Ser	His	Arg	Pro
	530				535					540					
Ser	Thr	Leu	Ala	Cys	Val	Asp	His	Leu	Phe	Cys	Val	Lys	Asn	Gly	Ser
545				550					555						560
Leu	Lys	Glu	Val	Asn	Lys	Lys									
				565											

<210> SEQ ID NO 217

<211> LENGTH: 777

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 217

ttggtttgta	ggaattgttc	ttgcaggagc	cttattaggg	tcagtttttg	cacattattt	60
actaaagaaa	cattttatca	aatcaggatt	gttatcatga	ggcttgatgt	tcgcaccaaa	120
ctgcttttgt	tggtagctgc	caatgcctgc	ttcttttttc	gtgttgatgg	cttttttagaa	180
tttataattg	ttatttttct	cttattactt	ttgtctgctt	taaataagaa	aaagctagcg	240
ttcaagttgg	cggttgttta	tctgttaatg	atcgggtctat	ctgtaatccc	gctatcgatt	300
ttcccttctt	atcttgacca	cttattgagt	tttgtctcaa	tagcaggaag	gttagttttc	360
ccttctttac	tagcagggtt	aattactatt	aagacaacta	ccatctacga	attggttcat	420
ggattacgca	aatggcggtt	cccagaagtc	tggctattga	ccttggccgt	tatgtgccgt	480
ttcataccaa	tgattagaca	agaatgttgt	gttattcatc	gctctttaaa	aatcaggggg	540
attattttta	caaaatggtc	tattttgatc	agacctaaac	aatacttgga	gtatttaatg	600
gttccattgc	ttttatcttt	gataagaagt	agccaagaac	taactatcgc	tagtctaact	660
aaagggctag	cagtcaacaa	aggcaccagt	gaatgcttta	gctcacactt	aacatggaaa	720
gattgggggg	tgcagatttg	gattactgtt	atcataatca	tcacgatact	gcaatga	777

<210> SEQ ID NO 218

<211> LENGTH: 258

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 218

```
Met Val Cys Arg Asn Cys Ser Cys Arg Ser Leu Ile Arg Val Ser Phe
1      5      10      15
Cys Thr Leu Phe Thr Lys Glu Thr Phe Tyr Gln Ile Arg Ile Val Ile
20     25     30
Met Arg Leu Asp Val Arg Thr Lys Leu Leu Leu Leu Val Leu Ala Asn
35     40     45
Ala Cys Phe Phe Phe Arg Val Asp Gly Phe Leu Glu Phe Ile Ile Val
50     55     60
Ile Phe Leu Leu Leu Leu Ser Ala Leu Asn Lys Lys Lys Leu Ala
65     70     75     80
Phe Lys Leu Ala Val Val Tyr Leu Leu Met Ile Gly Leu Ser Val Ile
85     90     95
Pro Leu Ser Ile Phe Pro Ser Tyr Leu Asp His Leu Leu Ser Phe Val
100    105    110
Ser Ile Ala Gly Arg Leu Val Phe Pro Ser Leu Leu Ala Gly Leu Ile
115    120    125
Thr Ile Lys Thr Thr Thr Ile Tyr Glu Leu Val His Gly Leu Arg Lys
130    135    140
Trp Arg Phe Pro Glu Val Trp Leu Leu Thr Leu Ala Val Met Cys Arg
145    150    155    160
Phe Ile Pro Met Ile Arg Gln Glu Cys Cys Val Ile His Arg Ser Leu
165    170    175
Lys Ile Arg Gly Ile Ile Leu Thr Lys Trp Ser Ile Leu Ile Arg Pro
180    185    190
Lys Gln Tyr Leu Glu Tyr Leu Met Val Pro Leu Leu Leu Ser Leu Ile
195    200    205
Arg Ser Ser Gln Glu Leu Thr Ile Ala Ser Leu Thr Lys Gly Leu Ala
210    215    220
Val Asn Lys Gly Thr Ser Glu Cys Phe Ser Ser His Leu Thr Trp Lys
225    230    235    240
Asp Trp Gly Val Gln Ile Trp Ile Thr Val Ile Ile Ile Thr Ile
245    250    255
Leu Gln
```

<210> SEQ ID NO 219

<211> LENGTH: 744

<212> TYPE: DNA

<213> ORGANISM: *Streptococcus pyogenes*

<400> SEQUENCE: 219

```
atgaaatata attcgttaaa ctatttagtg caattgctaa ttgttattgt ttttttagga      60
gggctttacc tctttataaa accagaagag tcagtaacac caactcagtt gaataaaaaa      120
gaaatccaac aaaaagatat caaaaaaacg gaccgtttac gagctttacc taaggatatct      180
gttgaagatt gggagttggt tttagtaaac cgcgatcaca ttacaaaaga aatgagtcct      240
gaattagctg acattaatgg tatttctgtg gataaacgca ttgagcaagc cactagtgac      300
tttttagcag cagcacaagc tatcgacttg caagaacatc ttatctctgg gtaccgttcc      360
gtagactacc aaacagagct ttaccaatct tatattaaaa aagagatggc taacgatcca      420
acattgacac aagaagctgc ggaggctttg gtgcaaacct attcacagcc gccaggggct      480
agtgaacatc aactgggtct tgctattgac atgagcactg tagatacttt aaatgccagt      540
gatccatcag tagctaaagc agttcaaaaa attgcacctg attatgggtt tgtcttgccg      600
tttccagaag gaaaaaagac tagtacaggg gttgattatg aggattggca ttaccgctat      660
gtaggcaagg cgtctgctcg ttatatggct cagcacaacc taacgttgga agagtacatt      720
gctgctttaa aggagaaacg atga                                     744
```

<210> SEQ ID NO 220

<211> LENGTH: 247

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 220

```
Met Lys Tyr Asn Ser Leu Asn Tyr Leu Val Gln Leu Leu Ile Val Ile
 1           5           10          15
Val Phe Leu Gly Gly Leu Tyr Leu Phe Ile Lys Pro Glu Glu Ser Val
          20          25          30
Thr Pro Thr Gln Leu Asn Lys Lys Glu Ile Gln Gln Lys Asp Ile Lys
          35          40          45
Lys Thr Asp Arg Leu Arg Ala Leu Pro Lys Val Ser Val Glu Asp Trp
          50          55          60
Glu Leu Val Leu Val Asn Arg Asp His Ile Thr Lys Glu Met Ser Pro
65          70          75          80
Glu Leu Ala Asp Ile Asn Gly Ile Ser Val Asp Lys Arg Ile Glu Gln
          85          90          95
Ala Thr Ser Asp Phe Leu Ala Ala Ala Gln Ala Ile Asp Leu Gln Glu
          100         105         110
His Leu Ile Ser Gly Tyr Arg Ser Val Asp Tyr Gln Thr Glu Leu Tyr
          115         120         125
Gln Ser Tyr Ile Lys Lys Glu Met Ala Asn Asp Pro Thr Leu Thr Gln
          130         135         140
Glu Ala Ala Glu Ala Leu Val Gln Thr Tyr Ser Gln Pro Pro Gly Ala
145         150         155         160
Ser Glu His His Thr Gly Leu Ala Ile Asp Met Ser Thr Val Asp Thr
          165         170         175
Leu Asn Ala Ser Asp Pro Ser Val Ala Lys Ala Val Gln Lys Ile Ala
          180         185         190
Pro Asp Tyr Gly Phe Val Leu Arg Phe Pro Glu Gly Lys Lys Thr Ser
          195         200         205
Thr Gly Val Asp Tyr Glu Asp Trp His Tyr Arg Tyr Val Gly Lys Ala
          210         215         220
Ser Ala Arg Tyr Met Ala Gln His Asn Leu Thr Leu Glu Glu Tyr Ile
225         230         235         240
Ala Ala Leu Lys Glu Lys Arg
          245
```

<210> SEQ ID NO 221

<211> LENGTH: 570

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 221

```
atgagaaaac gactaaagtt tccgtatttt ttaacgcttc tagcttgctt tttattgctg      60
attgtttgtc ctttactgag tagccaaagg atagctagtg cagataaaga agtaagggtg      120
aactacagcc aaaaacaatt tattacaaaa atgggtaaaag aagttaaacc attggcaaaa      180
tattatggca ttagaccatc tattttgatt gctcaaattc ttttggaac ccatgatgga      240
aaaacattac tagcgtctaa gtatcataat ctttttagca agaaagcaac tccaggacaa      300
gtggccatta ccctaaagtc ccctaaacaa accaaccaaa acgtgagata tgctatttat      360
aaagatgacg ctagtgcaat tagagattat ttacgaatgc ttcggcaggg aaaagaagtc      420
gataagcgtt tgtatcgtaa tcttgctaca gaaaaagggt ataaagcacc agctaaaagt      480
ttacaaaagt atttgcatta tactgataaa acctatgcta ggcgactaat tcaggtcatt      540
gaaagtaacg atttaacaaa ctatgactga
                                         570
```

<210> SEQ ID NO 222

<211> LENGTH: 189

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 222

```
Met Arg Lys Arg Leu Lys Phe Pro Tyr Phe Leu Thr Leu Leu Ala Cys
```


1				5					10					15			
Phe	Leu	Leu	Leu	Ile	Val	Cys	Pro	Leu	Leu	Ser	Ser	Gln	Arg	Ile	Ala		
			20						25				30				
Ser	Ala	Asp	Lys	Glu	Val	Arg	Val	Asn	Tyr	Ser	Gln	Lys	Gln	Phe	Ile		
		35					40					45					
Thr	Lys	Met	Gly	Lys	Glu	Val	Lys	Pro	Leu	Ala	Lys	Tyr	Tyr	Gly	Ile		
	50					55					60						
Arg	Pro	Ser	Ile	Leu	Ile	Ala	Gln	Ile	Leu	Leu	Glu	Thr	His	Asp	Gly		
65					70					75					80		
Lys	Thr	Leu	Leu	Ala	Ser	Lys	Tyr	His	Asn	Leu	Phe	Ser	Lys	Lys	Ala		
			85						90					95			
Thr	Pro	Gly	Gln	Val	Ala	Ile	Thr	Leu	Lys	Ser	Pro	Lys	Gln	Thr	Asn		
		100						105					110				
Gln	Asn	Val	Arg	Tyr	Ala	Ile	Tyr	Lys	Asp	Asp	Ala	Ser	Ala	Ile	Arg		
		115					120				125						
Asp	Tyr	Leu	Arg	Met	Leu	Arg	Gln	Gly	Lys	Glu	Val	Asp	Lys	Arg	Leu		
	130				135					140							
Tyr	Arg	Asn	Leu	Ala	Thr	Glu	Lys	Gly	Tyr	Lys	Ala	Pro	Ala	Lys	Ser		
145					150					155					160		
Leu	Gln	Lys	Tyr	Leu	His	Tyr	Thr	Asp	Lys	Thr	Tyr	Ala	Arg	Arg	Leu		
			165					170						175			
Ile	Gln	Val	Ile	Glu	Ser	Asn	Asp	Leu	Thr	Asn	Tyr	Asp					
		180						185									

<210> SEQ ID NO 223

<211> LENGTH: 912

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 223

atgactgaac	aaattaaatt	aactaaatca	gaccgtcaac	gtgtttggtg	gcgttcacaa	60
ttcttacaag	gttcttggaa	ctacgaacgt	atgcaaaaaca	tgggctgggc	ttatgcactt	120
atccctgctc	ttaaaaaatt	gtatacgtct	cctgaagacc	gtgcagctgc	tcttgagcgc	180
cacatggaat	tctttaacac	tcacccatac	gttgacgctc	caatcattgg	tgtaacactt	240
gcccttgaag	aagaacgcgc	aaatggtacg	ccaattgatg	acaaggctat	ccaagggggt	300
aaaatcggtg	tgatgggacc	tcttgctggt	atcggtgacc	cagtattctg	gtttacgatt	360
cgctcctatcc	ttggggcact	tggtgcttct	ttggcttcaa	caggtaacat	cgttggtcca	420
cttctgttct	tctttggatg	gaaccttatc	cgtatggcct	tcttatggta	tactcaagaa	480
tttggttaca	aagctgggtc	tgaaattact	aaagacatgt	caggcggtat	cctccaagac	540
attactaaag	gtgcttcaat	ccttggaatg	tttatccttg	cagtgccttg	tcaacgttgg	600
gtatctatca	actttactat	cgaccttcct	ggaaaaacaat	tgtcagatgg	tgcttatgtg	660
gtcttcccag	atggcgctgt	taaagggtgt	gaattgaaaa	ctatccttgc	caacgctatt	720
ggtggtatga	gccttgataa	agtccaagct	caaacccttc	aaggacaatt	ggactctctt	780
atcccagggt	tagctggatt	actccttaca	ttcctttgca	tgtggttatt	gaagaaaaaa	840
gtttctccaa	tcgcaatcat	catcggtctg	tttgcatctg	gtatccttgc	tcaccttgca	900
ggtattatgt	aa					912

<210> SEQ ID NO 224

<211> LENGTH: 303

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 224

Met	Thr	Glu	Gln	Ile	Lys	Leu	Thr	Lys	Ser	Asp	Arg	Gln	Arg	Val	Trp
1				5					10					15	
Trp	Arg	Ser	Gln	Phe	Leu	Gln	Gly	Ser	Trp	Asn	Tyr	Glu	Arg	Met	Gln
		20						25				30			
Asn	Met	Gly	Trp	Ala	Tyr	Ala	Leu	Ile	Pro	Ala	Leu	Lys	Lys	Leu	Tyr
	35						40					45			

Thr	Ser	Pro	Glu	Asp	Arg	Ala	Ala	Ala	Leu	Glu	Arg	His	Met	Glu	Phe
50						55					60				
Phe	Asn	Thr	His	Pro	Tyr	Val	Ala	Ala	Pro	Ile	Ile	Gly	Val	Thr	Leu
65					70					75					80
Ala	Leu	Glu	Glu	Glu	Arg	Ala	Asn	Gly	Thr	Pro	Ile	Asp	Asp	Lys	Ala
				85					90					95	
Ile	Gln	Gly	Val	Lys	Ile	Gly	Met	Met	Gly	Pro	Leu	Ala	Gly	Ile	Gly
			100					105					110		
Asp	Pro	Val	Phe	Trp	Phe	Thr	Ile	Arg	Pro	Ile	Leu	Gly	Ala	Leu	Gly
		115					120					125			
Ala	Ser	Leu	Ala	Ser	Thr	Gly	Asn	Ile	Val	Gly	Pro	Leu	Leu	Phe	Phe
130						135					140				
Phe	Gly	Trp	Asn	Leu	Ile	Arg	Met	Ala	Phe	Leu	Trp	Tyr	Thr	Gln	Glu
145				150						155					160
Phe	Gly	Tyr	Lys	Ala	Gly	Ser	Glu	Ile	Thr	Lys	Asp	Met	Ser	Gly	Gly
			165						170					175	
Ile	Leu	Gln	Asp	Ile	Thr	Lys	Gly	Ala	Ser	Ile	Leu	Gly	Met	Phe	Ile
		180					185						190		
Leu	Ala	Val	Leu	Val	Gln	Arg	Trp	Val	Ser	Ile	Asn	Phe	Thr	Ile	Asp
	195					200					205				
Leu	Pro	Gly	Lys	Gln	Leu	Ser	Asp	Gly	Ala	Tyr	Val	Val	Phe	Pro	Asp
210					215						220				
Gly	Ala	Val	Lys	Gly	Ala	Glu	Leu	Lys	Thr	Ile	Leu	Ala	Asn	Ala	Ile
225				230						235					240
Gly	Gly	Met	Ser	Leu	Asp	Lys	Val	Gln	Ala	Gln	Thr	Leu	Gln	Gly	Gln
			245					250					255		
Leu	Asp	Ser	Leu	Ile	Pro	Gly	Leu	Ala	Gly	Leu	Leu	Leu	Thr	Phe	Leu
		260					265						270		
Cys	Met	Trp	Leu	Leu	Lys	Lys	Lys	Val	Ser	Pro	Ile	Ala	Ile	Ile	Ile
	275					280					285				
Gly	Leu	Phe	Ala	Phe	Gly	Ile	Leu	Ala	His	Leu	Ala	Gly	Ile	Met	
290						295					300				

<210> SEQ ID NO 225

<211> LENGTH: 810

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 225

atgtcagata	tttcgattat	ttctgcaatt	ttggtcgcta	tcattgcctt	cttcgctggt	60
cttgaaggta	tcctcgacca	atttcaaagt	caccaaccac	ttgttgccctg	tactttgatt	120
ggacttgtaa	ctggacacct	tgaagctggt	gtcatccttg	gtggtacact	tcaaagtctt	180
gctcttggtt	gggcaaakat	cggtgctgcc	gttgcccctg	atgctgccct	tgccctctgtt	240
gcagctgcta	tcatcatggt	caaaagtggc	gactttactc	aaaaaggaat	taccttttgc	300
tactcaacag	ctatccact	tgctgttgct	ggctttttcc	ttacaatgat	cgttcgtact	360
ttgtcaactg	cccttgtaga	cgctggtagc	aaagctgccg	ctgaaggtaa	tttcgcaggt	420
attgaacgct	tcacttttat	tgcccttctt	cttcaaggat	tgctatcgc	tgtccctgca	480
gctcttcttg	ttgctgttcc	tacttcagcc	gtacaatctg	ttttgaatgc	tatgcaaacc	540
tggttgaaacg	aaggtagtga	aatcggtggt	gcatggttg	ttgctgtagg	ttatgctatg	600
gttatcaaca	tgatggctac	tcgtgaagta	tggccattct	tcgccctagg	ttttgctctt	660
gcagctatca	gccaattaac	ccttatcgct	atgggtgtta	tcggtgtagc	aattgccttc	720
atctacctta	atctttctaa	aaaagggtgt	aacgggtggt	atgcagcagg	ttcagctgat	780
ccaatcggcg	acatcttaga	agactactag				810

<210> SEQ ID NO 226

<211> LENGTH: 269

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 226

```
Met Ser Asp Ile Ser Ile Ile Ser Ala Ile Leu Val Val Ile Ile Ala
1           5           10          15
Phe Phe Ala Gly Leu Glu Gly Ile Leu Asp Gln Phe Gln Met His Gln
20          25          30
Pro Leu Val Ala Cys Thr Leu Ile Gly Leu Val Thr Gly His Leu Glu
35          40          45
Ala Gly Val Ile Leu Gly Gly Thr Leu Gln Met Leu Ala Leu Gly Trp
50          55          60
Ala Asn Ile Gly Ala Ala Val Ala Pro Asp Ala Ala Leu Ala Ser Val
65          70          75          80
Ala Ala Ala Ile Ile Met Val Lys Ser Gly Asp Phe Thr Gln Lys Gly
85          90          95
Ile Thr Phe Ala Tyr Ser Thr Ala Ile Pro Leu Ala Val Ala Gly Leu
100         105         110
Phe Leu Thr Met Ile Val Arg Thr Leu Ser Thr Ala Leu Val His Ala
115        120        125
Gly Asp Lys Ala Ala Ala Glu Gly Asn Phe Ala Gly Ile Glu Arg Phe
130        135        140
His Phe Ile Ala Leu Leu Leu Gln Gly Leu Arg Ile Ala Val Pro Ala
145        150        155        160
Ala Leu Leu Val Ala Val Pro Thr Ser Ala Val Gln Ser Val Leu Asn
165        170        175
Ala Met Pro Asn Trp Leu Asn Glu Gly Met Gln Ile Gly Gly Ala Met
180        185        190
Val Val Ala Val Gly Tyr Ala Met Val Ile Asn Met Met Ala Thr Arg
195        200        205
Glu Val Trp Pro Phe Phe Ala Leu Gly Phe Ala Leu Ala Ala Ile Ser
210        215        220
Gln Leu Thr Leu Ile Ala Met Gly Val Ile Gly Val Ala Ile Ala Phe
225        230        235        240
Ile Tyr Leu Asn Leu Ser Lys Lys Gly Gly Asn Gly Gly Asn Ala Ala
245        250        255
Gly Ser Ala Asp Pro Ile Gly Asp Ile Leu Glu Asp Tyr
260        265
```

<210> SEQ ID NO 227

<211> LENGTH: 1461

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 227

```
atggaaaagt tttttaagtt aagcgaaaat gggacaactg tctcaactga gattatggct      60
ggtttaacga ctttttttgc catgtcctat attttgtttg ttaacccaag tatttttaggt      120
gcagcgggga tgccctctaa tgctgtcttt ttggctacga ttatcgcagc agccatatca      180
accttaatta tgggactatt tgccaatgtg ccttatgcgt tggcaccagg aatgggactt      240
aacgcttttt tcacttatac agttgttttt gctttaaggt tttcatggca agaagccttg      300
gcaatgggtt tcatttgtgg attattcaat atttttatta ccgtaaccaa gtttcgtaaa      360
agtatcatca aggcgattcc agttagttta cagcatgcta ttggtggggg aattggtgtc      420
ttttagctt atttaggatt taaaaacgca aatatcatta ctttttctat ctctgctgaa      480
aatatagtaa tggtaaattg tgttgaaccg gctaaagcat cggctaaaac atttgcagat      540
ggtctattat ttgtagacgc caatggtgga gttgtacctt cgatttctag ttttacggat      600
tccggtgtat tacttgctat ttttggttta cttttgacga cagctcttgt gattcgaaat      660
tttagagggt ctattttaat tggattgtgc gcaacaactc ttgtagggtg tccttttagga      720
atagtggatg tgtccaacct caattttggg atcagccata ttggtgaagc ttggactgaa      780
ttaggtacaa ctttccttgc agctttcgat ggtttgagtt ctctttttag cgattcaagt      840
cgtttaccgc tagttttcat gactattttt gcttttagtc tatcagatac ttttgacaca      900
attggtacct ttatcggaac tggtcgtcga acagggtattt tctctcaaga cgatgagaat      960
```

```

gctttggaaa atagtatagg ctttagttca aaaatggacc gtgcgctttt tgcagatgct 1020
atcggtagctt ctattggggc tttgggttga acttcaaata cgactaccta tgttgaatca 1080
gcagcaggaa ttgctgaagg tggacgtact ggactaacag cagtctccac cgcagtatgc 1140
ttcttattat caatattgct attaccgctt gtaggtattg tcccagctgc tgctacggct 1200
ccagctttta ttattgtggg tgtcatgatg gtgtcttctt ttcttgatgt taattggagt 1260
aaatttgcag atgctcttcc agcttttttt gcagctttct ttatggcgct gtgttactct 1320
atttcctatg gtattgccgc tgcctttatt ttctattgtc tagtaaaagt tgttgaggga 1380
aaaacaaaag atattcaccc tattatttgg ggagcaacct tcttgttcat tgtaaatttc 1440
atcatattaa ctatcttata a 1461

```

<210> SEQ ID NO 228
 <211> LENGTH: 486
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 228

```

Met Glu Lys Phe Phe Lys Leu Ser Glu Asn Gly Thr Thr Val Ser Thr
1          5          10          15
Glu Ile Met Ala Gly Leu Thr Thr Phe Phe Ala Met Ser Tyr Ile Leu
20        25        30
Phe Val Asn Pro Ser Ile Leu Gly Ala Ala Gly Met Pro Ser Asn Ala
35        40        45
Val Phe Leu Ala Thr Ile Ile Ala Ala Ala Ile Ser Thr Leu Ile Met
50        55        60
Gly Leu Phe Ala Asn Val Pro Tyr Ala Leu Ala Pro Gly Met Gly Leu
65        70        75        80
Asn Ala Phe Phe Thr Tyr Thr Val Val Phe Ala Leu Arg Phe Ser Trp
85        90        95
Gln Glu Ala Leu Ala Met Val Phe Ile Cys Gly Leu Phe Asn Ile Phe
100       105       110
Ile Thr Val Thr Lys Phe Arg Lys Ser Ile Ile Lys Ala Ile Pro Val
115       120       125
Ser Leu Gln His Ala Ile Gly Gly Gly Ile Gly Val Phe Val Ala Tyr
130       135       140
Leu Gly Phe Lys Asn Ala Asn Ile Ile Thr Phe Ser Ile Ser Ala Glu
145       150       155       160
Asn Ile Val Met Val Asn Gly Val Glu Pro Ala Lys Ala Ser Ala Lys
165       170       175
Thr Phe Ala Asp Gly Leu Leu Phe Val Asp Ala Asn Gly Gly Val Val
180       185       190
Pro Thr Ile Ser Ser Phe Thr Asp Ser Gly Val Leu Leu Ala Ile Phe
195       200       205
Gly Leu Leu Leu Thr Thr Ala Leu Val Ile Arg Asn Phe Arg Gly Ala
210       215       220
Ile Leu Ile Gly Ile Val Ala Thr Thr Leu Val Gly Val Pro Leu Gly
225       230       235       240
Ile Val Asp Val Ser Asn Leu Asn Phe Gly Ile Ser His Ile Gly Glu
245       250       255
Ala Trp Thr Glu Leu Gly Thr Thr Phe Leu Ala Ala Phe Asp Gly Leu
260       265       270
Ser Ser Leu Phe Ser Asp Ser Ser Arg Leu Pro Leu Val Phe Met Thr
275       280       285
Ile Phe Ala Phe Ser Leu Ser Asp Thr Phe Asp Thr Ile Gly Thr Phe
290       295       300
Ile Gly Thr Gly Arg Arg Thr Gly Ile Phe Ser Gln Asp Asp Glu Asn
305       310       315       320
Ala Leu Glu Asn Ser Ile Gly Phe Ser Ser Lys Met Asp Arg Ala Leu
325       330       335

```


50		55		60	
Ile	Pro	Leu	Leu	Leu	Ser
65		70		75	
Ala	Asp	Gln	His	Phe	Leu
		85		90	
Ile	Lys	Gln	Ala	Glu	Arg
		100		105	
Thr	Ala	Val	Leu	Leu	Phe
		115		120	
Ser	Leu	Phe	Ile	Phe	Ile
		130		135	
Arg	Val	Val	Leu	Ser	Arg
145				150	
Leu	Asp	Trp	Ala	Lys	Ala
				165	
Ile	Leu	Lys	Phe	Tyr	Ser
				180	
Lys	Val	Lys	Glu	Arg	Thr
				195	
Gln	Thr	Pro	Ser	Asn	Leu
				210	
Arg	Ser	Ser	Asp	Tyr	Leu
225				230	
Ser	Leu	Ser	Val	Phe	Phe
				245	
Ala	Leu	Ile	Phe	Asn	Tyr
				260	
Tyr	His	Tyr	Asp	Tyr	His
				275	
Arg	Ser	Lys	Lys	Lys	Asn
				290	
Leu	Met	Leu	Ile	Val	Asn
305				310	
Leu	Ile	Leu	Ile	Val	Gly
				325	
Tyr	Lys	Leu	Lys	Lys	Ile
				340	

<210> SEQ ID NO 231

<211> LENGTH: 987

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 231

ttgaaacatc	ctattcgaaa	aacacttgtc	accttaggtc	tattactgac	cttatgcctg	60
ccgactccag	ttgcagctag	ttctcgttct	tggaagagct	ggtttatcga	gcaatatttc	120
tgggtaaaaac	gtgacaagag	ttactattct	aaacaagatg	acccaagctt	ccaaagatac	180
cttgatgcct	gtcgtgaaca	atctgataaa	ccttatcaac	tagatactaa	tttagtcaat	240
ggtccccttg	ttcaagaaaa	tctttatggc	atgcagggtt	actcttggaa	tgataatgga	300
aaacctgata	aaaaaacaat	tatttatctt	gccggtggtt	cttatcttaa	caatccaacg	360
acataccata	ttaatatggt	aaagacatta	tccacaagtc	ttgacgctaa	aattgtttta	420
cccatttatc	ctaaagcccc	acgttatacc	tataactata	ctatgccaaa	attgggtcaat	480
ctttaccaac	actattacca	taaaaatcag	aatgttttcc	ttatgggaga	ttcagcaggt	540
ggagggttag	ccttaggtct	agctcatgcc	ctacacaatg	aatcagtccc	tcaaccaaag	600
cagctcgttc	ttttatcacc	ttggttagat	gttactatgt	cacaccgaga	gattccagaa	660
tacgaagatg	ctgatcctat	tctatcttct	tggggattaa	aacgagtggg	agaattgtgg	720
gcctactctg	ctgataatac	caaccatatt	tatgtcagtc	ctaaaaatgg	tccgatcact	780
tatctaccac	caattacttt	atttactggg	acacgagaga	tcttttatcc	tgatattcgc	840

gattatgccg caaaactgaa agccgctaac cacaatatta cctttattac ccaagaaggc	900
atgaaccacg tttacccaat ttatcctatc gaagaggcaa aaacagctca ataccaaadc	960
attgatgccca tcaacaaaac tccttaa	987

<210> SEQ ID NO 232
 <211> LENGTH: 328
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 232

Met	Lys	His	Pro	Ile	Arg	Lys	Thr	Leu	Val	Thr	Leu	Gly	Leu	Leu	Leu	
1				5					10					15		
Thr	Leu	Cys	Leu	Pro	Thr	Pro	Val	Ala	Ala	Ser	Ser	Arg	Ser	Trp	Lys	
			20					25					30			
Ser	Trp	Phe	Ile	Glu	Gln	Tyr	Phe	Trp	Leu	Lys	Arg	Asp	Lys	Ser	Tyr	
		35					40					45				
Tyr	Ser	Lys	Gln	Asp	Asp	Pro	Ser	Phe	Gln	Arg	Tyr	Leu	Asp	Ala	Cys	
	50					55					60					
Arg	Glu	Gln	Ser	Asp	Lys	Pro	Tyr	Gln	Leu	Asp	Thr	Asn	Leu	Val	Asn	
65					70					75					80	
Gly	Pro	Leu	Val	Gln	Glu	Asn	Leu	Tyr	Gly	Met	Gln	Val	Tyr	Ser	Trp	
				85					90					95		
Asn	Asp	Asn	Gly	Lys	Pro	Asp	Gln	Lys	Thr	Ile	Ile	Tyr	Leu	Ala	Gly	
			100					105					110			
Gly	Ser	Tyr	Leu	Asn	Asn	Pro	Thr	Thr	Tyr	His	Ile	Asn	Met	Leu	Lys	
		115					120					125				
Thr	Leu	Ser	Thr	Ser	Leu	Asp	Ala	Lys	Ile	Val	Leu	Pro	Ile	Tyr	Pro	
	130					135					140					
Lys	Ala	Pro	Arg	Tyr	Thr	Tyr	Asn	Tyr	Thr	Met	Pro	Lys	Leu	Val	Asn	
145					150					155					160	
Leu	Tyr	Gln	His	Tyr	Tyr	His	Lys	Asn	Gln	Asn	Val	Phe	Leu	Met	Gly	
				165					170					175		
Asp	Ser	Ala	Gly	Gly	Gly	Leu	Ala	Leu	Gly	Leu	Ala	His	Ala	Leu	His	
			180					185					190			
Asn	Glu	Ser	Val	Pro	Gln	Pro	Lys	Gln	Leu	Val	Leu	Leu	Ser	Pro	Trp	
		195					200					205				
Leu	Asp	Val	Thr	Met	Ser	His	Pro	Glu	Ile	Pro	Glu	Tyr	Glu	Asp	Ala	
	210					215					220					
Asp	Pro	Ile	Leu	Ser	Ser	Trp	Gly	Leu	Lys	Arg	Val	Gly	Glu	Leu	Trp	
225					230					235					240	
Ala	Tyr	Ser	Ala	Asp	Asn	Thr	Asn	His	Ile	Tyr	Val	Ser	Pro	Lys	Asn	
				245					250					255		
Gly	Pro	Ile	Thr	Tyr	Leu	Pro	Pro	Ile	Thr	Leu	Phe	Thr	Gly	Thr	Arg	
			260					265					270			
Glu	Ile	Phe	Tyr	Pro	Asp	Ile	Arg	Asp	Tyr	Ala	Ala	Lys	Leu	Lys	Ala	
		275				280						285				
Ala	Asn	His	Asn	Ile	Thr	Phe	Ile	Thr	Gln	Glu	Gly	Met	Asn	His	Val	
	290					295					300					
Tyr	Pro	Ile	Tyr	Pro	Ile	Glu	Glu	Ala	Lys	Thr	Ala	Gln	Tyr	Gln	Ile	
305					310					315					320	
Ile	Asp	Ala	Ile	Asn	Lys	Thr	Pro									
				325												

<210> SEQ ID NO 233
 <211> LENGTH: 1452
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 233

```

atgatgcaac cttttttaga cattattaac aagattctgg gatttcctat tcagttggga      60
tcaggtgtgg tcatgctgat tgtcatgaca ggtttagcca tgattttcgg ggtaaatttc      120
acaaaggcac tgggaaggtgg gattaagtta gccatcgctt tgacagggat tggagccatt      180
attggaattt tgacggggggc tttttcagag tctttacagg cctttgttaa aaatacaggg      240
atcagtttaa acattattga tgtcgggttg gcaccgcttg caacaattac ctgggggttcc      300
ccttacaccc tttatttctt gctgggtgatg ctgggtggta atattgtcat gattgtcatg      360
aaaaaacgg acacccttga cgtcgatatt tttgatattt ggcatttgtc cattacgggt      420
ctattgatta tgtggtatgc ggctcgtaac catttaccag tctttgtgtc tcttttgatt      480
gctactgtgg cagttattct tgttggggta ctgaaaatca ttaactctga tttgatgaaa      540
ccgaccttgg atgaccttct tgggacaggg cctcaatcac caatgacttc aactcacatg      600
aactacatga tgaatccaat cattatgggtc ttagataaga tttttgacaa ggtctttccg      660
gggctggata aatatgactt tgatgctgct aaattgaaca aaaaaattgg cttctggggc      720
tctaagttct ttatcggaat ggctctaggc tttgtgattg ggattatggg agatcctcat      780
ttcactgttg aatctatcaa aaattgggtt ggcttaggct ttaccgcggg tgcctgcttg      840
gaacttttct ctttgattgg ctcttggttt atcgcagctg ttgagccttt gtcacaaggg      900
attaccaatt ttgccaatgc tagaatgcat gggcgctcgtt tcaatatcgg tttggactgg      960
cccttcattg ctggtcgtgc tgaaatctgg gcctgtgcc aatattcttg cccaatcatg     1020
ttgattgaag ccgttctcct atcaaaagtt ggcaatggga ttttaccact ggcaggaatt     1080
attgctatgg ggatgacacc agctcttctt gtggtcacac gtggtcgttt gattcgcatg     1140
attatttttg gttccctctt attgccatta ttcctcttgt caggaactat gattgctcca     1200
tttgcgacag agttggctaa aaaagtaggg gcttttccag caggtacaag cgctggttcc     1260
ttgattacgc attcaacact tgaaggacca atggaaaaaa tttttgggta tgtgattggg     1320
caagcgacaa caggtcagat tgcctcaatc atcacgctaa tcattcttgt ggccatttac     1380
ctaagtctct ttgcttggtg tgctaacc aa atgaaggcac gtaacgctga atatgcgaaa     1440
acaatgaaat aa                                     1452

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<210> SEQ ID NO 234
<211> LENGTH: 483
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 234

```

```

Met Met Gln Pro Phe Leu Asp Ile Ile Asn Lys Ile Leu Gly Phe Pro
1          5          10          15
Ile Gln Leu Gly Ser Gly Val Val Met Leu Ile Val Met Thr Gly Leu
          20          25          30
Ala Met Ile Phe Gly Val Lys Phe Thr Lys Ala Leu Glu Gly Gly Ile
          35          40          45
Lys Leu Ala Ile Ala Leu Thr Gly Ile Gly Ala Ile Ile Gly Ile Leu
          50          55          60
Thr Gly Ala Phe Ser Glu Ser Leu Gln Ala Phe Val Lys Asn Thr Gly
65          70          75          80
Ile Ser Leu Asn Ile Ile Asp Val Gly Trp Ala Pro Leu Ala Thr Ile
          85          90          95
Thr Trp Gly Ser Pro Tyr Thr Leu Tyr Phe Leu Leu Val Met Leu Val
          100         105         110
Val Asn Ile Val Met Ile Val Met Lys Lys Thr Asp Thr Leu Asp Val
          115         120         125
Asp Ile Phe Asp Ile Trp His Leu Ser Ile Thr Gly Leu Leu Ile Met
          130         135         140
Trp Tyr Ala Ala Arg Asn His Leu Pro Val Phe Val Ser Leu Leu Ile
145         150         155         160
Ala Thr Val Ala Val Ile Leu Val Gly Val Leu Lys Ile Ile Asn Ser
          165         170         175
Asp Leu Met Lys Pro Thr Phe Asp Asp Leu Leu Gly Thr Gly Pro Gln
          180         185         190
Ser Pro Met Thr Ser Thr His Met Asn Tyr Met Met Asn Pro Ile Ile
          195         200         205

```


Met	Val	Leu	Asp	Lys	Ile	Phe	Asp	Lys	Val	Phe	Pro	Gly	Leu	Asp	Lys
210						215					220				
Tyr	Asp	Phe	Asp	Ala	Ala	Lys	Leu	Asn	Lys	Lys	Ile	Gly	Phe	Trp	Gly
225				230						235					240
Ser	Lys	Phe	Phe	Ile	Gly	Met	Ala	Leu	Gly	Phe	Val	Ile	Gly	Ile	Met
				245					250					255	
Gly	Asp	Pro	His	Phe	Thr	Val	Glu	Ser	Ile	Lys	Asn	Trp	Phe	Gly	Leu
			260					265					270		
Gly	Phe	Thr	Ala	Gly	Ala	Cys	Leu	Glu	Leu	Phe	Ser	Leu	Ile	Gly	Ser
		275					280					285			
Trp	Phe	Ile	Ala	Ala	Val	Glu	Pro	Leu	Ser	Gln	Gly	Ile	Thr	Asn	Phe
290						295					300				
Ala	Asn	Ala	Arg	Met	His	Gly	Arg	Arg	Phe	Asn	Ile	Gly	Leu	Asp	Trp
305				310						315					320
Pro	Phe	Ile	Ala	Gly	Arg	Ala	Glu	Ile	Trp	Ala	Cys	Ala	Asn	Ile	Leu
				325					330					335	
Ala	Pro	Ile	Met	Leu	Ile	Glu	Ala	Val	Leu	Leu	Ser	Lys	Val	Gly	Asn
			340					345					350		
Gly	Ile	Leu	Pro	Leu	Ala	Gly	Ile	Ile	Ala	Met	Gly	Met	Thr	Pro	Ala
		355				360					365				
Leu	Leu	Val	Val	Thr	Arg	Gly	Arg	Leu	Ile	Arg	Met	Ile	Ile	Phe	Gly
370						375					380				
Ser	Leu	Leu	Leu	Pro	Leu	Phe	Leu	Leu	Ser	Gly	Thr	Met	Ile	Ala	Pro
385				390						395					400
Phe	Ala	Thr	Glu	Leu	Ala	Lys	Lys	Val	Gly	Ala	Phe	Pro	Ala	Gly	Thr
				405					410					415	
Ser	Ala	Gly	Ser	Leu	Ile	Thr	His	Ser	Thr	Leu	Glu	Gly	Pro	Met	Glu
			420					425					430		
Lys	Ile	Phe	Gly	Tyr	Val	Ile	Gly	Gln	Ala	Thr	Thr	Gly	Gln	Ile	Ala
		435					440					445			
Ser	Ile	Ile	Thr	Leu	Ile	Ile	Phe	Val	Ala	Ile	Tyr	Leu	Ser	Leu	Phe
	450					455					460				
Ala	Trp	Tyr	Ala	Asn	Gln	Met	Lys	Ala	Arg	Asn	Ala	Glu	Tyr	Ala	Lys
465				470						475					480
Thr	Met	Lys													

<210> SEQ ID NO 235

<211> LENGTH: 723

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 235

atggctacga	tgaacaata	tcataaagga	gattccatga	ctaaatcaca	aaaagaggcg	60
ctttattgga	tgttgagtgt	tctaactatc	actctaatag	gtggctcctg	ccttattttt	120
ggatccccacc	ctcaaacgca	agataaggta	gctaaacatt	ctaaaagtgc	tgctagttta	180
ctaaaaaaag	cagttaaagc	agttaatgac	gctgatcggt	tagccactgc	agctgctatc	240
caagaagccc	agaaagctgt	tgataaatta	gcagaatctt	ctaagaaaaa	aacgctacaa	300
gaacagctaa	acgttgccaa	agcaaagcaa	gagcaagaag	atgcagctac	tcaagcagtt	360
aaagctgctg	aggagactct	caatcaaaat	cttaaagata	tcgccccaaa	agcagttaac	420
gacttaagta	acaaaggtaa	aaaagccgct	ttacaatctc	ggttagacgc	tattttacca	480
gcgaaaccca	ttattgatga	atttccaaga	caaagtggag	aaataacaga	taactcttac	540
tggacacctt	tcccaggaga	cgtctcagat	acttatgata	attcccagtc	acctacttta	600
gacccaagct	cagaatcttc	agcttcagat	gttacaccac	aacctagtca	tcctgatcca	660
attccacctc	agacctcttc	agaaccttcc	gactcaggag	acaagcaatc	atcaaaagag	720
ttaa						723

<210> SEQ ID NO 236

<211> LENGTH: 240

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 236

```
Met Ala Thr Met Lys Gln Tyr His Lys Gly Asp Ser Met Thr Lys Ser
1          5          10          15
Gln Lys Glu Ala Leu Tyr Trp Met Leu Ser Val Leu Thr Ile Thr Leu
20          25          30
Ile Gly Gly Ser Cys Leu Ile Phe Gly Ser His Pro Gln Thr Gln Asp
35          40          45
Lys Val Ala Lys His Ser Lys Ser Ala Ala Ser Leu Leu Lys Lys Ala
50          55          60
Val Lys Ala Val Asn Asp Ala Asp Arg Leu Ala Thr Ala Ala Ala Ile
65          70          75          80
Gln Glu Ala Gln Lys Ala Val Asp Lys Leu Ala Glu Ser Ser Lys Lys
85          90          95
Lys Thr Leu Gln Glu Gln Leu Asn Val Ala Lys Ala Lys Gln Glu Gln
100         105         110
Glu Asp Ala Ala Thr Gln Ala Val Lys Ala Ala Glu Glu Thr Leu Asn
115         120         125
Gln Asn Leu Lys Asp Ile Ala Gln Lys Ala Val Asn Asp Leu Ser Asn
130         135         140
Lys Gly Lys Lys Ala Ala Leu Gln Ser Arg Leu Asp Ala Ile Leu Pro
145         150         155         160
Ala Lys Pro Ile Ile Asp Glu Phe Pro Arg Gln Ser Gly Glu Ile Thr
165         170         175
Asp Asn Ser Tyr Trp Thr Pro Phe Pro Gly Asp Val Ser Asp Thr Tyr
180         185         190
Asp Asn Ser Gln Ser Pro Thr Leu Asp Pro Ser Ser Glu Ser Ser Ala
195         200         205
Ser Asp Val Thr Pro Gln Pro Ser His Pro Asp Pro Ile Pro Pro Gln
210         215         220
Thr Ser Ser Glu Pro Ser Asp Ser Gly Asp Lys Gln Ser Ser Lys Glu
225         230         235         240
```

<210> SEQ ID NO 237

<211> LENGTH: 555

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 237

```
ttgaaaataa ggagccgtat tgtgaccatc tttttagtga tgtagctat gtttactatt      60
cgtttagtat ttttgaagaa atcgataaca aatgaaaaag ccatattagc ccaaggagga      120
caggaatttg gtgctcagaa cacgaaattt ttgacgttac ttcacattat gatttatgtg      180
tttgcggtga ttgaagcgct gcttaaacia attaatgttg atggcattag ttttttaggt      240
cttttggtga tgttattatc agtagctgtt ttatatgaag tgacacgtat cttaggtgac      300
atttggaactg taaaattgat gttagcaaaa gaccacaaat atgtggatca ctggttggtc      360
aaaacgatta aacatcctaa ctacttttta aatatcgccc ctgagctggt gggcatagcc      420
ttactttgcc atgctaaaat tacggctatg cttcttttcc catgctacat tgtagtaata      480
tatttacgta ttcgagaaga aaacaagcta ttagcggaag tgattattcc aaacggtact      540
cgaacaaaac cttaa                                         555
```

<210> SEQ ID NO 238

<211> LENGTH: 184

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 238

```
Met Lys Ile Arg Ser Arg Ile Val Thr Ile Phe Leu Val Met Leu Ala
1          5          10          15
```

Met	Phe	Thr	Ile	Arg	Leu	Val	Phe	Leu	Lys	Lys	Ser	Ile	Thr	Asn	Glu
			20					25				30			
Lys	Ala	Ile	Leu	Ala	Gln	Gly	Gly	Gln	Glu	Phe	Gly	Ala	Gln	Asn	Thr
	35					40					45				
Lys	Phe	Leu	Thr	Leu	Leu	His	Ile	Met	Ile	Tyr	Val	Phe	Ala	Val	Ile
	50					55				60					
Glu	Ala	Leu	Leu	Lys	Gln	Ile	Lys	Phe	Asp	Gly	Ile	Ser	Phe	Leu	Gly
65					70				75					80	
Leu	Leu	Leu	Met	Leu	Leu	Ser	Val	Ala	Val	Leu	Tyr	Glu	Val	Thr	Arg
			85					90						95	
Ile	Leu	Gly	Asp	Ile	Trp	Thr	Val	Lys	Leu	Met	Leu	Ala	Lys	Asp	His
		100						105					110		
Lys	Tyr	Val	Asp	His	Trp	Leu	Phe	Lys	Thr	Ile	Lys	His	Pro	Asn	Tyr
	115					120					125				
Phe	Leu	Asn	Ile	Ala	Pro	Glu	Leu	Val	Gly	Ile	Ala	Leu	Leu	Cys	His
	130					135					140				
Ala	Lys	Ile	Thr	Ala	Met	Leu	Leu	Phe	Pro	Cys	Tyr	Ile	Val	Val	Ile
145					150					155					160
Tyr	Leu	Arg	Ile	Arg	Glu	Glu	Asn	Lys	Leu	Leu	Ala	Glu	Val	Ile	Ile
			165					170						175	
Pro	Asn	Gly	Thr	Arg	Thr	Lys	Pro								
			180												

<210> SEQ ID NO 239

<211> LENGTH: 702

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 239

atggatatct	ttggcggaatt	tttgggtaca	gccttattgg	ttttactagg	aaatgggtgtg	60
gtagcagggg	ttgtcttgcc	caaaacgaaa	acccatgctt	ctggctggat	cgtgattgcg	120
actggctggg	gaattgcagt	tgctgtggca	gtctttatca	gtggcaaagt	tgcccctgcc	180
cacctcaatc	cagctgttag	ccttgctttt	gccatgagtg	gaaccattgc	ctggtcaaca	240
gccattgcct	atagccttgc	ccaactattg	ggagctatgg	ttggttcaac	tctggtattc	300
cttcagttca	ggccacatta	tctggctgct	gagagtcagg	ctgatatttt	agggacattt	360
gcgacaggtc	ctgctattcg	agatactagc	tcaaacctat	tgagtgaaat	ctttgggacc	420
tttgtcttga	tgcttggtat	tttggcattt	ggcttatatg	atatgccagc	aggactagga	480
accctctgtg	taggtacctt	ggttattggg	attgggttat	ccttaggagg	aacgacaggt	540
tacgccatta	acccagcacg	tgatttagga	cctcgtctag	ttcatgctat	tctaccactc	600
aacaacaagg	gagattctga	ttggctcttat	gcttggatac	ctgtttagg	accaattatt	660
ggagcggctc	tagcagtttt	gcttttccaa	gtcatgtcct	aa		702

<210> SEQ ID NO 240

<211> LENGTH: 233

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 240

Met	Asp	Ile	Phe	Gly	Glu	Phe	Leu	Gly	Thr	Ala	Leu	Leu	Val	Leu	Leu
1			5					10					15		
Gly	Asn	Gly	Val	Val	Ala	Gly	Val	Val	Leu	Pro	Lys	Thr	Lys	Thr	His
		20					25				30				
Ala	Ser	Gly	Trp	Ile	Val	Ile	Ala	Thr	Gly	Trp	Gly	Ile	Ala	Val	Ala
	35					40					45				
Val	Ala	Val	Phe	Ile	Ser	Gly	Lys	Val	Ala	Pro	Ala	His	Leu	Asn	Pro
	50					55				60					
Ala	Val	Ser	Leu	Ala	Phe	Ala	Met	Ser	Gly	Thr	Ile	Ala	Trp	Ser	Thr
65				70					75					80	
Ala	Ile	Ala	Tyr	Ser	Leu	Ala	Gln	Leu	Leu	Gly	Ala	Met	Val	Gly	Ser

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 242

Met	Asn	Ser	Leu	Gly	Val	Arg	Arg	Lys	Lys	Arg	Gly	Asp	Gly	Met	Asn	
1				5					10					15		
Trp	Ser	Thr	Ile	Trp	Glu	Leu	Ile	Lys	Ile	Asn	Ile	Leu	Tyr	Ser	Asn	
			20					25					30			
Pro	Gln	Ser	Leu	Ala	Asn	Leu	Lys	Lys	Arg	Gln	Glu	Lys	His	Pro	Lys	
			35				40					45				
Glu	Asn	Phe	Lys	Ala	Tyr	Lys	Ser	Met	Met	Arg	Gln	Gln	Ala	Leu	Met	
	50					55					60					
Ile	Ala	Met	Phe	Leu	Val	Ile	Tyr	Leu	Phe	Met	Phe	Ile	Gly	Val	Asp	
65					70					75					80	
Phe	Ser	His	Tyr	Pro	Gly	Leu	Phe	Ser	Phe	Asp	Val	Ala	Met	Phe	Phe	
				85					90					95		
Ile	Met	Ser	Thr	Leu	Thr	Ala	Phe	Ser	Ser	Leu	Tyr	Thr	Ile	Phe	Tyr	
			100					105					110			
Glu	Ser	Asn	Asp	Leu	Lys	Leu	Tyr	Ile	His	Leu	Pro	Val	Thr	Ser	Glu	
		115					120					125				
Glu	Leu	Tyr	Ile	Ala	Lys	Ile	Val	Ser	Ser	Leu	Gly	Met	Gly	Ala	Val	
	130					135					140					
Phe	Leu	Met	Pro	Leu	Ile	Ser	Leu	Leu	Leu	Ile	Ala	Tyr	Trp	Gln	Leu	
145					150					155					160	
Leu	Gly	Asn	Pro	Leu	Ser	Ile	Leu	Val	Ala	Ile	Val	Leu	Phe	Leu	Val	
				165					170					175		
Leu	Leu	Val	Ser	Ser	Met	Val	Leu	Ala	Ile	Tyr	Ile	Asn	Ala	Trp	Val	
			180					185					190			
Gly	Lys	Ile	Ile	Val	Arg	Ser	Arg	Lys	Arg	Lys	Leu	Ile	Ser	Thr	Ile	
		195					200					205				
Met	Met	Phe	Val	Ser	Thr	Phe	Gly	Ala	Phe	Val	Leu	Ile	Phe	Ala	Ile	
	210					215					220					
Asn	Ile	Ser	Asn	Asn	Lys	Arg	Thr	Met	Thr	Asp	Gly	Val	Phe	Thr	Asp	
225				230						235				240		
Tyr	Pro	Thr	Ile	Pro	Tyr	Phe	Lys	Gly	Phe	Tyr	Asp	Val	Val	Gln	Ala	
				245					250					255		
Pro	Phe	Ser	Thr	Ala	Ala	Leu	Leu	Asn	Phe	Trp	Leu	Pro	Leu	Leu	Leu	
			260					265					270			
Ile	Leu	Ala	Met	Val	Tyr	Gly	Ile	Val	Thr	Lys	Val	Met	Pro	Thr	Tyr	
		275					280					285				
Tyr	Arg	Glu	Ala	Phe	Tyr	Ile	Ser	Asn	Glu	Asn	Lys	Val	Lys	Gln	Thr	
	290					295					300					
Lys	Lys	Pro	Val	Asn	Arg	Pro	His	Gln	Asn	Gln	Ser	Leu	Ala	Gln	Leu	
305				310						315				320		
Leu	Arg	Lys	His	His	Leu	Leu	Thr	Leu	Gln	Asn	Ala	Thr	Leu	Leu	Thr	
				325					330					335		
Gln	Thr	Tyr	Leu	Met	Pro	Leu	Met	Tyr	Val	Met	Leu	Phe	Ile	Gly	Pro	
			340					345					350			
Ser	Leu	Ser	Arg	Gly	Thr	Gly	Phe	Phe	Lys	His	Ile	Ser	Pro	Asp	Tyr	
		355					360					365				
Phe	Gly	Val	Ala	Leu	Leu	Phe	Gly	Val	Ser	Leu	Gly	Val	Met	Cys	Ala	
	370					375					380					
Thr	Pro	Thr	Ser	Phe	Ile	Gly	Val	Gly	Ile	Ser	Leu	Glu	Lys	Asp	Asn	
385				390						395				400		
Phe	Thr	Phe	Ile	Lys	Ser	Leu	Pro	Ile	Thr	Leu	Lys	Lys	Phe	Leu	Met	
				405					410					415		
Asp	Lys	Phe	Cys	Leu	Leu	Val	Gly	Leu	Gln	Leu	Ile	Val	Pro	Met	Val	
			420					425					430			
Ile	Tyr	Leu	Val	Phe	Gly	Leu	Phe	Val	Leu	His	Leu	His	Pro	Leu	Leu	

aaaggaacag attctgggtcg tgttatgaaa caaagtgttg atgttggttaa gtccttgaaa 2220
 aaaataaaaa aaatgaccat tacttttagga gattaa 2256

<210> SEQ ID NO 244
 <211> LENGTH: 751
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 244

Met	Lys	Lys	Trp	Gln	Lys	Tyr	Val	Leu	Asp	Tyr	Val	Val	Arg	Asp	Arg
1				5					10					15	
Arg	Thr	Pro	Val	Glu	Asn	Arg	Val	Arg	Val	Gly	Gln	Asn	Met	Met	Leu
			20					25					30		
Leu	Thr	Ile	Phe	Ile	Phe	Phe	Ile	Phe	Ile	Ile	Asn	Phe	Met	Ile	Ile
			35				40					45			
Ile	Gly	Thr	Asp	Gln	Lys	Phe	Gly	Val	Ser	Leu	Ser	Glu	Gly	Ala	Lys
	50					55					60				
Lys	Val	Tyr	Gln	Glu	Thr	Val	Thr	Ile	Gln	Ala	Lys	Arg	Gly	Thr	Ile
65					70					75					80
Tyr	Asp	Arg	Asn	Gly	Thr	Ala	Ile	Ala	Val	Asp	Ser	Thr	Thr	Tyr	Ser
				85					90					95	
Ile	Tyr	Ala	Ile	Leu	Asp	Lys	Ser	Phe	Val	Ser	Ala	Ser	Asp	Glu	Lys
			100					105					110		
Leu	Tyr	Val	Gln	Pro	Ser	Gln	Tyr	Glu	Thr	Val	Ala	Asp	Ile	Leu	Lys
			115				120					125			
Lys	His	Leu	Gly	Met	Lys	Lys	Thr	Asp	Val	Ile	Lys	Gln	Leu	Lys	Arg
	130					135					140				
Lys	Gly	Leu	Phe	Gln	Val	Ser	Phe	Gly	Pro	Ser	Gly	Ser	Gly	Ile	Ser
145					150					155					160
Tyr	Ser	Thr	Met	Ser	Thr	Ile	Gln	Lys	Ala	Met	Glu	Asp	Ala	Lys	Ile
				165					170					175	
Lys	Gly	Ile	Ala	Phe	Thr	Thr	Ser	Pro	Gly	Arg	Met	Tyr	Pro	Asn	Gly
			180					185						190	
Thr	Phe	Ala	Ser	Glu	Phe	Ile	Gly	Leu	Ala	Ser	Leu	Thr	Glu	Asp	Lys
			195				200						205		
Lys	Thr	Gly	Val	Lys	Ser	Leu	Val	Gly	Lys	Thr	Gly	Leu	Glu	Ala	Ser
	210					215					220				
Phe	Asp	Lys	Ile	Leu	Ser	Gly	Gln	Asp	Gly	Val	Ile	Thr	Tyr	Gln	Lys
225					230					235					240
Asp	Arg	Asn	Gly	Thr	Thr	Leu	Leu	Gly	Thr	Gly	Lys	Thr	Val	Lys	Lys
				245					250					255	
Ala	Ile	Asp	Gly	Lys	Asp	Ile	Tyr	Thr	Thr	Leu	Ser	Glu	Pro	Ile	Gln
			260					265					270		
Thr	Phe	Leu	Glu	Thr	Gln	Met	Asp	Val	Phe	Gln	Ala	Lys	Ser	Asn	Gly
			275				280					285			
Gln	Leu	Ala	Ser	Ala	Thr	Leu	Val	Asn	Ala	Lys	Thr	Gly	Glu	Ile	Leu
	290					295					300				
Ala	Thr	Thr	Gln	Arg	Pro	Thr	Tyr	Asn	Ala	Asp	Thr	Leu	Lys	Gly	Leu
305					310					315					320
Glu	Asn	Thr	Asn	Tyr	Lys	Trp	Tyr	Ser	Ala	Leu	His	Gln	Gly	Asn	Phe
				325					330					335	
Glu	Pro	Gly	Ser	Thr	Met	Lys	Val	Met	Thr	Leu	Ala	Ala	Ala	Ile	Asp
			340					345					350		
Asp	Lys	Val	Phe	Asn	Pro	Asn	Glu	Thr	Phe	Ser	Asn	Ala	Asn	Gly	Leu
			355				360					365			
Thr	Ile	Ala	Asp	Ala	Thr	Ile	Gln	Asp	Trp	Ser	Ile	Asn	Glu	Gly	Ile
	370					375					380				
Ser	Thr	Gly	Gln	Tyr	Met	Asn	Tyr	Ala	Gln	Gly	Phe	Ala	Phe	Ser	Ser

385					390					395				400	
Asn	Val	Gly	Met	Thr	Lys	Leu	Glu	Gln	Lys	Met	Gly	Asn	Ala	Lys	Trp
				405					410					415	
Met	Asn	Tyr	Leu	Thr	Lys	Phe	Arg	Phe	Gly	Phe	Pro	Thr	Arg	Phe	Gly
			420					425					430		
Leu	Lys	Asp	Glu	Asp	Ala	Gly	Ile	Phe	Pro	Ser	Asp	Asn	Ile	Val	Thr
		435				440						445			
Gln	Ala	Met	Ser	Ala	Phe	Gly	Gln	Gly	Ile	Ser	Val	Thr	Gln	Ile	Gln
	450					455					460				
Met	Leu	Arg	Ala	Phe	Thr	Ala	Ile	Ser	Asn	Asn	Gly	Glu	Met	Leu	Glu
465					470					475				480	
Pro	Gln	Phe	Ile	Ser	Gln	Ile	Tyr	Asp	Pro	Asn	Thr	Ala	Ser	Phe	Arg
				485					490					495	
Thr	Ala	Asn	Lys	Glu	Ile	Val	Gly	Lys	Pro	Val	Ser	Lys	Lys	Ala	Ala
		500						505					510		
Ser	Glu	Thr	Arg	Gln	Tyr	Met	Ile	Gly	Val	Gly	Thr	Asp	Pro	Glu	Phe
	515					520						525			
Gly	Thr	Leu	Tyr	Ser	Lys	Thr	Phe	Gly	Pro	Ile	Ile	Lys	Val	Gly	Asp
	530					535					540				
Leu	Pro	Val	Ala	Val	Lys	Ser	Gly	Thr	Ala	Gln	Ile	Gly	Ser	Glu	Asp
545					550					555				560	
Gly	Ser	Gly	Tyr	Gln	Asp	Gly	Gly	Leu	Thr	Asn	Tyr	Val	Tyr	Ser	Val
				565				570						575	
Val	Ala	Met	Val	Pro	Ala	Asp	Lys	Pro	Asp	Phe	Leu	Met	Tyr	Val	Thr
		580						585					590		
Met	Thr	Lys	Pro	Gln	His	Phe	Gly	Pro	Leu	Phe	Trp	Gln	Asp	Val	Val
	595					600						605			
Asn	Pro	Val	Leu	Glu	Glu	Ala	Tyr	Leu	Met	Gln	Asp	Thr	Leu	Thr	Lys
	610					615					620				
Pro	Val	Val	Ser	Asp	Ala	Asn	Arg	Gln	Thr	Thr	Tyr	Lys	Leu	Pro	Asn
625					630					635				640	
Phe	Val	Gly	Lys	Asn	Pro	Gly	Glu	Thr	Ser	Ser	Glu	Leu	Arg	Arg	Asn
				645					650					655	
Leu	Val	Gln	Pro	Val	Val	Leu	Gly	Thr	Gly	Ser	Lys	Ile	Lys	Lys	Val
		660						665					670		
Ser	His	Gln	Pro	Gly	Gln	Thr	Leu	Thr	Glu	Asn	Gln	Gln	Val	Leu	Ile
	675						680					685			
Leu	Ser	Asp	Arg	Phe	Val	Glu	Val	Pro	Asp	Met	Tyr	Gly	Trp	Thr	Lys
	690					695					700				
Ser	Asn	Val	Lys	Thr	Phe	Ala	Lys	Trp	Thr	Gly	Ile	Asp	Ile	Ser	Phe
705					710					715				720	
Lys	Gly	Thr	Asp	Ser	Gly	Arg	Val	Met	Lys	Gln	Ser	Val	Asp	Val	Gly
				725					730					735	
Lys	Ser	Leu	Lys	Lys	Ile	Lys	Lys	Met	Thr	Ile	Thr	Leu	Gly	Asp	
		740						745					750		

<210> SEQ ID NO 245

<211> LENGTH: 855

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 245

ttgcagcaat	catatccttt	atggatatctg	ctttcacaat	gcccttatttt	tatcaaattc	60
tatcaattga	aaaaaattgg	tgggcaacaa	atgcatgaag	atgtcaagca	acatttagct	120
aaagctggaa	caccgactat	ggggggaact	gtttttcttt	tagtagctac	ggcagtatcg	180
ttattgggta	gtctattttc	gatcaaaaac	actcaaagtt	tagctttgat	ttcaggcatt	240
ttatcaattg	ttgtcattta	cgggattatc	ggatttttgg	atgatttttt	aaaaattttt	300
aagcaaatca	atgaaggatt	gacagccaaa	caaaagttag	ccttgcagtt	ggttggagga	360

ttgatgttct	atTTTTtaca	tgtagtcca	agtggcattt	cctctattaa	tgtgtttggt	420
tatcagctgc	cgctgggaat	tttctaccta	ttctttgttt	tgttttgggt	ggttggtttt	480
tcaaatgccg	ttaatttgac	agatgggtatc	gatggccttag	cttctatctc	agtgggtgatt	540
agtctagtga	cttacggcgt	tattgcctac	gttcagagtc	aatttgatgt	tttgttactg	600
attggagcaa	tgattggagc	cttgcttggc	ttcttctgct	ttaatcacia	acctgctaaa	660
gtatttatgg	gagatgtagg	tagtttagcc	cttggagcta	tgttggctgc	catttctatt	720
gcgcttcgtc	aagaatggac	tctcctgatt	attgggatcg	tttatgttct	tgaacaagt	780
tctgtgatgt	tgcaagtgtc	ctatttcaag	tacaccaaga	aaaaatatgg	agaagtcgtc	840
gtatttttag	aatga					855

<210> SEQ ID NO 246
 <211> LENGTH: 284
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 246

Met	Gln	Gln	Ser	Tyr	Pro	Leu	Trp	Tyr	Leu	Leu	Ser	Gln	Cys	Pro	Tyr
1				5					10					15	
Phe	Ile	Lys	Phe	Tyr	Gln	Leu	Lys	Lys	Ile	Gly	Gly	Gln	Gln	Met	His
			20					25					30		
Glu	Asp	Val	Lys	Gln	His	Leu	Ala	Lys	Ala	Gly	Thr	Pro	Thr	Met	Gly
		35					40					45			
Gly	Thr	Val	Phe	Leu	Leu	Val	Ala	Thr	Ala	Val	Ser	Leu	Leu	Val	Ser
	50					55					60				
Leu	Phe	Ser	Ile	Lys	Asn	Thr	Gln	Ser	Leu	Ala	Leu	Ile	Ser	Gly	Ile
65				70						75				80	
Leu	Ser	Ile	Val	Val	Ile	Tyr	Gly	Ile	Ile	Gly	Phe	Leu	Asp	Asp	Phe
			85						90				95		
Leu	Lys	Ile	Phe	Lys	Gln	Ile	Asn	Glu	Gly	Leu	Thr	Ala	Lys	Gln	Lys
			100					105					110		
Leu	Ala	Leu	Gln	Leu	Val	Gly	Gly	Leu	Met	Phe	Tyr	Phe	Leu	His	Val
		115				120					125				
Ser	Pro	Ser	Gly	Ile	Ser	Ser	Ile	Asn	Val	Phe	Gly	Tyr	Gln	Leu	Pro
	130					135					140				
Leu	Gly	Ile	Phe	Tyr	Leu	Phe	Phe	Val	Leu	Phe	Trp	Val	Val	Gly	Phe
145				150						155				160	
Ser	Asn	Ala	Val	Asn	Leu	Thr	Asp	Gly	Ile	Asp	Gly	Leu	Ala	Ser	Ile
			165					170					175		
Ser	Val	Val	Ile	Ser	Leu	Val	Thr	Tyr	Gly	Val	Ile	Ala	Tyr	Val	Gln
			180					185					190		
Ser	Gln	Phe	Asp	Val	Leu	Leu	Leu	Ile	Gly	Ala	Met	Ile	Gly	Ala	Leu
		195					200					205			
Leu	Gly	Phe	Phe	Cys	Phe	Asn	His	Lys	Pro	Ala	Lys	Val	Phe	Met	Gly
	210					215					220				
Asp	Val	Gly	Ser	Leu	Ala	Leu	Gly	Ala	Met	Leu	Ala	Ala	Ile	Ser	Ile
225					230					235				240	
Ala	Leu	Arg	Gln	Glu	Trp	Thr	Leu	Leu	Ile	Ile	Gly	Ile	Val	Tyr	Val
			245						250					255	
Leu	Glu	Thr	Ser	Ser	Val	Met	Leu	Gln	Val	Ser	Tyr	Phe	Lys	Tyr	Thr
			260					265					270		
Lys	Lys	Lys	Tyr	Gly	Glu	Val	Val	Phe	Leu	Glu					
		275					280								

<210> SEQ ID NO 247
 <211> LENGTH: 894
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 247

ttgcttattg	ctataatacg	aatttactat	tttacatgtg	ggctctaagag	tgttagaata	60
ttaagacaaa	caaatacaaa	ggggaaatac	atgacatcag	tgtttttaac	cagtgggttg	120
gctttttatg	attacctcat	ctcaccgatt	ccacatggga	aacttttttag	ttggcatgct	180
gtttttgatg	ccattccaaa	tattatccaa	cggcttccaa	ttacgcttgg	tttgacacta	240
tcaggagcaa	cctttggctt	ggttttggct	ttgatttttg	cccttggtcaa	aattaataaa	300
gtgaagctac	tataccctat	tcaagctatt	tttgtgagtt	tcttgcgagg	aactcctatt	360
ttggtacagt	tgatgttgac	ctactacggt	attcccctct	ttctaaaatt	tctcaatcag	420
aagtatggct	ttgattggaa	tgtaaatgca	attccggcct	ctattttttgc	cattacagcc	480
tttgctttta	atgaagcagc	ctacgctagt	gaaactattc	gggcagccat	tttatcagta	540
gatacagggtg	aaattgaagc	agcaaaaagt	ctaggcatga	cttctgtgca	ggtttaccgt	600
cgtgtcatta	ttcctaatac	aactgttggt	gctattccaa	ccttgattaa	tgggttaatt	660
ggcttaacta	aaggaacatc	gcttgccctt	aatgcaggga	ttgtcgaaat	gtttgccag	720
gctcaaattc	taggcggatc	agattaccgt	tattttgaac	gttatatctc	tgttgctctt	780
gtctattggg	ctatcagtat	tttgatggag	caagtaggtc	gcttgattga	aaacaagatg	840
gccatcaaag	caccagaaca	agctagaaat	gaaaagttag	gagaattgcy	ttga	894

<210> SEQ ID NO 248

<211> LENGTH: 297

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 248

Met	Leu	Ile	Ala	Ile	Ile	Arg	Ile	Tyr	Tyr	Phe	Thr	Cys	Gly	Ser	Lys
1				5					10					15	
Ser	Val	Arg	Ile	Leu	Arg	Gln	Thr	Asn	Thr	Lys	Gly	Lys	Tyr	Met	Thr
			20					25					30		
Ser	Val	Phe	Leu	Thr	Ser	Gly	Trp	Ala	Phe	Tyr	Asp	Tyr	Leu	Ile	Ser
		35				40					45				
Pro	Ile	Pro	His	Gly	Lys	Leu	Phe	Ser	Trp	His	Ala	Val	Phe	Asp	Ala
	50				55					60					
Ile	Pro	Asn	Ile	Ile	Gln	Arg	Leu	Pro	Ile	Thr	Leu	Gly	Leu	Thr	Leu
65				70					75				80		
Ser	Gly	Ala	Thr	Phe	Gly	Leu	Val	Leu	Ala	Leu	Ile	Phe	Ala	Leu	Val
			85					90					95		
Lys	Ile	Asn	Lys	Val	Lys	Leu	Leu	Tyr	Pro	Ile	Gln	Ala	Ile	Phe	Val
		100						105					110		
Ser	Phe	Leu	Arg	Gly	Thr	Pro	Ile	Leu	Val	Gln	Leu	Met	Leu	Thr	Tyr
	115					120					125				
Tyr	Gly	Ile	Pro	Leu	Phe	Leu	Lys	Phe	Leu	Asn	Gln	Lys	Tyr	Gly	Phe
	130				135					140					
Asp	Trp	Asn	Val	Asn	Ala	Ile	Pro	Ala	Ser	Ile	Phe	Ala	Ile	Thr	Ala
145				150					155				160		
Phe	Ala	Phe	Asn	Glu	Ala	Ala	Tyr	Ala	Ser	Glu	Thr	Ile	Arg	Ala	Ala
			165					170					175		
Ile	Leu	Ser	Val	Asp	Thr	Gly	Glu	Ile	Glu	Ala	Ala	Lys	Ser	Leu	Gly
		180				185						190			
Met	Thr	Ser	Val	Gln	Val	Tyr	Arg	Arg	Val	Ile	Ile	Pro	Asn	Ala	Thr
	195				200							205			
Val	Val	Ala	Ile	Pro	Thr	Leu	Ile	Asn	Gly	Leu	Ile	Gly	Leu	Thr	Lys
	210				215					220					
Gly	Thr	Ser	Leu	Ala	Phe	Asn	Ala	Gly	Ile	Val	Glu	Met	Phe	Ala	Gln
225			230						235				240		
Ala	Gln	Ile	Leu	Gly	Gly	Ser	Asp	Tyr	Arg	Tyr	Phe	Glu	Arg	Tyr	Ile
			245					250					255		
Ser	Val	Ala	Leu	Val	Tyr	Trp	Ser	Ile	Ser	Ile	Leu	Met	Glu	Gln	Val
		260				265						270			
Gly	Arg	Leu	Ile	Glu	Asn	Lys	Met	Ala	Ile	Lys	Ala	Pro	Glu	Gln	Ala
	275					280						285			

Arg Asn Glu Lys Leu Gly Glu Leu Arg
290 295

<210> SEQ ID NO 249

<211> LENGTH: 1392

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 249

```

atggagttta gaatgtctat aaaagaacaa acagacaata acgaactaga aaatggaatg      60
gtaaggggct tagaaaatcg tcatgtgcag ttaattgcga tcgcaggaac gattggaaca      120
ggctctcttt taggggcagg acgctctatt gccctaacag gaccatctat tatttttgtg      180
tatatgatta caggtgcctt catgtttatg atgatgcgtg ccatcggtga aatgctctat      240
tatgatccag atcaacacac ctttatcaat tttatttcca aatacattgg tccaggctgg      300
ggttattttt cgggtctatc ctattggatt tcccttattt ttattggaat ggcagaaatc      360
acagcagtag gtgcttatgt gcaattttgg ttcccaagct ggccagcctg gttgattcag      420
ttggttttct tagtcttact tagttcgatc aacttaattg ctgtgcgcgt ttttggggaa      480
acagagtttt ggtttgccat gattaagatt ttagctattt tagctttgat tgcaacagct      540
attttcatgg tattgacagg ttttgaaact cacacaggcc atgctagcct ttccaatatt      600
tttgaccatt tttccatgtt cccaaatggg aaactaaagt tctttatggc cttccaaatg      660
gttttctttg cttatcaagc tatcgaattt gtgggaatta ccacttctga gacggctaac      720
ccaagaaaag ttctaccaa ggctattcaa gaaattccaa cccgtattgt gatcttttat      780
gtgggagcct tggctctctat tatggcaatt gtgccatggc atcagttacc agttgatgaa      840
tctccttttg tgatgggtgtt caaattgatt ggtattaaat gggcagcagc cttgattaac      900
tttgtggtct tgacatcagc agcgtcagcg cttaactcaa ccctttattc aaccggtcgt      960
catctctatc agattgctaa tgagactcca aacgctttga ccaatcgctt aaagattaat     1020
actttatctc gacaaggggt gccaaagtcgt gccattattg cttcagcggg tgtggttggg     1080
atctcagctt tgattaatat cctaccagga gttgcagatg cgttctcact cattacggcc     1140
tcctcatcag gtgtatatat tgctatctac gccttaacca tgattgctca ctggaagtac     1200
cgtcaatcta aggactttat ggcagatggg tattttgatgc caaaatataa agtgacaacg     1260
cctttgacct ttgctttctt tgccctttgtc tttatctctc ttttcttaca agaatccacc     1320
tatatcggcg ccattggagc aacgatttgg attattattt ttgggattta tagcaatgtc     1380
aaatttaaat aa                                     1392

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<210> SEQ ID NO 250

<211> LENGTH: 463

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 250

```

Met Glu Phe Arg Met Ser Ile Lys Glu Gln Thr Asp Asn Asn Glu Leu
1      5      10      15
Glu Asn Gly Met Val Arg Gly Leu Glu Asn Arg His Val Gln Leu Ile
20      25      30
Ala Ile Ala Gly Thr Ile Gly Thr Gly Leu Phe Leu Gly Ala Gly Arg
35      40      45
Ser Ile Ala Leu Thr Gly Pro Ser Ile Ile Phe Val Tyr Met Ile Thr
50      55      60
Gly Ala Phe Met Phe Met Met Met Arg Ala Ile Gly Glu Met Leu Tyr
65      70      75      80
Tyr Asp Pro Asp Gln His Thr Phe Ile Asn Phe Ile Ser Lys Tyr Ile
85      90      95
Gly Pro Gly Trp Gly Tyr Phe Ser Gly Leu Ser Tyr Trp Ile Ser Leu
100     105     110
Ile Phe Ile Gly Met Ala Glu Ile Thr Ala Val Gly Ala Tyr Val Gln
115     120     125
Phe Trp Phe Pro Ser Trp Pro Ala Trp Leu Ile Gln Leu Val Phe Leu
130     135     140
Val Leu Leu Ser Ser Ile Asn Leu Ile Ala Val Arg Val Phe Gly Glu

```

145					150					155				160	
Thr	Glu	Phe	Trp	Phe	Ala	Met	Ile	Lys	Ile	Leu	Ala	Ile	Leu	Ala	Leu
				165					170					175	
Ile	Ala	Thr	Ala	Ile	Phe	Met	Val	Leu	Thr	Gly	Phe	Glu	Thr	His	Thr
			180					185					190		
Gly	His	Ala	Ser	Leu	Ser	Asn	Ile	Phe	Asp	His	Phe	Ser	Met	Phe	Pro
	195						200					205			
Asn	Gly	Lys	Leu	Lys	Phe	Phe	Met	Ala	Phe	Gln	Met	Val	Phe	Phe	Ala
	210					215					220				
Tyr	Gln	Ala	Ile	Glu	Phe	Val	Gly	Ile	Thr	Thr	Ser	Glu	Thr	Ala	Asn
225					230					235					240
Pro	Arg	Lys	Val	Leu	Pro	Lys	Ala	Ile	Gln	Glu	Ile	Pro	Thr	Arg	Ile
			245						250					255	
Val	Ile	Phe	Tyr	Val	Gly	Ala	Leu	Val	Ser	Ile	Met	Ala	Ile	Val	Pro
	260							265					270		
Trp	His	Gln	Leu	Pro	Val	Asp	Glu	Ser	Pro	Phe	Val	Met	Val	Phe	Lys
	275						280					285			
Leu	Ile	Gly	Ile	Lys	Trp	Ala	Ala	Ala	Leu	Ile	Asn	Phe	Val	Val	Leu
	290					295					300				
Thr	Ser	Ala	Ala	Ser	Ala	Leu	Asn	Ser	Thr	Leu	Tyr	Ser	Thr	Gly	Arg
305					310					315					320
His	Leu	Tyr	Gln	Ile	Ala	Asn	Glu	Thr	Pro	Asn	Ala	Leu	Thr	Asn	Arg
			325						330					335	
Leu	Lys	Ile	Asn	Thr	Leu	Ser	Arg	Gln	Gly	Val	Pro	Ser	Arg	Ala	Ile
			340					345					350		
Ile	Ala	Ser	Ala	Val	Val	Val	Gly	Ile	Ser	Ala	Leu	Ile	Asn	Ile	Leu
	355						360					365			
Pro	Gly	Val	Ala	Asp	Ala	Phe	Ser	Leu	Ile	Thr	Ala	Ser	Ser	Ser	Gly
	370					375					380				
Val	Tyr	Ile	Ala	Ile	Tyr	Ala	Leu	Thr	Met	Ile	Ala	His	Trp	Lys	Tyr
385					390					395					400
Arg	Gln	Ser	Lys	Asp	Phe	Met	Ala	Asp	Gly	Tyr	Leu	Met	Pro	Lys	Tyr
			405						410					415	
Lys	Val	Thr	Thr	Pro	Leu	Thr	Leu	Ala	Phe	Phe	Ala	Phe	Val	Phe	Ile
			420					425					430		
Ser	Leu	Phe	Leu	Gln	Glu	Ser	Thr	Tyr	Ile	Gly	Ala	Ile	Gly	Ala	Thr
	435						440					445			
Ile	Trp	Ile	Ile	Ile	Phe	Gly	Ile	Tyr	Ser	Asn	Val	Lys	Phe	Lys	
	450					455					460				

<210> SEQ ID NO 251

<211> LENGTH: 573

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 251

ttgatctggt	ttcttagcct	tttctcctcc	acaagtagcc	actttctcac	tatttgtggt	60
atgataaagt	gtaaaacaaa	ggagattgaa	atgacaaaag	aagttatcgt	cgaaagtgtt	120
gagctagatc	atactattgt	aaaggcccct	tatgttcgtc	ttattttctga	agaatttgga	180
cccaagggcg	atcgtattac	aaattttgat	gttcgcctag	tgcagcctaa	ccaaaattct	240
attgaaacag	ccggtttgca	taccattgaa	cacttacttg	ccaagctcat	ccgccaacgc	300
attgatggga	tgattgattg	ctctcctttt	ggctgtcgaa	caggttttca	ccttatcatg	360
tggggaaaac	acagttctac	tgatattgcc	aaggtgatta	aatccagcct	agaagaaatt	420
gcaactggga	ttacttggga	agatgttcct	ggaacaactc	ttgaatcctg	tgggaactat	480
aaggatcata	gcctctttgc	cgccaaagaa	tgggctcaat	tgattattga	tcaagggtatt	540
tcagacgata	cttttagtcg	ccatgtcatc	tga			573

<210> SEQ ID NO 252

<211> LENGTH: 190

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 252

```
Met Ile Cys Phe Leu Ser Leu Phe Ser Ser Thr Ser Ser His Phe Leu
1           5           10           15
Thr Ile Cys Val Met Ile Lys Cys Lys Thr Lys Glu Ile Glu Met Thr
          20          25          30
Lys Glu Val Ile Val Glu Ser Phe Glu Leu Asp His Thr Ile Val Lys
          35          40          45
Ala Pro Tyr Val Arg Leu Ile Ser Glu Glu Phe Gly Pro Lys Gly Asp
          50          55          60
Arg Ile Thr Asn Phe Asp Val Arg Leu Val Gln Pro Asn Gln Asn Ser
65          70          75          80
Ile Glu Thr Ala Gly Leu His Thr Ile Glu His Leu Leu Ala Lys Leu
          85          90          95
Ile Arg Gln Arg Ile Asp Gly Met Ile Asp Cys Ser Pro Phe Gly Cys
          100         105         110
Arg Thr Gly Phe His Leu Ile Met Trp Gly Lys His Ser Ser Thr Asp
          115         120         125
Ile Ala Lys Val Ile Lys Ser Ser Leu Glu Glu Ile Ala Thr Gly Ile
          130         135         140
Thr Trp Glu Asp Val Pro Gly Thr Thr Leu Glu Ser Cys Gly Asn Tyr
145         150         155         160
Lys Asp His Ser Leu Phe Ala Ala Lys Glu Trp Ala Gln Leu Ile Ile
          165         170         175
Asp Gln Gly Ile Ser Asp Asp Pro Phe Ser Arg His Val Ile
          180         185         190
```

<210> SEQ ID NO 253

<211> LENGTH: 1608

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 253

```
atgggttaata ttatttttatt aattgttttct gccctcattg gtttaatatatt aggttatgca      60
cttattttcga ttagactcaa gtctgcgaag gaagctgcag agttgactct tttaaacgct    120
gaacaagaag ctggtgatat tcgtggcaaa gcagaagtag atgctgaaca catcaaaaaa    180
acagctaaac gtgaaagtaa agcaaatcgt aaagaattac ttttagaagc aaaagaagag    240
gcaagaaaat atcgtgaaga gattgaacaa gaatttaagt ctgaaagaca agagcttaaa    300
caactcgaga cacgcttagc ggagcgctcc ttaactcttg accgtaaaga tgaaaaccta    360
tcaagtaaag aaaaggtact agatagtaaa gaacaaagtc tgaccgataa atctaaacac    420
attgatgagc ggcaacttca agtggaaaaa cttgaagagg agaaaaaagc agaactggaa    480
aaagttgctg cgatgacgat tgcagaagcg cgtgaagtga ttttaatgga gacggaaaaa    540
aaactgaccc atgaaattgc gacgcgcatt cgagatgccg aacgtgacat caaggaccga    600
acagttaaaa cagccaagga cttgttagcg caagccatgc aacgccttgc tggtagtat    660
gtgactgaac aaactattac cagtgtccat ctcccagacg acaacatgaa gggccgaatt    720
attggacgtg aaggccgtaa tattcgctact ttagagagct tgactggcat tgacgttatt    780
attgacgata ctcttgaagt tgttatctta tcaggatttg atcctattcg acgtgaaatt    840
gctcgtatga ccttggaatc tctgattgct gatggctcga tccatccagc tcgtatcgag    900
gaattggttg agaaaaatcg tcttgaaatg gataatcgta ttcgtgagta cgggtgaagct    960
gcagcctatg agattggtgc accaaacctt catcctgatt tgattaaaaat catgggacgc   1020
ctgcaattcc gtacctcgtt tgggtcaaaat gtcctacgtc actctgttga gggttgtaag   1080
ttagctggta ttttagctgg tgagttagggt gaaaatgttg ctcttgcccc cgtgtctggg   1140
ttcttgcatg atatgggtaa agctattgac cgtgaggttg aaggcagtca cgttgagatt   1200
ggaaatggaat ttgcacgtaa atacaaagaa catccagttg ttgtcaacac tattgttagc   1260
caccacggag atgtggagcc agattctgtg atcgctgtgc tagtagctgc agcagacgct   1320
ctcagttcgg ctcgtccagg cgctcgtaat gagtcaatgg agaattacat caagcgtctt   1380
```

cgtgatttag	aagaaatcgc	gacaagtttt	gatgggggtac	aaaatagttt	tgctctacaa	1440
gctggacgtg	agattcgtat	tatgggttcaa	cctgaaaaaa	tttcagatga	tcagggttgtc	1500
atattgtcgc	ataaagtaag	agaaaaaatt	gaaaacaatc	tagattaccc	aggaaatatt	1560
aaagtaactg	ttattcgtga	gatgagagcg	gttgattatg	ccaagtag		1608

<210> SEQ ID NO 254

<211> LENGTH: 535

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 254

Met	Val	Asn	Ile	Ile	Leu	Leu	Ile	Val	Ser	Ala	Leu	Ile	Gly	Leu	Ile
1			5						10				15		
Leu	Gly	Tyr	Ala	Leu	Ile	Ser	Ile	Arg	Leu	Lys	Ser	Ala	Lys	Glu	Ala
		20						25					30		
Ala	Glu	Leu	Thr	Leu	Leu	Asn	Ala	Glu	Gln	Glu	Ala	Val	Asp	Ile	Arg
		35					40					45			
Gly	Lys	Ala	Glu	Val	Asp	Ala	Glu	His	Ile	Lys	Lys	Thr	Ala	Lys	Arg
	50					55					60				
Glu	Ser	Lys	Ala	Asn	Arg	Lys	Glu	Leu	Leu	Leu	Glu	Ala	Lys	Glu	Glu
65					70					75					80
Ala	Arg	Lys	Tyr	Arg	Glu	Glu	Ile	Glu	Gln	Glu	Phe	Lys	Ser	Glu	Arg
			85						90					95	
Gln	Glu	Leu	Lys	Gln	Leu	Glu	Thr	Arg	Leu	Ala	Glu	Arg	Ser	Leu	Thr
		100						105					110		
Leu	Asp	Arg	Lys	Asp	Glu	Asn	Leu	Ser	Ser	Lys	Glu	Lys	Val	Leu	Asp
	115						120					125			
Ser	Lys	Glu	Gln	Ser	Leu	Thr	Asp	Lys	Ser	Lys	His	Ile	Asp	Glu	Arg
	130					135					140				
Gln	Leu	Gln	Val	Glu	Lys	Leu	Glu	Glu	Glu	Lys	Lys	Ala	Glu	Leu	Glu
145					150					155					160
Lys	Val	Ala	Ala	Met	Thr	Ile	Ala	Glu	Ala	Arg	Glu	Val	Ile	Leu	Met
			165						170					175	
Glu	Thr	Glu	Asn	Lys	Leu	Thr	His	Glu	Ile	Ala	Thr	Arg	Ile	Arg	Asp
		180						185					190		
Ala	Glu	Arg	Asp	Ile	Lys	Asp	Arg	Thr	Val	Lys	Thr	Ala	Lys	Asp	Leu
	195						200					205			
Leu	Ala	Gln	Ala	Met	Gln	Arg	Leu	Ala	Gly	Glu	Tyr	Val	Thr	Glu	Gln
	210					215					220				
Thr	Ile	Thr	Ser	Val	His	Leu	Pro	Asp	Asp	Asn	Met	Lys	Gly	Arg	Ile
225					230					235					240
Ile	Gly	Arg	Glu	Gly	Arg	Asn	Ile	Arg	Thr	Leu	Glu	Ser	Leu	Thr	Gly
			245						250					255	
Ile	Asp	Val	Ile	Ile	Asp	Asp	Thr	Pro	Glu	Val	Val	Ile	Leu	Ser	Gly
		260						265					270		
Phe	Asp	Pro	Ile	Arg	Arg	Glu	Ile	Ala	Arg	Met	Thr	Leu	Glu	Ser	Leu
	275						280					285			
Ile	Ala	Asp	Gly	Arg	Ile	His	Pro	Ala	Arg	Ile	Glu	Glu	Leu	Val	Glu
	290					295					300				
Lys	Asn	Arg	Leu	Glu	Met	Asp	Asn	Arg	Ile	Arg	Glu	Tyr	Gly	Glu	Ala
305					310					315					320
Ala	Ala	Tyr	Glu	Ile	Gly	Ala	Pro	Asn	Leu	His	Pro	Asp	Leu	Ile	Lys
			325						330					335	
Ile	Met	Gly	Arg	Leu	Gln	Phe	Arg	Thr	Ser	Phe	Gly	Gln	Asn	Val	Leu
		340						345					350		
Arg	His	Ser	Val	Glu	Val	Gly	Lys	Leu	Ala	Gly	Ile	Leu	Ala	Gly	Glu
	355						360					365			
Leu	Gly	Glu	Asn	Val	Ala	Leu	Ala	Arg	Arg	Ala	Gly	Phe	Leu	His	Asp

370		375		380
Met Gly Lys Ala Ile Asp Arg Glu Val Glu Gly Ser His Val Glu Ile				
385		390		400
Gly Met Glu Phe Ala Arg Lys Tyr Lys Glu His Pro Val Val Val Asn				
	405		410	415
Thr Ile Ala Ser His His Gly Asp Val Glu Pro Asp Ser Val Ile Ala				
	420		425	430
Val Leu Val Ala Ala Ala Asp Ala Leu Ser Ser Ala Arg Pro Gly Ala				
	435		440	445
Arg Asn Glu Ser Met Glu Asn Tyr Ile Lys Arg Leu Arg Asp Leu Glu				
	450		455	460
Glu Ile Ala Thr Ser Phe Asp Gly Val Gln Asn Ser Phe Ala Leu Gln				
465		470		475
Ala Gly Arg Glu Ile Arg Ile Met Val Gln Pro Glu Lys Ile Ser Asp				
	485		490	495
Asp Gln Val Val Ile Leu Ser His Lys Val Arg Glu Lys Ile Glu Asn				
	500		505	510
Asn Leu Asp Tyr Pro Gly Asn Ile Lys Val Thr Val Ile Arg Glu Met				
	515		520	525
Arg Ala Val Asp Tyr Ala Lys				
530		535		

<210> SEQ ID NO 255

<211> LENGTH: 687

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 255

atgcaatttt	ccaggaattc	tgataaaata	caaagaaata	aggggaaact	aatgaaaaaa	60
tttcaattct	ttttacttat	cgagtgtata	ctgctagcta	tgggtatcat	gacaatcttg	120
gataatgatt	tatcaagttt	tatcctaatt	ctagttctta	tcttattagc	attacgcttt	180
tataaccaag	atagccgcaa	taatttttta	ctaactgtca	gtttattggt	tcttttttta	240
attttcattg	ttaatcccta	cattatcatg	gctgttcttt	tggggatagt	ttacattttc	300
attaaccatt	ttcacaaagt	caaaaagaag	aatcgctttg	ccttgattcg	tttcaaggaa	360
gaaaagattg	aagtgaacaa	taccaagcat	caatggattg	gtactgctaa	ttatgaaagt	420
gattattatt	gttttgatga	cattaacatc	attcgaatct	caggaaatga	cacggttgac	480
ttaaccaatg	ttattgtgac	aggaatggat	aatatcattg	tgatacgtaa	aatttttggg	540
aatacgacta	tattgggtacc	tattgatgtc	actgttactt	tagatgttag	ttccatatac	600
ggaagcgttg	attttttttag	atgtcagcaa	tatgatttgc	gcaacgaatc	tattaagttg	660
aaagaaacgg	ataaccaatc	ccttttaa				687

<210> SEQ ID NO 256

<211> LENGTH: 228

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 256

Met Gln Phe Ser Arg Asn Ser Asp Lys Ile Gln Arg Asn Lys Gly Lys	
1	15
Leu Met Lys Lys Phe Gln Phe Phe Leu Leu Ile Glu Cys Ile Leu Leu	
	30
Ala Met Gly Ile Met Thr Ile Leu Asp Asn Asp Leu Ser Ser Phe Ile	
	45
Leu Ile Leu Val Leu Ile Leu Leu Ala Leu Arg Phe Tyr Asn Gln Asp	
	60
Ser Arg Asn Asn Phe Leu Leu Thr Val Ser Leu Leu Phe Leu Phe Leu	
65	80
Ile Phe Met Leu Asn Pro Tyr Ile Ile Met Ala Val Leu Leu Gly Ile	
	95

Val	Tyr	Ile	Phe	Ile	Asn	His	Phe	Ser	Gln	Val	Lys	Lys	Lys	Asn	Arg
			100					105					110		
Phe	Ala	Leu	Ile	Arg	Phe	Lys	Glu	Glu	Lys	Ile	Glu	Val	Asn	Asn	Thr
		115					120					125			
Lys	His	Gln	Trp	Ile	Gly	Thr	Ala	Asn	Tyr	Glu	Ser	Asp	Tyr	Tyr	Cys
	130					135					140				
Phe	Asp	Asp	Ile	Asn	Ile	Ile	Arg	Ile	Ser	Gly	Asn	Asp	Thr	Val	Asp
145					150					155				160	
Leu	Thr	Asn	Val	Ile	Val	Thr	Gly	Met	Asp	Asn	Ile	Ile	Val	Ile	Arg
			165					170						175	
Lys	Ile	Phe	Gly	Asn	Thr	Thr	Ile	Leu	Val	Pro	Ile	Asp	Val	Thr	Val
		180					185						190		
Thr	Leu	Asp	Val	Ser	Ser	Ile	Tyr	Gly	Ser	Val	Asp	Phe	Phe	Arg	Cys
	195						200				205				
Gln	Gln	Tyr	Asp	Leu	Arg	Asn	Glu	Ser	Ile	Lys	Leu	Lys	Glu	Thr	Asp
	210					215					220				
Asn	Gln	Ser	Leu												
225															

<210> SEQ ID NO 257
 <211> LENGTH: 1005
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 257

atgaaaaaac	gttactatgc	tcttgtttgg	ctctactcaa	ccattaccat	tttatctatt	60
gtttttgtgg	tcatggataa	tttaggaatc	acttttaact	accttcgcaa	tcatttatgg	120
caggtcgaac	gtctagggtt	ttcgatttta	ttggttgattg	tttctgtgac	tttattattg	180
ttgttattgt	ggattattat	ggatgataac	agtaagcgta	acatcaacca	aaatctaaaa	240
tatattctca	ataatcgacg	actctatcta	gatgagacat	cagaaatcaa	tactaattta	300
agtcgacttt	ctaaaaaaat	gtctcacctg	actgctaaca	tgcaaaaagaa	agaaagtgct	360
tatattcttg	atagccaaga	agttgtaaaa	caagagcgca	aacgaattgc	aagagattta	420
catgacacag	tcagtcaaga	gctattcgct	tcgtcattga	ttttatcagg	aatttcgatg	480
agtttggaac	aactggacaa	aacacaatta	caaacacagt	taacaacggt	tgaagcaatg	540
ttgcaaaatg	ctcaaaaatga	tctacgcatt	ctccttttgc	atcttagacc	taccgagcta	600
gctaatacga	ctttatctga	gggccttcat	atgattctta	aggaattaac	agataaaaagt	660
gatattgaag	tcattttataa	ggaaaccatt	gctcagcttc	ctaaaaacaat	ggaagataat	720
cttttttagaa	ttgccaaga	attcattagc	aacacgttaa	aacatgctaa	agctagtcga	780
attgaagttt	atctcaatca	aacctcaaca	gaattacaat	tgaagatgat	tgatgatggt	840
gtaggatttg	atatggatca	ggtaagggat	ttgagttatg	gtctgaagaa	tattgaagac	900
cgtgtcaatg	athtagcagg	aaacctacat	ttaattagtc	aaaaaggcaa	aggagtttcc	960
atggatatta	gactgccgat	agtgaaggga	gatgacgatg	agtaa		1005

<210> SEQ ID NO 258
 <211> LENGTH: 334
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 258

Met	Lys	Lys	Arg	Tyr	Tyr	Ala	Leu	Val	Trp	Leu	Tyr	Ser	Thr	Ile	Thr
1			5					10					15		
Ile	Leu	Ser	Ile	Val	Phe	Val	Val	Met	Asp	Asn	Leu	Gly	Ile	Thr	Phe
		20						25				30			
Asn	Tyr	Leu	Arg	Asn	His	Leu	Trp	Gln	Val	Glu	Arg	Leu	Gly	Phe	Ser
	35					40					45				
Ile	Leu	Leu	Leu	Ile	Val	Ser	Val	Thr	Leu	Leu	Leu	Leu	Leu	Leu	Trp
	50					55				60					
Ile	Ile	Met	Asp	Asp	Asn	Ser	Lys	Arg	Asn	Ile	Asn	Gln	Asn	Leu	Lys
65					70				75					80	

Met	Ile	Phe	Ala	Pro	Tyr	Ile	Gln	Gly	Leu	His	His	Leu	Thr	Ile	Gln
65					70					75					80
Asn	Phe	Cys	Leu	Leu	Trp	Ile	Lys	Leu	Val	Lys	Ser	Ser	Arg		
				85					90						

<210> SEQ ID NO 261

<211> LENGTH: 1356

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 261

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atggttagaag attttcttca atttttagga tttatatattt tagatattat tgaaattatg      60
ttaacggttaa agcttttttag ctttgtaagt gcaattccgc ttcgcctgaa aaatatatttt      120
tatttatcac ttagtatggg tttgtttcaa gtagtttttt gggctttctt tccagaccat      180
ttcattcttg atgttgtgat gttggctcag tttcttttct ttgcgcttat agccctatac      240
tatggtaaat caataaaagc taagttttta atgttttatg ccttttttcc actagtgtct      300
attagtttgg ttaagcgatt tattgtattt tttgttatgc cattgtttgg tatgccttat      360
tcagttgtta aacataatac actactgatt tacagcatta cttgttttag tatttttttg      420
atztatcgct gcattcaagt ttttcatttc gatttttcaa cctggcgcca atattttcaa      480
tcacatagag ctagtaaaact attagtgttt actaactctt cgatggctct atattacttg      540
tgtgtccaag ggatagatgt gatgtcgctt tctttatcag gacttgctac aacgactgct      600
cgttcaatca tagtgctctt ttatttcatt ttgtttctta ctttattaat tcatttagag      660
cgttatgtaa aacaaaactc tattgaggca attgtgcaac aaaaagaata tcgtgagctg      720
attaattata gtcagcacct tggattgctg tatcaagata ttcaagagct taggcggcta      780
ttaactaccg tgtctagtcg tcttaagatt ggaatcgaac aaaatgatat ctctattgtg      840
agacttactt atgaagggtat cttgaatgct gaaaagaata atgctaaaga tgacagactt      900
gatttaactt gtttagataa attacaagtt gaagcaatca gacatattgt ttagctaaa      960
ttaattgagg caaaaaataa gaagcttaag gttgaggtat cgatccctaa ttgtattgca     1020
acgttttttc tagaagtagt agatttcact aagctattgt catttttgtt agataatgct     1080
atagaaatga gtttgagac aaagcaacct tgcttatcaa tagcatttct ggatcaaac      1140
cataaacttg tcatagtcac tcaaagcagt actaaacaag gacaagatga tagtcaaagc     1200
gtgtttgcta taccggcttt gaaaaaaga gatgactggc aatttgactt aaggaatgtc     1260
acgaccattt taaatcgtta tgactatctc acaattagct cgcagattca tgatggcatt     1320
ttaaccacgt taatagaaat agctaagcct gactga                                1356

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<210> SEQ ID NO 262

<211> LENGTH: 451

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 262

Met	Leu	Glu	Asp	Phe	Leu	Gln	Phe	Leu	Gly	Phe	Ile	Phe	Leu	Asp	Ile
1				5					10					15	
Ile	Glu	Ile	Met	Leu	Thr	Leu	Lys	Leu	Phe	Ser	Phe	Val	Ser	Ala	Ile
			20					25					30		
Pro	Leu	Arg	Leu	Lys	Asn	Ile	Phe	Tyr	Leu	Ser	Leu	Ser	Met	Val	Leu
		35				40					45				
Phe	Gln	Val	Val	Phe	Trp	Ala	Phe	Phe	Pro	Asp	His	Phe	Ile	Leu	Asp
	50				55				60						
Val	Val	Met	Leu	Ala	Gln	Phe	Leu	Phe	Phe	Ala	Leu	Ile	Ala	Leu	Tyr
65				70					75					80	
Tyr	Gly	Lys	Ser	Ile	Lys	Ala	Lys	Phe	Leu	Met	Phe	Tyr	Ala	Phe	Phe
			85					90					95		
Pro	Leu	Val	Ser	Ile	Ser	Leu	Val	Lys	Arg	Phe	Ile	Val	Phe	Phe	Val
			100					105					110		
Met	Pro	Leu	Phe	Gly	Met	Pro	Tyr	Ser	Val	Val	Lys	His	Asn	Thr	Leu
		115				120						125			
Leu	Ile	Tyr	Ser	Ile	Thr	Cys	Phe	Ser	Ile	Phe	Leu	Ile	Tyr	Arg	Cys
		130				135						140			

tatgaagctg	ctatggtgga	tgggtgcaagc	aaatggcaac	aaattaggaa	catcaccatt	720
ccacaattat	tgccaatgat	gtctatctta	ttgatcatta	atattggtaa	tatttttaaa	780
tctgatttcg	gacttttcta	cgttattcct	aagaattcag	gcccacttta	tgacgtgacc	840
agtgtgtcag	atacctatgt	ctacaatgcc	ttgactgcta	caggagatat	tgggatggca	900
tcggcagcta	gccttttatca	gtcagtagtt	gggaccagca	tcttgttagt	caccaatgcg	960
attgttcgctc	gcatggaccc	tgatgcagcc	ttgttttag			999

<210> SEQ ID NO 264
 <211> LENGTH: 332
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 264

Met	Ile	Tyr	Cys	Asn	Tyr	Asn	Val	Ile	Asn	Thr	Lys	Gly	Gly	Trp	Glu	1	5	10	15
Met	Ile	Arg	Gln	Thr	Asn	Lys	Lys	Thr	Ser	Phe	Trp	Lys	Asn	Val	Ile	20	25	30	
Lys	Tyr	Arg	Ala	Leu	Leu	Leu	Met	Val	Leu	Pro	Gly	Phe	Ile	Trp	Phe	35	40	45	
Ile	Phe	Phe	Phe	Tyr	Ile	Pro	Val	Leu	Ala	Asn	Val	Val	Ala	Phe	Lys	50	55	60	
Asp	Phe	His	Tyr	Ser	Ala	Gly	Gly	Phe	Met	Glu	Ser	Leu	Lys	Glu	Ser	65	70	75	80
Pro	Trp	Val	Gly	Leu	Ala	Asn	Phe	Lys	Tyr	Leu	Phe	Ala	Ser	Lys	Asp	85	90	95	
Ala	Trp	Leu	Ile	Thr	Arg	Asn	Thr	Ile	Ala	Tyr	Asn	Val	Ile	Phe	Leu	100	105	110	
Leu	Phe	Asn	Val	Phe	Phe	Ala	Ile	Ala	Phe	Ala	Ile	Ile	Met	Ser	Glu	115	120	125	
Leu	Arg	Asn	Lys	Arg	Thr	Val	Lys	Val	Tyr	His	Thr	Met	Ser	Leu	Leu	130	135	140	
Pro	Tyr	Phe	Leu	Ser	Trp	Val	Val	Ile	Glu	Tyr	Phe	Val	Ser	Ala	Phe	145	150	155	160
Leu	Asn	Thr	Asp	Lys	Gly	Phe	Ile	Asn	Gln	Leu	Leu	Thr	Gly	Ser	Gly	165	170	175	
Ala	Asp	Pro	Ile	Lys	Trp	Tyr	Ser	Asn	Pro	Thr	Trp	Trp	Pro	Leu	Ile	180	185	190	
Leu	Leu	Phe	Met	Ser	Val	Trp	Lys	Gly	Leu	Gly	Tyr	Asn	Ser	Ile	Ile	195	200	205	
Tyr	Tyr	Ala	Ser	Val	Lys	Gly	Ile	Ser	Asp	Thr	Tyr	Tyr	Glu	Ala	Ala	210	215	220	
Met	Val	Asp	Gly	Ala	Ser	Lys	Trp	Gln	Gln	Ile	Arg	Asn	Ile	Thr	Ile	225	230	235	240
Pro	Gln	Leu	Leu	Pro	Met	Met	Ser	Ile	Leu	Leu	Ile	Ile	Asn	Ile	Gly	245	250	255	
Asn	Ile	Phe	Lys	Ser	Asp	Phe	Gly	Leu	Phe	Tyr	Val	Ile	Pro	Lys	Asn	260	265	270	
Ser	Gly	Pro	Leu	Tyr	Asp	Val	Thr	Ser	Val	Ser	Asp	Thr	Tyr	Val	Tyr	275	280	285	
Asn	Ala	Leu	Thr	Ala	Thr	Gly	Asp	Ile	Gly	Met	Ala	Ser	Ala	Ala	Ser	290	295	300	
Leu	Tyr	Gln	Ser	Val	Val	Gly	Thr	Ser	Ile	Leu	Leu	Val	Thr	Asn	Ala	305	310	315	320
Ile	Val	Arg	Arg	Met	Asp	Pro	Asp	Ala	Ala	Leu	Phe					325	330		

<210> SEQ ID NO 265
 <211> LENGTH: 927

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 265

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atggagaaaa agaaaaaagt cgaaaagggt aatgtttagaa cctttgatcg aaaaaccaat    60
gctatcttta atattctgat tggctctgtt gccatctctt gtatcattcc ttttatcttc    120
gtgattatta tttccttcac tgatgaaagt tacttgatta atcatgggta tagttttttt    180
ccagatgtct ggtcaactaa ggcttaccag tatatttttc aaggagccat gtcccataga    240
atcatgaggt catttgggat atccgtgttt attacagtgg tgggaacctt tattaacacg    300
accatgacat caacctatgc ttatgcgatt tcaagacctt atttcccata cagacgtttt    360
tttactgttt atgcacttat caccatgctc tttgcaccag ggatgggtgc taattacttg    420
gtggtcagca atctccttca tttgaaggat acggtttggg ccttgatttt accaatggct    480
ctgggcccat ttggcatctt ggcatgaga acgttcttta aaaagacagt tccagatagc    540
attattgagt cggctcgtat ggatggggct agtgaatgga tgatttttat gaaaattgtc    600
ttaccattag ctgttccagg gattgccacc atcagtttat tttctgcctt aacttattgg    660
aatgattggt ttaacgcctt gctttatgtg caaagtgaga atctttacc atgcagtagc    720
ttactgatga aaattcagag caacctacag gcttggcac aaaatgctgg catgagtgc    780
caaatggcag atagcttagc atcgctgcca aaagaatcag ttcgtatggc tatcgtgggt    840
attgcaacct tgccgattgc cttgacttac ccattcttcc aaaagtactt tgtcggtggt    900
ttgaaccattg gtggggtgaa ggaatag                                927
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<210> SEQ ID NO 266

<211> LENGTH: 308

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 266

```
Met Glu Lys Lys Lys Lys Val Glu Lys Val Asn Val Arg Thr Phe Asp
1          5          10          15
Arg Lys Thr Asn Ala Ile Phe Asn Ile Leu Ile Gly Leu Phe Ala Ile
          20          25          30
Ser Cys Ile Ile Pro Phe Ile Phe Val Ile Ile Ile Ser Phe Thr Asp
          35          40          45
Glu Ser Tyr Leu Ile Asn His Gly Tyr Ser Phe Phe Pro Asp Val Trp
          50          55          60
Ser Thr Lys Ala Tyr Gln Tyr Ile Phe Gln Gly Ala Met Ser His Arg
          65          70          75          80
Ile Met Arg Ser Phe Gly Ile Ser Val Phe Ile Thr Val Val Gly Thr
          85          90          95
Phe Ile Asn Thr Thr Met Thr Ser Thr Tyr Ala Tyr Ala Ile Ser Arg
          100          105          110
Pro Tyr Phe Pro Tyr Arg Arg Phe Phe Thr Val Tyr Ala Leu Ile Thr
          115          120          125
Met Leu Phe Ala Pro Gly Met Val Ala Asn Tyr Leu Val Val Ser Asn
          130          135          140
Leu Leu His Leu Lys Asp Thr Val Trp Ala Leu Ile Leu Pro Met Ala
          145          150          155          160
Leu Gly Pro Phe Gly Ile Leu Val Met Arg Thr Phe Phe Lys Lys Thr
          165          170          175
Val Pro Asp Ser Ile Ile Glu Ser Ala Arg Met Asp Gly Ala Ser Glu
          180          185          190
Trp Met Ile Phe Met Lys Ile Val Leu Pro Leu Ala Val Pro Gly Ile
          195          200          205
Ala Thr Ile Ser Leu Phe Ser Ala Leu Thr Tyr Trp Asn Asp Trp Phe
          210          215          220
Asn Ala Leu Leu Tyr Val Gln Ser Glu Asn Leu Tyr Pro Met Gln Tyr
          225          230          235          240
Leu Leu Met Lys Ile Gln Ser Asn Leu Gln Ala Leu Ala Gln Asn Ala
          245          250          255
```

Gly	Met	Ser	Ala	Gln	Met	Ala	Asp	Ser	Leu	Ala	Ser	Leu	Pro	Lys	Glu
			260					265					270		
Ser	Val	Arg	Met	Ala	Ile	Val	Val	Ile	Ala	Thr	Leu	Pro	Ile	Ala	Leu
		275					280					285			
Thr	Tyr	Pro	Phe	Phe	Gln	Lys	Tyr	Phe	Val	Gly	Gly	Leu	Thr	Ile	Gly
	290					295					300				
Gly	Val	Lys	Glu												
305															

<210> SEQ ID NO 267
 <211> LENGTH: 1728
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 267

ttgatgagtg	ttaaaacatt	gggaaggat	gtgactaacc	actttaagca	gggttttttg	60
attaatcgac	tgatgaaatt	atatagcctg	ctaattgtaa	gtttttttcac	tttagcagct	120
attggccttga	gcagttattc	tattagtagt	acttataaaa	gggtggatgc	tgaggcgcag	180
atgcgattgg	aggagactct	aggtagattg	cagtcacaaa	acgatattac	cctacgggtt	240
ttagaccagt	tggttgccg	ttcagaagat	taccataatc	tctatcaata	catgacgtta	300
accccaaacc	aataattttc	aaacgttttt	gaagactggg	aaaaaggaaa	agacacgggtc	360
ctattttctg	aagaggtgag	gcgtcttttt	gacttgtacc	ctgatgtgac	ttctatgacc	420
ctactgctag	aggacagtag	tgcttatctg	tacgccgata	aggtcattaa	gacgggtcgt	480
ttgctttata	gcaagcctga	aaaagtaacc	ggaaatgttt	tagttcgctc	tattcgaaat	540
ccagaatcag	gagatgtgac	aggtcgtctt	tacctgacct	ttgacaaacc	accgactttg	600
gtagagacac	agcaggatca	ctatttagct	acttttgctt	ttgattacta	tggccgcaaa	660
ctcttccatc	aaggaggctg	gagatttcct	catttagagg	ctgagggttaa	aaaggctatc	720
aaggcagatc	gggcagctga	tcttagtaat	cttagcaagg	cttatcggat	gcagtacaat	780
cgctcgggag	acctcttggc	ttatgtggct	gtcagaaaat	cctattttatt	agcgggaagct	840
gtcaggacag	tttttgtgta	tggccttggt	tctctacttt	tagcttggct	gttattgcag	900
ttgctcttta	gggttttccg	aaattatatc	cagcagggtt	ctgaaattac	ggatactggt	960
gaaatggttg	cagcaggcga	tttgtcttta	accatcgaca	acagccacat	ggaattggaa	1020
ctgtatcata	tctcagaagc	cattaatcag	atggttgcca	gcattaaagc	ttatattgac	1080
gaagtttatg	tgttagagg	agagcaacga	gatgcccaaa	tgagagctct	gcagtctcaa	1140
atcaaccctc	attttttata	caacacgtta	gagtatatc	ggatgtacgc	ccttagttgt	1200
caacaagaag	aattagcaga	tgtcatttat	gcctttgcga	gtctgcttcg	caacaatatt	1260
agccaagata	agatgaccac	cttaaaagaa	gaactgggctt	tttgtgaaaa	gtacattttac	1320
ctttatcaaa	tgcggtatcc	agatagcttc	gcttatcatg	taaaaattga	tgagagtgtt	1380
gctgacttag	ccattcctaa	atttgtcatt	caacctctcg	ttgaaaatta	ttttgtgcat	1440
gggattgatt	atagtcgcca	tgacaatgca	ctaagcatca	aggctttaga	tgagacggat	1500
catctcttga	ttcaggtgct	tgataatgga	cgtgggtatta	gtcaagagcg	cttagcagat	1560
atggaaaaaa	ggcttcaaga	gcaccaaaca	acaggcaata	gctctattgg	tttgcaaaat	1620
gtttacctcc	gtctctttca	tcattttcga	gacagggttt	cttgggtccat	ggctaaggag	1680
ccaaatggtg	gctttatcat	tcaaattagg	attagaaagg	atgcttga		1728

<210> SEQ ID NO 268
 <211> LENGTH: 575
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 268

Met	Met	Ser	Val	Lys	Thr	Leu	Gly	Arg	Tyr	Val	Thr	Asn	His	Phe	Lys
1			5						10					15	
Gln	Gly	Phe	Leu	Ile	Asn	Arg	Leu	Met	Lys	Leu	Tyr	Ser	Leu	Leu	Ile
		20					25					30			
Val	Ser	Phe	Phe	Thr	Leu	Ala	Ala	Ile	Gly	Leu	Ser	Ser	Tyr	Ser	Ile
	35					40					45				
Ser	Ser	Thr	Tyr	Lys	Arg	Val	Asp	Ala	Glu	Ala	Gln	Met	Arg	Leu	Glu
50						55					60				

Glu	Thr	Leu	Gly	Arg	Leu	Gln	Ser	Gln	Asn	Asp	Ile	Thr	Leu	Arg	Val
65					70				75						80
Leu	Asp	Gln	Leu	Val	Gly	Arg	Ser	Glu	Asp	Tyr	His	Asn	Leu	Tyr	Gln
				85					90					95	
Tyr	Met	Thr	Leu	Thr	Pro	Asn	Gln	Tyr	Phe	Ser	Asn	Val	Phe	Glu	Asp
			100					105					110		
Trp	Glu	Lys	Gly	Lys	Asp	Thr	Val	Leu	Phe	Ser	Glu	Glu	Val	Arg	Arg
		115					120					125			
Leu	Phe	Asp	Leu	Tyr	Pro	Asp	Val	Thr	Ser	Met	Thr	Leu	Leu	Leu	Glu
	130					135					140				
Asp	Ser	Ser	Ala	Tyr	Leu	Tyr	Ala	Asp	Lys	Val	Ile	Lys	Thr	Gly	Arg
145					150					155					160
Leu	Leu	Tyr	Ser	Lys	Pro	Glu	Lys	Val	Thr	Gly	Asn	Val	Leu	Val	Arg
			165						170					175	
Ser	Ile	Arg	Asn	Pro	Glu	Ser	Gly	Asp	Val	Thr	Gly	Arg	Leu	Tyr	Leu
			180					185					190		
Thr	Phe	Asp	Lys	Pro	Pro	Thr	Leu	Val	Glu	Thr	Gln	Gln	Asp	His	Tyr
		195					200					205			
Leu	Ala	Thr	Phe	Ala	Phe	Asp	Tyr	Tyr	Gly	Arg	Lys	Leu	Phe	His	Gln
	210					215					220				
Gly	Gly	Arg	Arg	Phe	Pro	His	Leu	Glu	Ala	Glu	Val	Lys	Lys	Ala	Ile
225					230					235					240
Lys	Ala	Asp	Arg	Ala	Ala	Asp	Leu	Ser	Asn	Leu	Ser	Lys	Ala	Tyr	Arg
			245						250					255	
Met	Gln	Tyr	Asn	Arg	Ser	Gly	Asp	Leu	Leu	Ala	Tyr	Val	Ala	Val	Arg
			260					265					270		
Lys	Ser	Tyr	Leu	Leu	Ala	Glu	Ala	Val	Arg	Thr	Val	Phe	Val	Tyr	Gly
		275					280					285			
Leu	Val	Ser	Leu	Leu	Leu	Ala	Trp	Leu	Leu	Leu	Gln	Leu	Leu	Phe	Arg
	290					295					300				
Val	Phe	Arg	Asn	Tyr	Ile	Gln	Gln	Val	Ser	Glu	Ile	Thr	Asp	Thr	Val
305				310						315					320
Glu	Met	Val	Ala	Ala	Gly	Asp	Leu	Ser	Leu	Thr	Ile	Asp	Asn	Ser	His
			325						330					335	
Met	Glu	Leu	Glu	Leu	Tyr	His	Ile	Ser	Glu	Ala	Ile	Asn	Gln	Met	Leu
			340					345					350		
Ala	Ser	Ile	Lys	Ala	Tyr	Ile	Asp	Glu	Val	Tyr	Val	Leu	Glu	Val	Glu
		355					360					365			
Gln	Arg	Asp	Ala	Gln	Met	Arg	Ala	Leu	Gln	Ser	Gln	Ile	Asn	Pro	His
	370				375						380				
Phe	Leu	Tyr	Asn	Thr	Leu	Glu	Tyr	Ile	Arg	Met	Tyr	Ala	Leu	Ser	Cys
385				390					395						400
Gln	Gln	Glu	Glu	Leu	Ala	Asp	Val	Ile	Tyr	Ala	Phe	Ala	Ser	Leu	Leu
			405						410					415	
Arg	Asn	Asn	Ile	Ser	Gln	Asp	Lys	Met	Thr	Thr	Leu	Lys	Glu	Glu	Leu
			420					425					430		
Ala	Phe	Cys	Glu	Lys	Tyr	Ile	Tyr	Leu	Tyr	Gln	Met	Arg	Tyr	Pro	Asp
		435					440					445			
Ser	Phe	Ala	Tyr	His	Val	Lys	Ile	Asp	Glu	Ser	Val	Ala	Asp	Leu	Ala
	450					455					460				
Ile	Pro	Lys	Phe	Val	Ile	Gln	Pro	Leu	Val	Glu	Asn	Tyr	Phe	Val	His
465				470						475					480
Gly	Ile	Asp	Tyr	Ser	Arg	His	Asp	Asn	Ala	Leu	Ser	Ile	Lys	Ala	Leu
			485						490					495	
Asp	Glu	Thr	Asp	His	Leu	Leu	Ile	Gln	Val	Leu	Asp	Asn	Gly	Arg	Gly
			500					505					510		
Ile	Ser	Gln	Glu	Arg	Leu	Ala	Asp	Met	Glu	Lys	Arg	Leu	Gln	Glu	His

145		150		155		160									
Ala	Ile	Ile	Asp	Glu	Val	Phe	Lys	Glu	Lys	Ala	Lys	Asp	Tyr	Lys	Lys
		165		170		175									
Lys	Ile	Val	Val	Glu	Lys	Ala	Pro	Leu	Lys	His	Phe	Ile	Lys	Ala	Glu
		180		185		190									
Asp	Tyr	His	Gln	Asp	Tyr	Leu	Lys	Lys	Asn	Pro	Asn	Gly	Tyr	Cys	His
		195		200		205									
Ile	Asp	Ile	Asn	Gln	Ala	Thr	Tyr	Pro	Val	Ile	Asp	Glu	Ser	Lys	Tyr
		210		215		220									
Pro	Lys	Pro	Ser	Ala	Thr	Glu	Ile	Lys	Glu	Lys	Leu	Ser	Ala	Asp	Glu
		225		230		235									
Tyr	Arg	Val	Thr	Gln	Lys	Asn	Glu	Thr	Glu	Lys	Ala	Phe	Ser	Asn	Arg
		245		250		255									
Tyr	Trp	Asp	Ser	Phe	Asp	Ala	Gly	Ile	Tyr	Val	Asp	Val	Val	Thr	Gly
		260		265		270									
Glu	Pro	Leu	Phe	Ser	Ser	Lys	Asp	Lys	Phe	Glu	Ser	Gly	Cys	Gly	Trp
		275		280		285									
Pro	Ser	Phe	Ser	Arg	Pro	Ile	Ser	Pro	Asp	Val	Val	Arg	Tyr	Lys	Glu
		290		295		300									
Asp	Lys	Ser	Phe	Asn	Met	Thr	Arg	Thr	Glu	Val	Arg	Ser	Arg	Ser	Gly
		305		310		315									
Asn	Ser	His	Leu	Gly	His	Val	Phe	Thr	Asp	Gly	Pro	Lys	Asp	Gln	Gly
		325		330		335									
Gly	Leu	Arg	Tyr	Cys	Ile	Asn	Ser	Leu	Ser	Ile	Thr	Phe	Ile	Pro	Lys
		340		345		350									
Ala	Asp	Met	Glu	Ala	Lys	Gly	Tyr	Gly	Tyr	Leu	Leu	Ser	Ser	Val	Glu
		355		360		365									

<210> SEQ ID NO 271

<211> LENGTH: 1035

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 271

atgaagcggtt	atccccctact	ggtccagttg	atttcgtatg	tttttgtgat	cgtaattgcc	60
ctcattacca	cgcttggttt	gctttattac	cagacgagtt	ctcgtaatat	caggcaacta	120
attgaacgtg	ataccgggca	gagcattcgg	caaagttccc	aatttattga	cgcttacatc	180
aagcctctta	aagaaacaac	ttcggtgctg	gcgaaaaata	cggaaattca	agcctttgct	240
agtcaaatc	atcaagaaaa	tgacaaacag	gttcttcagc	tcatgaagat	ggttcttgcg	300
accaattccg	atttacaagc	agctgttctg	gtgactaagg	atgggtcgaac	ggtgtctacc	360
aattctcagt	tgaccatgaa	aacctccagt	gacatgatgg	cagaaccctg	gtataaagca	420
gccatagacc	gtcaagccat	gccaatctta	accccagctc	ggcaattatc	cctttcttct	480
aaaaaagaat	gggtagtttc	tgtgacccaa	gaggtagtag	atagggctgg	gcataattta	540
ggtgtgctaa	gacttgatat	tgcatacccg	accattaaag	cgtctttaga	tcagcttcag	600
ctaggccgcc	aaggctttgc	ctttattgtg	aatgataagc	atgaatttgt	ttaccatccc	660
aaaaagagtg	tttacagttc	ttctaaggag	atggctgcga	tgaaacctta	tttagcgatt	720
cagaatgggt	acactaagga	caagacatct	tttgtttacc	aaaaactcat	tcctaacagt	780
caatggactt	tagtgggagt	ggcgtcactg	gatcagttgc	accgggtgca	gcgccaaatt	840
ttttggctct	tttcttgga	cagggcttct	accctgtctg	atttgtggct	ttgcaactgt	900
cttagtcctta	cgcagatgga	ttcgtcccat	tcaacaattg	cagcaagtta	ttcttgctat	960
tcaaaaagga	gatcgtcagt	tacgtgccca	agaaacgggt	tctccagaat	tgacagacct	1020
tgcccaacag	tttaa					1035

<210> SEQ ID NO 272

<211> LENGTH: 344

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 272

Met	Lys	Arg	Tyr	Pro	Leu	Leu	Val	Gln	Leu	Ile	Ser	Tyr	Val	Phe	Val
1				5					10					15	
Ile	Val	Ile	Ala	Leu	Ile	Thr	Thr	Leu	Gly	Leu	Leu	Tyr	Tyr	Gln	Thr
			20					25					30		
Ser	Ser	Arg	Asn	Ile	Arg	Gln	Leu	Ile	Glu	Arg	Asp	Thr	Arg	Gln	Ser
		35					40					45			
Ile	Arg	Gln	Ser	Ser	Gln	Phe	Ile	Asp	Ala	Tyr	Ile	Lys	Pro	Leu	Lys
	50				55				60						
Glu	Thr	Thr	Ser	Val	Leu	Ala	Lys	Asn	Thr	Glu	Ile	Gln	Ala	Phe	Ala
65					70				75					80	
Ser	Gln	Ile	His	Gln	Glu	Asn	Asp	Lys	Gln	Val	Leu	Gln	Leu	Met	Lys
			85					90						95	
Met	Val	Leu	Ala	Thr	Asn	Ser	Asp	Leu	Gln	Ala	Ala	Val	Leu	Val	Thr
			100					105					110		
Lys	Asp	Gly	Arg	Thr	Val	Ser	Thr	Asn	Ser	Gln	Leu	Thr	Met	Lys	Thr
		115					120					125			
Ser	Ser	Asp	Met	Met	Ala	Glu	Pro	Trp	Tyr	Lys	Ala	Ala	Ile	Asp	Arg
	130				135						140				
Gln	Ala	Met	Pro	Ile	Leu	Thr	Pro	Ala	Arg	Gln	Leu	Ser	Leu	Ser	Ser
145					150				155					160	
Lys	Lys	Glu	Trp	Val	Val	Ser	Val	Thr	Gln	Glu	Val	Val	Asp	Arg	Ala
			165					170					175		
Gly	His	Asn	Leu	Gly	Val	Leu	Arg	Leu	Asp	Ile	Ala	Tyr	Pro	Thr	Ile
		180						185					190		
Lys	Ala	Ser	Leu	Asp	Gln	Leu	Gln	Leu	Gly	Arg	Gln	Gly	Phe	Ala	Phe
	195						200					205			
Ile	Val	Asn	Asp	Lys	His	Glu	Phe	Val	Tyr	His	Pro	Lys	Lys	Ser	Val
	210				215						220				
Tyr	Ser	Ser	Ser	Lys	Glu	Met	Ala	Ala	Met	Lys	Pro	Tyr	Leu	Ala	Ile
225					230					235				240	
Gln	Asn	Gly	Tyr	Thr	Lys	Asp	Lys	Thr	Ser	Phe	Val	Tyr	Gln	Lys	Leu
			245					250					255		
Ile	Pro	Asn	Ser	Gln	Trp	Thr	Leu	Val	Gly	Val	Ala	Ser	Leu	Asp	Gln
			260				265						270		
Leu	His	Arg	Val	Gln	Arg	Gln	Ile	Phe	Trp	Ser	Phe	Ser	Trp	Asn	Arg
	275					280						285			
Ala	Ser	Thr	Leu	Ser	Asp	Leu	Trp	Leu	Cys	Asn	Cys	Leu	Ser	Leu	Thr
	290					295					300				
Gln	Met	Asp	Ser	Ser	His	Ser	Thr	Ile	Ala	Ala	Ser	Tyr	Ser	Cys	Tyr
305					310				315					320	
Ser	Lys	Arg	Arg	Ser	Ser	Val	Thr	Cys	Pro	Arg	Asn	Gly	Phe	Ser	Arg
			325					330					335		
Ile	Asp	Arg	Pro	Cys	Pro	Thr	Val								
			340												

<210> SEQ ID NO 273

<211> LENGTH: 798

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 273

ttgcagcaag	ttattcttgc	tattcaaaaa	ggagatcgtc	agttacgtgc	ccaagaaacg	60
ggttctccag	aattgacaga	ccttgcccaa	cagtttaatg	cgctcttaga	tcaaattgat	120
agcttgatgg	ttgccgttgc	ggataaggaa	aaggcgattg	ggcagtatag	gttacaagcc	180
ttggctagtc	agattaaccc	gcattttctc	tataacacct	tggacactat	tatttggatg	240
gcagaattta	atgacagcaa	gcgcgtggta	gaagtgacca	agtctctagc	taagtatttt	300
cgtttggccc	ttaatcaggg	gaacgaatac	attcgtttgg	cagatgaact	ggatcacgtt	360
agccaatacc	tctttattca	aaaacagcgc	tatggagaca	agctaagtta	tgaagtgcaa	420

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ggcttagatg tctacgcaga ctttgttatt cctaagctta tcttacagcc cttagtagaa 480
aatgctatct accatggcat caaagaagtc gatcgcaagg gcatgatcaa ggttacggta 540
tctgatacag ctcagcatct gatgttgact gtttgggata atggtaaagg cattgaagac 600
tcttcactga ccaatagtca gagcttggtg gctaggggag gtgtgggcct taaaaatgtt 660
gaccagcggg taaaacttca ctatggtgaa ggctaccaca tgaccattca tagccagtca 720
gaccagttca ctgaaatata attaagcctt cctaaaatgc atgaattaat ggcagacgac 780
acacaggaaa acgagtaa 798

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<210> SEQ ID NO 274
 <211> LENGTH: 265
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 274

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Met Gln Gln Val Ile Leu Ala Ile Gln Lys Gly Asp Arg Gln Leu Arg
1          5          10          15
Ala Gln Glu Thr Gly Ser Pro Glu Leu Thr Asp Leu Ala Gln Gln Phe
20        25        30
Asn Ala Leu Leu Asp Gln Ile Asp Ser Leu Met Val Ala Val Ala Asp
35        40        45
Lys Glu Lys Ala Ile Gly Gln Tyr Arg Leu Gln Ala Leu Ala Ser Gln
50        55        60
Ile Asn Pro His Phe Leu Tyr Asn Thr Leu Asp Thr Ile Ile Trp Met
65        70        75        80
Ala Glu Phe Asn Asp Ser Lys Arg Val Val Glu Val Thr Lys Ser Leu
85        90        95
Ala Lys Tyr Phe Arg Leu Ala Leu Asn Gln Gly Asn Glu Tyr Ile Arg
100       105       110
Leu Ala Asp Glu Leu Asp His Val Ser Gln Tyr Leu Phe Ile Gln Lys
115       120       125
Gln Arg Tyr Gly Asp Lys Leu Ser Tyr Glu Val Gln Gly Leu Asp Val
130       135       140
Tyr Ala Asp Phe Val Ile Pro Lys Leu Ile Leu Gln Pro Leu Val Glu
145       150       155       160
Asn Ala Ile Tyr His Gly Ile Lys Glu Val Asp Arg Lys Gly Met Ile
165       170       175
Lys Val Thr Val Ser Asp Thr Ala Gln His Leu Met Leu Thr Val Trp
180       185       190
Asp Asn Gly Lys Gly Ile Glu Asp Ser Ser Leu Thr Asn Ser Gln Ser
195       200       205
Leu Leu Ala Arg Gly Gly Val Gly Leu Lys Asn Val Asp Gln Arg Leu
210       215       220
Lys Leu His Tyr Gly Glu Gly Tyr His Met Thr Ile His Ser Gln Ser
225       230       235       240
Asp Gln Phe Thr Glu Ile Gln Leu Ser Leu Pro Lys Met His Glu Leu
245       250       255
Met Ala Asp Asp Thr Gln Glu Asn Glu
260       265

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<210> SEQ ID NO 275
 <211> LENGTH: 1494
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 275

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atgacagaag aaaaaaaacg gggttttaga attccttctt cttacaccgt tctttttatc 60
attatagcca tcatggcagt gttaacttgg tttattccag ctggcgccta cgaaaccgct 120
aagggcggtg gtgttatttc aggaacctac aaaacagtag catccaatcc tcaaggattt 180
tttgacatct tgatggctcc cgttcgaggc atgttaggtg ttgaaggcac tgatggtgct 240

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attcaagtgt ctttctttat cttaatgggt gggggccttt taggagttgt caacaaaaca 300
ggtgctcttg acacagggat tgcgtcagtg gttcgtaaaa acaaaggtag agaaaaaatg 360
ctgattgcta ttttaatccc tttgtttgct ctagggtggaa cgacctatgg tatgggggaa 420
gaaaccatgg cctttttaccc actttttaatt cctgttatga ttgcggttg ttttgacagt 480
attgttgctg tagccattat tttgattggg tctcaaattg ggtgtctagc ctccactatt 540
aaccattttg caactgggtg agcagctgat gctgctggtg tcagcattgc agatggaatg 600
atttggcgtg ttatccaatg gggtattcct gtcggcatgt ctatttggtt tgtttacaat 660
tacgctagta agattgaaga agaccaagt aaatcattgg ttgcagacaa ggaagaagag 720
cataaggaac tcttccagtt gcaaaattct ggagaagact taaacaagcg ccaacgaaac 780
gttttgacca tttttacttt gacctttgtc attatgattc ttagtttgat tccgtgggaa 840
gattttggca tcaaattcct tactaatatc aatacttggg taaccacaat gcctatctta 900
ggggggagtt ttgggaaaac catgggagca tttgggtact ggtatttccc agaaatcacc 960
atgctcttta tcatgatggg tgtcttagtt gctattggtt atcgtatgag tgaagaagac 1020
tttttttagct cttttttgac tgggtgcagg gaatttttag gtgttgccat gatctgtgct 1080
attgcacgcg gtattcaagt tatcatgaat ggtgggtatga ttacagccac tatcttacac 1140
ttaggtgaaa caagtctttc tggtttatct tctcaagttt ttgtgatatt agcttatatt 1200
ttctacctcc caatgtcctt cttgattcca tcaacatcag gacttgctgg ggctacaatg 1260
ggaattatgg caccgcttgg acaattctca aatgtccctg ctcaccttgt tattacagcc 1320
ttccagtcag cttctggaat cttaaacaatg atttctccaa cttcagcaat cgttatggga 1380
gcacttgccg ttggtgcgct tgaccttggg acttgggtgga aattcattgg taaatttatt 1440
gtaatggtga tgcttgtaag cgtgctatta cttgtagttg caacattctt ttaa 1494

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<210> SEQ ID NO 276

<211> LENGTH: 497

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 276

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Met Thr Glu Glu Lys Lys Arg Gly Phe Arg Ile Pro Ser Ser Tyr Thr
1          5          10          15
Val Leu Phe Ile Ile Ala Ile Met Ala Val Leu Thr Trp Phe Ile
20          25          30
Pro Ala Gly Ala Tyr Glu Thr Ala Lys Gly Gly Gly Val Ile Ser Gly
35          40          45
Thr Tyr Lys Thr Val Ala Ser Asn Pro Gln Gly Phe Phe Asp Ile Leu
50          55          60
Met Ala Pro Val Arg Gly Met Leu Gly Val Glu Gly Thr Asp Gly Ala
65          70          75          80
Ile Gln Val Ser Phe Phe Ile Leu Met Val Gly Gly Phe Leu Gly Val
85          90          95
Val Asn Lys Thr Gly Ala Leu Asp Thr Gly Ile Ala Ser Val Val Arg
100         105         110
Lys Asn Lys Gly Arg Glu Lys Met Leu Ile Ala Ile Leu Ile Pro Leu
115         120         125
Phe Ala Leu Gly Gly Thr Thr Tyr Gly Met Gly Glu Glu Thr Met Ala
130         135         140
Phe Tyr Pro Leu Leu Ile Pro Val Met Ile Ala Val Gly Phe Asp Ser
145         150         155         160
Ile Val Ala Val Ala Ile Ile Leu Ile Gly Ser Gln Ile Gly Cys Leu
165         170         175
Ala Ser Thr Ile Asn Pro Phe Ala Thr Gly Val Ala Ala Asp Ala Ala
180         185         190
Gly Val Ser Ile Ala Asp Gly Met Ile Trp Arg Val Ile Gln Trp Val
195         200         205
Ile Leu Val Gly Met Ser Ile Trp Phe Val Tyr Asn Tyr Ala Ser Lys
210         215         220
Ile Glu Glu Asp Pro Ser Lys Ser Leu Val Ala Asp Lys Glu Glu Glu
225         230         235         240

```

His	Lys	Glu	Leu	Phe	Gln	Leu	Gln	Asn	Ser	Gly	Glu	Asp	Leu	Asn	Lys		
				245					250					255			
Arg	Gln	Arg	Asn	Val	Leu	Thr	Ile	Phe	Thr	Leu	Thr	Phe	Val	Ile	Met		
			260					265					270				
Ile	Leu	Ser	Leu	Ile	Pro	Trp	Glu	Asp	Phe	Gly	Ile	Lys	Phe	Phe	Thr		
		275					280					285					
Asn	Ile	Asn	Thr	Trp	Leu	Thr	Thr	Met	Pro	Ile	Leu	Gly	Gly	Val	Ile		
	290					295					300						
Gly	Lys	Thr	Met	Gly	Ala	Phe	Gly	Thr	Trp	Tyr	Phe	Pro	Glu	Ile	Thr		
305				310						315					320		
Met	Leu	Phe	Ile	Met	Met	Gly	Val	Leu	Val	Ala	Ile	Val	Tyr	Arg	Met		
			325					330						335			
Ser	Glu	Glu	Asp	Phe	Phe	Ser	Ser	Phe	Leu	Thr	Gly	Ala	Gly	Glu	Phe		
			340					345					350				
Leu	Gly	Val	Ala	Met	Ile	Cys	Ala	Ile	Ala	Arg	Gly	Ile	Gln	Val	Ile		
	355					360						365					
Met	Asn	Gly	Gly	Met	Ile	Thr	Ala	Thr	Ile	Leu	His	Leu	Gly	Glu	Thr		
370						375					380						
Ser	Leu	Ser	Gly	Leu	Ser	Ser	Gln	Val	Phe	Val	Ile	Leu	Ala	Tyr	Ile		
385				390					395					400			
Phe	Tyr	Leu	Pro	Met	Ser	Phe	Leu	Ile	Pro	Ser	Thr	Ser	Gly	Leu	Ala		
			405					410					415				
Gly	Ala	Thr	Met	Gly	Ile	Met	Ala	Pro	Leu	Gly	Gln	Phe	Ser	Asn	Val		
		420					425					430					
Pro	Ala	His	Leu	Val	Ile	Thr	Ala	Phe	Gln	Ser	Ala	Ser	Gly	Ile	Leu		
	435					440					445						
Asn	Met	Ile	Ser	Pro	Thr	Ser	Ala	Ile	Val	Met	Gly	Ala	Leu	Ala	Leu		
450					455						460						
Gly	Arg	Val	Asp	Leu	Gly	Thr	Trp	Trp	Lys	Phe	Ile	Gly	Lys	Phe	Ile		
465				470					475					480			
Val	Met	Val	Met	Leu	Val	Ser	Val	Leu	Leu	Val	Val	Ala	Thr	Phe			
			485					490					495				

Phe

<210> SEQ ID NO 277

<211> LENGTH: 1365

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 277

atggctagaa	atggcttttt	tactggtttg	gacattggaa	caagctcgat	aaaagtttta	60
gtagcagaat	ttatttctgg	tgagatgaac	gtcattggtg	ttagtaatgt	tccaagtacc	120
ggcgtaaaag	atggcataat	aatcgatata	gaggcagctg	cgactgccat	caaaactgcg	180
gtagaacaag	cagaagaaaa	agcagggatg	acaattgaaa	aggttaatgt	tgggctaccg	240
gcaaaccttc	ttcaaattga	accaacacaa	ggaatgattc	ctgtcccaag	tgagtctaaa	300
gagataaaag	atgaggatgt	tgatagcggt	gttaaatcgg	ctttaacaaa	aagtatcaca	360
ccagaacgag	aggttatctc	tttagttcca	gaagagttca	ttgtggatgg	ctttcagggc	420
attcgagatc	cacgtggtat	gatggggatt	agattagaga	tgcgcgggct	tatttatact	480
ggaccaagca	ccattttaca	taatctgcgt	aaaacggtag	aaagagcagg	cattaaagtt	540
gaaaacatca	ttatttctcc	gtagctatg	gctaaaacca	ttttaaacga	aggtgagcgc	600
gagtttggag	ctactgtaat	tgatatggga	ggtggacaga	caactgtcgc	ttctatgcga	660
gcacaagaat	tgcagtatac	caatatatat	gccgaaggcg	gcgaatacat	tactaaagat	720
atatcaaaaag	tattaaaaac	gtctttggct	attgcagaag	cacttaagtt	taattttggt	780
caagcggaga	tatcagaagc	tagtataact	gaaacagtaa	aagttgatgt	ggtaggtagt	840
gaagagcctg	ttgaggtaac	tgaacgttat	ttatctgaaa	ttatttcagc	gcgtattcgt	900
catatttttag	atcgtgtgaa	gcaagatttg	gaaagaggtc	gtttactaga	cttaccagga	960
ggcattgttt	tgattggtgg	cggtgcaatc	atgcctggag	tggtagaaat	tgcacaagaa	1020
atctttggag	taactgtaaa	gctccatggt	ccaaaccaag	tcggtattag	aaatccaatg	1080

ttttcaaacg ttatcagttt ggtagaatat gttggtatga tgtctgaagt agacgtttta	1140
gcacaaactg cagtttcagg agaagaactt ttgcgacgca agcctatcga tttcagtggc	1200
caagaatcctt atttaccaga ttatgatgat tcaagaagac cagaatcgac cattggctat	1260
gaacaacaag cgtcacaaac agcatatgat tcacaagttc cgagtgatcc taaacaaaaa	1320
atttcagaac gtgttcgtgg catatttggg agtatgtttg attaa	1365

<210> SEQ ID NO 278

<211> LENGTH: 454

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 278

Met Ala Arg Asn Gly Phe Phe Thr Gly Leu Asp Ile Gly Thr Ser Ser	
1	5 10 15
Ile Lys Val Leu Val Ala Glu Phe Ile Ser Gly Glu Met Asn Val Ile	
	20 25 30
Gly Val Ser Asn Val Pro Ser Thr Gly Val Lys Asp Gly Ile Ile Ile	
	35 40 45
Asp Ile Glu Ala Ala Ala Thr Ala Ile Lys Thr Ala Val Glu Gln Ala	
	50 55 60
Glu Glu Lys Ala Gly Met Thr Ile Glu Lys Val Asn Val Gly Leu Pro	
65	70 75 80
Ala Asn Leu Leu Gln Ile Glu Pro Thr Gln Gly Met Ile Pro Val Pro	
	85 90 95
Ser Glu Ser Lys Glu Ile Lys Asp Glu Asp Val Asp Ser Val Val Lys	
	100 105 110
Ser Ala Leu Thr Lys Ser Ile Thr Pro Glu Arg Glu Val Ile Ser Leu	
	115 120 125
Val Pro Glu Glu Phe Ile Val Asp Gly Phe Gln Gly Ile Arg Asp Pro	
	130 135 140
Arg Gly Met Met Gly Ile Arg Leu Glu Met Arg Gly Leu Ile Tyr Thr	
145	150 155 160
Gly Pro Ser Thr Ile Leu His Asn Leu Arg Lys Thr Val Glu Arg Ala	
	165 170 175
Gly Ile Lys Val Glu Asn Ile Ile Ile Ser Pro Leu Ala Met Ala Lys	
	180 185 190
Thr Ile Leu Asn Glu Gly Glu Arg Glu Phe Gly Ala Thr Val Ile Asp	
	195 200 205
Met Gly Gly Gly Gln Thr Thr Val Ala Ser Met Arg Ala Gln Glu Leu	
	210 215 220
Gln Tyr Thr Asn Ile Tyr Ala Glu Gly Gly Glu Tyr Ile Thr Lys Asp	
225	230 235 240
Ile Ser Lys Val Leu Lys Thr Ser Leu Ala Ile Ala Glu Ala Leu Lys	
	245 250 255
Phe Asn Phe Gly Gln Ala Glu Ile Ser Glu Ala Ser Ile Thr Glu Thr	
	260 265 270
Val Lys Val Asp Val Val Gly Ser Glu Glu Pro Val Glu Val Thr Glu	
	275 280 285
Arg Tyr Leu Ser Glu Ile Ile Ser Ala Arg Ile Arg His Ile Leu Asp	
	290 295 300
Arg Val Lys Gln Asp Leu Glu Arg Gly Arg Leu Leu Asp Leu Pro Gly	
305	310 315 320
Gly Ile Val Leu Ile Gly Gly Gly Ala Ile Met Pro Gly Val Val Glu	
	325 330 335
Ile Ala Gln Glu Ile Phe Gly Val Thr Val Lys Leu His Val Pro Asn	
	340 345 350
Gln Val Gly Ile Arg Asn Pro Met Phe Ser Asn Val Ile Ser Leu Val	
	355 360 365

Glu	Tyr	Val	Gly	Met	Met	Ser	Glu	Val	Asp	Val	Leu	Ala	Gln	Thr	Ala
370						375					380				
Val	Ser	Gly	Glu	Glu	Leu	Leu	Arg	Arg	Lys	Pro	Ile	Asp	Phe	Ser	Gly
385					390					395					400
Gln	Glu	Ser	Tyr	Leu	Pro	Asp	Tyr	Asp	Asp	Ser	Arg	Arg	Pro	Glu	Ser
				405					410					415	
Thr	Ile	Gly	Tyr	Glu	Gln	Gln	Ala	Ser	Gln	Thr	Ala	Tyr	Asp	Ser	Gln
			420					425					430		
Val	Pro	Ser	Asp	Pro	Lys	Gln	Lys	Ile	Ser	Glu	Arg	Val	Arg	Gly	Ile
	435						440					445			
Phe	Gly	Ser	Met	Phe	Asp										
450															

<210> SEQ ID NO 279

<211> LENGTH: 1320

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 279

atggcatttt	catttgatac	tgcatacaatt	caaggtgcaa	ttataaaaagt	aattggagtc	60
ggcggagggtg	gcggaatgc	cattaatcgt	atgattgatg	aaggtgttgc	tggtgtcgag	120
ttcatcgag	caaacacaga	cattcaggca	ttaagctcat	caaaagctga	aacggttatt	180
caactaggcc	ctaaattaac	tcgtggactt	ggtgctggag	gacaacctga	agtaggacgt	240
aaagctgctg	aagaaagcga	agaaatttta	acagaagctc	ttacaggagc	ggacatggta	300
tttattactg	ccggtatggg	tggtggctct	gggacagggg	ctgcaccggt	tattgctcgt	360
atcgctaaaa	gtttgggagc	cttgacagta	gctgttgta	ctcgcccgtt	tggttttgaa	420
ggtaacaaac	gtggtaattt	tgctattgaa	ggtatcgaag	aactacgtga	acaagtgtgat	480
actttgttaa	ttatttcaaa	taataacctt	cttgagattg	ttgataaaaa	gacaccttta	540
ttagaagcac	ttagtgaagc	tgataatggt	ttacgccagg	gagttcaagg	gataaccgac	600
ttaattacta	gtcctggcct	tatcaatctc	gattttgccc	acgtgaaaac	agttatggca	660
aataaaggga	atgccttgat	ggggattggg	attggctctg	gagaagagcg	cattgttgag	720
gcggcgcgta	aggcaatcta	ttcaccctta	ttagaaacga	ctattgatgg	tgcacaagac	780
gttattgtga	acgttacagg	aggtctcgac	atgacactta	cagaagctga	agaagcctct	840
gaaattgttg	ggcaagctgc	tggtcaaggc	gttaacattt	ggtaggaac	atctattgat	900
gatactatga	aagatgacat	ccgtgtgact	gttgtagcaa	ctggagtgcg	ccaagaaaaa	960
gccgaacaag	tttcagggtt	tcgtcagcct	aggactttta	cccaaaccac	cgcgcagcaa	1020
gtagcgggtg	cacaatagtc	atcagatcaa	gcaaaacagt	cggttcaacc	agggtttgat	1080
cgtcgctcaa	attttgattt	tgacatgggg	gagtcctcgcg	agataccaag	tgcacaaaag	1140
gtaatttcta	atcataatca	aaatcaagg	tctgcttttg	gaaattggga	tttgagacgt	1200
gataatatatt	ctcgtccaac	agaaggtgaa	ttggataacc	atcttaatat	gtcaacgttc	1260
tcagctaacg	atgacagtga	tgatgaatta	gaaacgcctc	cattctttta	aaaccgttaa	1320

<210> SEQ ID NO 280

<211> LENGTH: 439

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 280

Met	Ala	Phe	Ser	Phe	Asp	Thr	Ala	Ser	Ile	Gln	Gly	Ala	Ile	Ile	Lys
1				5					10					15	
Val	Ile	Gly	Val	Gly	Gly	Gly	Gly	Gly	Asn	Ala	Ile	Asn	Arg	Met	Ile
			20					25					30		
Asp	Glu	Gly	Val	Ala	Gly	Val	Glu	Phe	Ile	Ala	Ala	Asn	Thr	Asp	Ile
		35					40					45			
Gln	Ala	Leu	Ser	Ser	Ser	Lys	Ala	Glu	Thr	Val	Ile	Gln	Leu	Gly	Pro
	50					55					60				
Lys	Leu	Thr	Arg	Gly	Leu	Gly	Ala	Gly	Gly	Gln	Pro	Glu	Val	Gly	Arg
65				70					75					80	
Lys	Ala	Ala	Glu	Glu	Ser	Glu	Glu	Ile	Leu	Thr	Glu	Ala	Leu	Thr	Gly

				85					90					95			
Ala	Asp	Met	Val	Phe	Ile	Thr	Ala	Gly	Met	Gly	Gly	Gly	Ser	Gly	Thr		
			100					105					110				
Gly	Ala	Ala	Pro	Val	Ile	Ala	Arg	Ile	Ala	Lys	Ser	Leu	Gly	Ala	Leu		
		115					120					125					
Thr	Val	Ala	Val	Val	Thr	Arg	Pro	Phe	Gly	Phe	Glu	Gly	Asn	Lys	Arg		
	130					135					140						
Gly	Asn	Phe	Ala	Ile	Glu	Gly	Ile	Glu	Glu	Leu	Arg	Glu	Gln	Val	Asp		
145					150					155					160		
Thr	Leu	Leu	Ile	Ile	Ser	Asn	Asn	Asn	Leu	Leu	Glu	Ile	Val	Asp	Lys		
			165					170					175				
Lys	Thr	Pro	Leu	Leu	Glu	Ala	Leu	Ser	Glu	Ala	Asp	Asn	Val	Leu	Arg		
		180						185					190				
Gln	Gly	Val	Gln	Gly	Ile	Thr	Asp	Leu	Ile	Thr	Ser	Pro	Gly	Leu	Ile		
	195					200						205					
Asn	Leu	Asp	Phe	Ala	Asp	Val	Lys	Thr	Val	Met	Ala	Asn	Lys	Gly	Asn		
	210					215					220						
Ala	Leu	Met	Gly	Ile	Gly	Ile	Gly	Ser	Gly	Glu	Glu	Arg	Ile	Val	Glu		
225					230					235					240		
Ala	Ala	Arg	Lys	Ala	Ile	Tyr	Ser	Pro	Leu	Leu	Glu	Thr	Thr	Ile	Asp		
			245					250						255			
Gly	Ala	Gln	Asp	Val	Ile	Val	Asn	Val	Thr	Gly	Gly	Leu	Asp	Met	Thr		
		260					265						270				
Leu	Thr	Glu	Ala	Glu	Glu	Ala	Ser	Glu	Ile	Val	Gly	Gln	Ala	Ala	Gly		
	275						280					285					
Gln	Gly	Val	Asn	Ile	Trp	Leu	Gly	Thr	Ser	Ile	Asp	Asp	Thr	Met	Lys		
	290				295					300							
Asp	Asp	Ile	Arg	Val	Thr	Val	Val	Ala	Thr	Gly	Val	Arg	Gln	Glu	Lys		
305					310					315					320		
Ala	Glu	Gln	Val	Ser	Gly	Phe	Arg	Gln	Pro	Arg	Thr	Phe	Thr	Gln	Thr		
			325					330						335			
Asn	Ala	Gln	Gln	Val	Ala	Gly	Ala	Gln	Tyr	Ala	Ser	Asp	Gln	Ala	Lys		
		340						345					350				
Gln	Ser	Val	Gln	Pro	Gly	Phe	Asp	Arg	Arg	Ser	Asn	Phe	Asp	Phe	Asp		
	355						360					365					
Met	Gly	Glu	Ser	Arg	Glu	Ile	Pro	Ser	Ala	Gln	Lys	Val	Ile	Ser	Asn		
	370					375					380						
His	Asn	Gln	Asn	Gln	Gly	Ser	Ala	Phe	Gly	Asn	Trp	Asp	Leu	Arg	Arg		
385					390					395					400		
Asp	Asn	Ile	Ser	Arg	Pro	Thr	Glu	Gly	Glu	Leu	Asp	Asn	His	Leu	Asn		
			405					410					415				
Met	Ser	Thr	Phe	Ser	Ala	Asn	Asp	Asp	Ser	Asp	Asp	Glu	Leu	Glu	Thr		
		420					425					430					
Pro	Pro	Phe	Lys	Asn	Arg												
		435															

<210> SEQ ID NO 281

<211> LENGTH: 687

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 281

atggatttgt	catttttggc	caaatactgg	gcctacttta	actacggtgt	acttgtcacc	60
attatgattt	cagtcagcgt	tgtctttttt	ggaaccctta	ttggtgtctt	ggtaaccctg	120
attaagcgta	gtcatgtgaa	gccgttgacc	tggttcgtta	atctttacgt	ttggatcttt	180
cggggaacac	ctatggtggt	tcaaatcatg	attgcctttg	cttggatgca	ttttaacaat	240
atgcctacta	ttggttttgg	gggttttagac	ttggactttt	caagactact	tcctggaatt	300
attatcattt	cattgaatag	cggtgcttat	atttcagaaa	ttgttagagc	aggtattgag	360

gctgtaccaa	aagggcaatt	agaagcagct	tattcactag	gtattcgtcc	tcaaaatgcc	420
atgcgttatg	tgattttgcc	tcaggccttt	aaaaatattt	tgccagcctt	aggaaatgaa	480
tttattacca	ttattaagga	tagtgctctt	ttacaaacca	ttggagtgat	ggaactttgg	540
aatggtgccc	aatcgtgtgt	aacggctact	tattctccaa	tttccccttt	actggtggct	600
gctttttact	acttaatggt	cacaacagtg	atggcacagt	tattggcagt	cttagaacgt	660
cacatggcgc	aaggaggtaa	tcattga				687

<210> SEQ ID NO 282
 <211> LENGTH: 228
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 282

Met	Asp	Leu	Ser	Phe	Leu	Pro	Lys	Tyr	Trp	Ala	Tyr	Phe	Asn	Tyr	Gly
1				5					10				15		
Val	Leu	Val	Thr	Ile	Met	Ile	Ser	Val	Ser	Val	Val	Phe	Phe	Gly	Thr
			20					25					30		
Leu	Ile	Gly	Val	Leu	Val	Thr	Leu	Ile	Lys	Arg	Ser	His	Val	Lys	Pro
		35					40					45			
Leu	Thr	Trp	Val	Val	Asn	Leu	Tyr	Val	Trp	Ile	Phe	Arg	Gly	Thr	Pro
	50					55					60				
Met	Val	Val	Gln	Ile	Met	Ile	Ala	Phe	Ala	Trp	Met	His	Phe	Asn	Asn
65				70					75					80	
Met	Pro	Thr	Ile	Gly	Phe	Gly	Val	Leu	Asp	Leu	Asp	Phe	Ser	Arg	Leu
			85					90					95		
Leu	Pro	Gly	Ile	Ile	Ile	Ile	Ser	Leu	Asn	Ser	Gly	Ala	Tyr	Ile	Ser
		100						105					110		
Glu	Ile	Val	Arg	Ala	Gly	Ile	Glu	Ala	Val	Pro	Lys	Gly	Gln	Leu	Glu
	115						120					125			
Ala	Ala	Tyr	Ser	Leu	Gly	Ile	Arg	Pro	Gln	Asn	Ala	Met	Arg	Tyr	Val
	130					135					140				
Ile	Leu	Pro	Gln	Ala	Phe	Lys	Asn	Ile	Leu	Pro	Ala	Leu	Gly	Asn	Glu
145				150					155					160	
Phe	Ile	Thr	Ile	Ile	Lys	Asp	Ser	Ala	Leu	Leu	Gln	Thr	Ile	Gly	Val
			165					170					175		
Met	Glu	Leu	Trp	Asn	Gly	Ala	Gln	Ser	Val	Val	Thr	Ala	Thr	Tyr	Ser
		180						185					190		
Pro	Ile	Ser	Pro	Leu	Leu	Val	Ala	Ala	Phe	Tyr	Tyr	Leu	Met	Val	Thr
	195					200						205			
Thr	Val	Met	Ala	Gln	Leu	Leu	Ala	Val	Leu	Glu	Arg	His	Met	Ala	Gln
	210				215						220				
Gly	Gly	Asn	His												
225															

<210> SEQ ID NO 283
 <211> LENGTH: 432
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 283

gtgccgccag	ttgatccaac	aatgttagct	gtaactgtgg	cagtttcaga	cgtgtcttcc	60
agtttagctt	taatgtcagc	taagctatcc	ttgctaaaac	cggctttggc	caaagcatca	120
tcaatctgct	tttcatcaac	ttcaaggctc	ttaagagacg	ttctaaattc	ttcaagtttt	180
ttatcaaaat	cttgctcttt	agtgtcagca	tcagataaaa	attttttgag	tcgctcatcg	240
actgccttgg	ctagctcctc	agcttccagc	acttttagcgt	taacctcagc	aactttgacc	300
tctgcattag	cttcagcttt	tttgatgcca	tcttcaatct	cttcacggag	tttagcttct	360
tttgtgtcaa	aaatacgatt	agcattatca	atctgctttt	gtaattttgc	ttcaaatgct	420
gcgtcatggt	ga					432

<210> SEQ ID NO 284
 <211> LENGTH: 143
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 284

```

Met Pro Pro Val Asp Pro Thr Met Leu Ala Val Thr Val Ala Val Ser
1          5          10          15
Asp Val Ser Ser Ser Leu Ala Leu Met Ser Ala Lys Leu Ser Leu Leu
          20          25          30
Lys Pro Ala Leu Ala Lys Ala Ser Ser Ile Cys Phe Ser Ser Thr Ser
          35          40          45
Arg Ser Leu Arg Asp Val Leu Asn Ser Ser Ser Phe Leu Ser Lys Ser
          50          55          60
Cys Ser Leu Val Ser Ala Ser Asp Lys Asn Phe Leu Ser Arg Ser Ser
65          70          75          80
Thr Ala Leu Ala Ser Ser Ser Ala Ser Ser Thr Leu Ala Leu Thr Ser
          85          90          95
Ala Thr Leu Thr Ser Ala Leu Ala Ser Ala Phe Leu Met Pro Ser Ser
          100         105         110
Ile Ser Ser Arg Ser Leu Ala Ser Phe Val Ser Lys Ile Arg Leu Ala
          115         120         125
Leu Ser Ile Cys Phe Cys Asn Phe Ala Ser Asn Ala Ala Ser Cys
          130         135         140

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<210> SEQ ID NO 285
 <211> LENGTH: 807
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 285

```

atggatatgt ctaaatacaaa tcgtcgtact tggcaagggt tagttgttat tttaatagct      60
attctcacca cttttaccac aagtactgtt acggcagcca gaaaaattag aaatttcctt      120
gataccacgg aaattttgtt aggaacgaag gcgactgaga caccaggaat cttaccattc      180
actggtagct accaattagt ttggggcgat cttgacaatc tgcaaaggcc aaccttcgca      240
cacatccagc taaaagatca agatgagcct aatattaaac gaaaaggact taaattcaat      300
cctcctggct ggcataatta caaattgact gacgctaatt gaaaaacaac ttggttaatt      360
gaccgtggcc atttagttgg ttaccaattt agcggcttaa atgacgagcc taaaaaccta      420
gttacaatga caaaatatct taatactggc tttagtgaac aaaatccttt aggaatgctc      480
tattatgaaa atagattaga tagctggtta gctctacacc ctaacttctg gctagactat      540
aaagttactc ctgtttatca taaaaatgag ttagttcctc gccaaagtag tctacagtat      600
gttggaattg atgaaaatgg agatctactt caaattaagt taggtagtga aaaagaaagt      660
gtagacaact ttggagtaac atcagttaca ttagataacg tatctccttt agctgaattg      720
gattaccaaa caggaatgat gctagattca actcaaaacg aagaagatag taatttagaa      780
accgaagagt ttgaagaagc ggcttaa                                807

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<210> SEQ ID NO 286
 <211> LENGTH: 268
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 286

```

Met Asp Met Ser Lys Ser Asn Arg Arg Thr Trp Gln Gly Leu Val Val
1          5          10          15
Ile Leu Ile Ala Ile Leu Thr Thr Phe Thr Thr Ser Thr Val Thr Ala
          20          25          30
Ala Arg Lys Ile Arg Asn Phe Pro Asp Thr Thr Glu Ile Leu Leu Gly
          35          40          45
Thr Lys Ala Thr Glu Thr Pro Gly Ile Leu Pro Phe Thr Gly Ser Tyr
          50          55          60

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Gln	Leu	Val	Leu	Gly	Asp	Leu	Asp	Asn	Leu	Gln	Arg	Pro	Thr	Phe	Ala
65					70					75					80
His	Ile	Gln	Leu	Lys	Asp	Gln	Asp	Glu	Pro	Asn	Ile	Lys	Arg	Lys	Gly
				85						90					95
Leu	Lys	Phe	Asn	Pro	Pro	Gly	Trp	His	Asn	Tyr	Lys	Leu	Thr	Asp	Ala
			100						105					110	
Asn	Gly	Lys	Thr	Thr	Trp	Leu	Met	Asp	Arg	Gly	His	Leu	Val	Gly	Tyr
		115					120					125			
Gln	Phe	Ser	Gly	Leu	Asn	Asp	Glu	Pro	Lys	Asn	Leu	Val	Thr	Met	Thr
	130					135					140				
Lys	Tyr	Leu	Asn	Thr	Gly	Phe	Ser	Asp	Lys	Asn	Pro	Leu	Gly	Met	Leu
145					150					155					160
Tyr	Tyr	Glu	Asn	Arg	Leu	Asp	Ser	Trp	Leu	Ala	Leu	His	Pro	Asn	Phe
			165						170						175
Trp	Leu	Asp	Tyr	Lys	Val	Thr	Pro	Val	Tyr	His	Lys	Asn	Glu	Leu	Val
			180						185				190		
Pro	Arg	Gln	Val	Val	Leu	Gln	Tyr	Val	Gly	Ile	Asp	Glu	Asn	Gly	Asp
	195						200					205			
Leu	Leu	Gln	Ile	Lys	Leu	Gly	Ser	Glu	Lys	Glu	Ser	Val	Asp	Asn	Phe
	210					215					220				
Gly	Val	Thr	Ser	Val	Thr	Leu	Asp	Asn	Val	Ser	Pro	Leu	Ala	Glu	Leu
225					230					235					240
Asp	Tyr	Gln	Thr	Gly	Met	Met	Leu	Asp	Ser	Thr	Gln	Asn	Glu	Glu	Asp
			245						250					255	
Ser	Asn	Leu	Glu	Thr	Glu	Glu	Phe	Glu	Glu	Ala	Ala				
			260						265						

<210> SEQ ID NO 287

<211> LENGTH: 1863

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 287

atgacaatca	gacaatggat	ggcagaccat	cttcatttga	tggagacttt	agcgtgtttg	60
gtattaataa	taattggcct	agccttttta	cactcatttc	cacaagtggc	ttccgctatt	120
ttcattacag	ccttccttgat	tggaggatat	gcgtctgcaa	aaacgggtat	attggatttg	180
gtgaagaaca	aacacttgtc	agtggatatt	ttgatgattt	tggcagctat	cggtgctgga	240
attatcggtc	attggctgga	gggtgctctg	cttattttta	tcttttcgtt	gtccaatacg	300
cttgaagaaa	tggccatgga	aaaaagtaag	gatgctattt	cagccttgat	gtccttgacg	360
ccagatacag	ctcgtcaata	ccaagaagat	ggccatattt	tagaagtga	gaccagatcc	420
ttgagtgttg	gtgaccgttt	acaagttcgt	aaaggcgaag	ctgttccaat	tgacgggcag	480
ttgcttagtc	cttttggtca	atttgatgaa	tctatggtca	ctggtgagcc	tatcactggt	540
gataaggcag	aaggccagga	tctgattggg	ggaaccatta	accaaggaca	aaccatagat	600
atgttggtta	ctattgaaaa	tgacgatact	ctctttgcc	agattattaa	tctggtggaa	660
tctgccccag	aaaagaaaa	caaaaccgcc	acctttatcg	aaagcttaga	agatggttat	720
gtcaaatttg	tgctcgtcct	tattcctgcc	tttatcctct	ttagccactt	tgtgctttct	780
tggacttggt	tggctgcttt	ttaccgaggg	atgattctct	taacagtagc	ttcaccatgt	840
gccctaattg	ccagttccac	acctgctagc	ttggctgcta	tttctcgtgc	agccagaaa	900
ggattgatta	tcaaaggagg	ggatattgtc	gataacatgg	gagatattaa	ggctgtgtgc	960
atggataaaa	cgggaacgct	cacccaagga	aaaccttctg	ttgtgaatgc	tcattatttg	1020
gaagatgagt	tgctcgtgaa	tagactggta	aaaggagcag	agactgctag	taccatcctt	1080
atttctaaag	cccttcttga	atacactgaa	aaattggagc	cactgacctt	tgaccactta	1140
gaagaaaattt	ctgggaaaag	ttttcagggc	ttctatcaag	ggcaagaatg	gcgaattggc	1200
aagaaaacct	acattttgga	aaaggttcaa	gacctatcag	cttttgaaga	aactattcaa	1260
gtggaagaaa	atcaagggaa	aaccctaata	tttgtttcac	gtgaccatca	attgatagct	1320
tactatgccc	tcttggtatga	tatcaaaaata	gaatcaaaac	gtgctattaa	gtctcttcac	1380
gccatgggaa	tcaaaacagt	catgttaaca	ggtgaccaag	aacgaaccgc	caattatgtg	1440
gcacaaaaaac	ttggtattga	tgaagtggta	gcccaactgta	tgccctcaaga	taagggtggct	1500

aagttagcag aattaaagac taaatatggt tttgtggcta tggtaggaga tggtattaat	1560
gatgctcctg cccttgctca agcagatggt tcttatgcta ttggatcagg aacagatatt	1620
gcaatggaaa gtgcagacag tgtgattatg gatgacttga ctcgtattcc attttcgatt	1680
caactttccc gcacaatgaa gaccattatc aaacaaaata ttgtttttgc cttatctgtg	1740
attaccttat tgatttttagc caatgttttt caggtagtta acttgccgct tggtgttggt	1800
ggacacgaag gctcaacgat tttagtgttt ttaaattggct tgcgtttact ttcttttaaa	1860
taa	1863

<210> SEQ ID NO 288
 <211> LENGTH: 620
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 288

Met Thr Ile Arg Gln Trp Met Ala Asp His Leu His Leu Met Glu Thr	
1 5 10 15	
Leu Ala Cys Leu Val Leu Ile Ile Ile Gly Leu Ala Phe Leu His Ser	
20 25 30	
Phe Pro Gln Val Ala Ser Ala Ile Phe Ile Thr Ala Phe Leu Ile Gly	
35 40 45	
Gly Tyr Ala Ser Ala Lys Thr Gly Ile Leu Asp Leu Val Lys Asn Lys	
50 55 60	
His Leu Ser Val Asp Ile Leu Met Ile Leu Ala Ala Ile Gly Ala Gly	
65 70 75 80	
Ile Ile Gly Tyr Trp Leu Glu Gly Ala Leu Leu Ile Phe Ile Phe Ser	
85 90 95	
Leu Ser Asn Thr Leu Glu Glu Met Ala Met Glu Lys Ser Lys Asp Ala	
100 105 110	
Ile Ser Ala Leu Met Ser Leu Thr Pro Asp Thr Ala Arg Gln Tyr Gln	
115 120 125	
Glu Asp Gly His Ile Leu Glu Val Glu Thr Arg Ser Leu Ser Val Gly	
130 135 140	
Asp Arg Leu Gln Val Arg Lys Gly Glu Ala Val Pro Ile Asp Gly Gln	
145 150 155 160	
Leu Leu Ser Pro Phe Gly Gln Phe Asp Glu Ser Met Val Thr Gly Glu	
165 170 175	
Pro Ile Thr Val Asp Lys Ala Glu Gly Gln Asp Leu Ile Gly Gly Thr	
180 185 190	
Ile Asn Gln Gly Gln Thr Ile Asp Met Leu Val Thr Ile Glu Asn Asp	
195 200 205	
Asp Thr Leu Phe Ala Lys Ile Ile Asn Leu Val Glu Ser Ala Gln Glu	
210 215 220	
Lys Lys Ser Lys Thr Ala Thr Phe Ile Glu Ser Leu Glu Asp Gly Tyr	
225 230 235 240	
Val Lys Phe Val Leu Val Leu Ile Pro Ala Phe Ile Leu Phe Ser His	
245 250 255	
Phe Val Leu Ser Trp Thr Trp Leu Ala Ala Phe Tyr Arg Gly Met Ile	
260 265 270	
Leu Leu Thr Val Ala Ser Pro Cys Ala Leu Ile Ala Ser Ser Thr Pro	
275 280 285	
Ala Ser Leu Ala Ala Ile Ser Arg Ala Ala Arg Lys Gly Leu Ile Ile	
290 295 300	
Lys Gly Gly Asp Ile Val Asp Asn Met Gly Asp Ile Lys Ala Val Val	
305 310 315 320	
Met Asp Lys Thr Gly Thr Leu Thr Gln Gly Lys Pro Ser Val Val Asn	
325 330 335	
Ala His Tyr Leu Glu Asp Glu Leu Leu Val Asn Arg Leu Val Lys Gly	
340 345 350	

<211> LENGTH: 293

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 290

```
Met Ile Met Thr Ser Pro Phe Leu Leu Lys Gly Leu Ala Phe Phe Arg
1           5           10          15
Lys Ile Asp Ile Leu Lys Cys Val Phe Val Asn Thr Val Thr Lys Gly
20          25          30
Asp Ile Met Lys Thr Pro Glu Gln Ile Leu Glu Ala Thr Ile His Ile
35          40          45
Gly Glu His Lys Val Thr Lys Thr Phe Leu Ala Lys Ser Ile Leu Gly
50          55          60
Phe Ile Gly Gly Ala Met Ile Ser Leu Gly Tyr Leu Leu Tyr Val Arg
65          70          75          80
Ile Ala Ala Ser Gly Leu Glu Thr Phe Gly Ala Phe Ser Ser Ile Val
85          90          95
Gly Ala Cys Ala Phe Pro Ile Gly Leu Ile Ile Ile Leu Met Ala Gly
100         105         110
Gly Glu Leu Ile Thr Gly Asn Met Met Ala Val Ser Ala Ala Leu Leu
115         120         125
Ala Lys Lys Ile Lys Phe Ser Glu Leu Ala Lys Asn Trp Leu Ile Ile
130         135         140
Thr Leu Phe Asn Val Ile Gly Ala Val Phe Val Ala Phe Val Phe Gly
145         150         155         160
His Phe Leu Gly Leu Thr Ser Ala Gly Ile Phe Lys Glu Glu Val Ile
165         170         175
Glu Val Ala His Ala Lys Ile Ala Ala Ser Pro Leu Gln Ala Leu Val
180         185         190
Ser Gly Ile Gly Cys Asn Trp Phe Val Gly Leu Ala Leu Trp Leu Cys
195         200         205
Tyr Gly Ala Asn Asp Ala Ala Gly Lys Phe Leu Gly Thr Trp Phe Pro
210         215         220
Val Met Thr Phe Val Ala Leu Gly Phe Gln His Ser Val Ala Asn Ala
225         230         235         240
Phe Val Ile Pro Ala Ala Ile Phe Glu Gly Gly Ala Thr Trp Leu Asp
245         250         255
Phe Val Thr Asn Phe Ile Phe Val Tyr Ser Gly Asn Ile Ile Gly Gly
260         265         270
Ala Ile Phe Val Ser Phe Leu Tyr Phe Lys Val Tyr Tyr His Pro Gln
275         280         285
Lys Ser Lys Thr Gln
290
```

<210> SEQ ID NO 291

<211> LENGTH: 696

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 291

```
atggattttt ttgcaattga ccccatcgga ctgcctcata cctcacttat cttttacttg      60
tcgtcactct tgatagcgct tttgcttggt tttttgactt ttcaagcata taggttaaaa      120
tctcatcggt attttttctt gtttttacag ttatctcagg tgattggctt atacacatgg      180
tacgtggttaa ggggggtttcc tttagatgaa gctttgccgt tgtatcattg tcgcatcgct      240
atgtagtcta tcttttttct acctgatcgt aacaagttta agcaattatt tatggttttg      300
gggtaggttg gaacattcct tgcactttta tcgccagatc tttatccgtt tagattatgg      360
catgtagcaa atgtctcggt ttattttggt cattatgctt tgtagtgtaa tggtttgatt      420
tacctcttgc gtttttacga tgccagtcag ttaagactgc tatcagtagt acgctattta      480
gcaactgtta actttcttct tctgttggtc agtttagcca cgaaaggaaa ttatggtttt      540
```

gtgatggata	ttccagtgat	tcatacgcgt	catttgctac	ttaattttgt	gatcggtaca	600
agtggcttga	cttttatggt	taaaataacc	gaatattttt	accttaaatt	tggtgaagct	660
caacagctgg	cacttgcttt	ctctaaagaa	aagtag			696

<210> SEQ ID NO 292
 <211> LENGTH: 231
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 292

Met	Asp	Phe	Phe	Ala	Ile	Asp	Pro	Ile	Gly	Leu	Pro	His	Thr	Ser	Leu
1				5					10					15	
Ile	Phe	Tyr	Leu	Ser	Ser	Leu	Leu	Ile	Ala	Leu	Leu	Leu	Val	Phe	Leu
			20					25					30		
Thr	Phe	Gln	Ala	Tyr	Arg	Leu	Lys	Ser	His	Arg	Tyr	Phe	Phe	Leu	Phe
			35				40					45			
Leu	Gln	Leu	Ser	Gln	Val	Ile	Gly	Leu	Tyr	Thr	Trp	Tyr	Val	Leu	Arg
	50					55					60				
Gly	Phe	Pro	Leu	Asp	Glu	Ala	Leu	Pro	Leu	Tyr	His	Cys	Arg	Ile	Ala
65				70					75					80	
Met	Leu	Ala	Ile	Phe	Phe	Leu	Pro	Asp	Arg	Asn	Lys	Phe	Lys	Gln	Leu
			85					90						95	
Phe	Met	Val	Leu	Gly	Ile	Gly	Gly	Thr	Phe	Leu	Ala	Leu	Leu	Ser	Pro
			100					105						110	
Asp	Leu	Tyr	Pro	Phe	Arg	Leu	Trp	His	Val	Ala	Asn	Val	Ser	Phe	Tyr
		115					120					125			
Phe	Gly	His	Tyr	Ala	Leu	Leu	Val	Asn	Gly	Leu	Ile	Tyr	Leu	Leu	Arg
	130						135				140				
Phe	Tyr	Asp	Ala	Ser	Gln	Leu	Arg	Leu	Leu	Ser	Val	Val	Arg	Tyr	Leu
145					150					155				160	
Ala	Thr	Val	Asn	Phe	Leu	Leu	Leu	Val	Ser	Leu	Ala	Thr	Lys	Gly	
			165					170						175	
Asn	Tyr	Gly	Phe	Val	Met	Asp	Ile	Pro	Val	Ile	His	Thr	Arg	His	Leu
			180					185					190		
Leu	Leu	Asn	Phe	Val	Ile	Val	Thr	Ser	Gly	Leu	Thr	Phe	Met	Val	Lys
		195					200					205			
Ile	Thr	Glu	Tyr	Phe	Tyr	Leu	Lys	Phe	Gly	Glu	Ala	Gln	Gln	Leu	Ala
	210					215					220				
Leu	Ala	Phe	Ser	Lys	Glu	Lys									
225						230									

<210> SEQ ID NO 293
 <211> LENGTH: 663
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 293

atgtagacg	aattattaat	taaaggaaaa	tcgtttttga	gagagcggta	ttttctgcca	60
tacctaatta	gtcttttatt	aggacttttt	ctaatactaa	gcttcagttt	tttggtctgg	120
ggaaataggc	agagcaaggc	agccgttcct	gctttgagag	aaatatcgcc	tgtgaaacag	180
caggtttagt	aagaaaaaaa	ggaaattcaa	gaagatagca	gtatttttagt	ggatttaaaa	240
ggcgccgtac	aaaaagaggg	agttttataa	ctaactgcta	gcagtcgtgt	gcgagatgtc	300
attgaactag	ctggaggcct	aacttcagaa	gctgataaac	atgctattaa	ttttgcagaa	360
aaactaactg	atgagcaagt	tgtttatgta	cctaaacaag	gagaagagat	ttctgtgcta	420
ccaagatcat	tagtttctg	taaaaaagaa	actgccagca	aggatcagtc	aaaggttcat	480
attaataagg	ccagcttaga	agaactacaa	catatcccag	gtattggtgc	taaaagagct	540
caggatatta	ttgatatgag	agataagtta	ggtgggttta	aagcgtaga	agatctccgt	600
cagggttcgg	ggattggcga	aaaaacgctc	gagaaaattaa	aagatgacat	tttcttggtac	660
taa						663

aaggaactgg	ctacattaca	tgggtatata	ttgacagctt	gggcaatagc	tgcattaact	1080
ggacctatgt	tattatctat	cactgttgaa	tggaactcata	attatcttct	taccttatgt	1140
gtttttattg	tcttatacat	tttaggatta	atggtagcat	taagggtaaa	gaaatga	1197

<210> SEQ ID NO 296
 <211> LENGTH: 398
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 296

Met	Glu	Lys	Thr	Lys	Arg	Tyr	Ile	Ile	Ala	Thr	Ala	Gly	Ile	Leu	Leu	1	5	10	15
His	Leu	Met	Leu	Gly	Ser	Thr	Tyr	Ala	Trp	Ser	Val	Tyr	Arg	Asn	Pro	20	25	30	
Ile	Leu	Gln	Glu	Thr	Gly	Trp	Asp	Gln	Ala	Pro	Val	Ala	Phe	Ala	Phe	35	40	45	
Ser	Leu	Ala	Ile	Phe	Cys	Leu	Gly	Leu	Ser	Ala	Ala	Phe	Met	Gly	Asn	50	55	60	
Leu	Val	Glu	Gln	Tyr	Gly	Pro	Arg	Leu	Thr	Gly	Thr	Val	Ser	Ala	Ile	65	70	75	80
Leu	Tyr	Ala	Ser	Gly	Asn	Met	Leu	Thr	Gly	Leu	Ala	Ile	Asp	Arg	Lys	85	90	95	
Glu	Ile	Trp	Leu	Leu	Tyr	Ile	Gly	Tyr	Gly	Val	Ile	Gly	Gly	Leu	Gly	100	105	110	
Leu	Gly	Ala	Gly	Tyr	Ile	Thr	Pro	Ile	Ser	Thr	Ile	Ile	Lys	Trp	Phe	115	120	125	
Pro	Asp	Lys	Arg	Gly	Met	Ala	Thr	Gly	Phe	Ala	Ile	Met	Gly	Phe	Gly	130	135	140	
Phe	Ala	Ser	Leu	Leu	Thr	Ser	Pro	Ile	Ala	Gln	Trp	Leu	Ile	Glu	Thr	145	150	155	160
Glu	Gly	Leu	Val	Ala	Thr	Phe	Tyr	Leu	Leu	Gly	Leu	Ile	Tyr	Leu	Ile	165	170	175	
Val	Met	Leu	Phe	Ala	Ser	Gln	Leu	Ile	Lys	Pro	Thr	Ala	Ala	Glu		180	185	190	
Ile	Ala	Ile	Leu	Asp	Lys	Lys	Arg	Leu	Gln	Asn	Asn	Ser	Tyr	Leu	Ile	195	200	205	
Glu	Gly	Met	Thr	Ala	Lys	Glu	Ala	Leu	Lys	Thr	Lys	Ser	Phe	Tyr	Cys	210	215	220	
Leu	Trp	Val	Ile	Leu	Phe	Ile	Asn	Ile	Thr	Cys	Gly	Leu	Gly	Leu	Ile	225	230	235	240
Ser	Val	Val	Ala	Pro	Met	Ala	Gln	Asp	Leu	Thr	Gly	Met	Ser	Pro	Glu	245	250	255	
Met	Ser	Ala	Ile	Val	Val	Gly	Ala	Met	Gly	Ile	Phe	Asn	Gly	Phe	Gly	260	265	270	
Arg	Leu	Val	Trp	Ala	Ser	Leu	Ser	Asp	Tyr	Ile	Gly	Arg	Arg	Val	Thr	275	280	285	
Val	Ile	Leu	Leu	Phe	Leu	Val	Ser	Ile	Ile	Met	Thr	Ile	Ser	Leu	Ile	290	295	300	
Phe	Ala	His	Ser	Ser	Leu	Ile	Phe	Met	Ile	Ser	Ile	Ala	Thr	Leu	Met	305	310	315	320
Thr	Cys	Tyr	Gly	Ala	Gly	Phe	Ser	Leu	Ile	Pro	Pro	Tyr	Leu	Ser	Asp	325	330	335	
Leu	Phe	Gly	Ala	Lys	Glu	Leu	Ala	Thr	Leu	His	Gly	Tyr	Ile	Leu	Thr	340	345	350	
Ala	Trp	Ala	Ile	Ala	Ala	Leu	Thr	Gly	Pro	Met	Leu	Leu	Ser	Ile	Thr	355	360	365	
Val	Glu	Trp	Thr	His	Asn	Tyr	Leu	Leu	Thr	Leu	Cys	Val	Phe	Ile	Val	370	375	380	

Leu Tyr Ile Leu Gly Leu Met Val Ala Leu Arg Leu Lys Lys
 385 390 395

<210> SEQ ID NO 297
 <211> LENGTH: 696
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 297

```

atgaaaggat tcattaatta tttaaaaata gcagtgtcga ttattctggc tatgggttttc      60
aatgtccttc cgatgatttt attgcaaaaag caacacgata ttcctatggg acttaattgg      120
ggaattggta ttttctactt gggtattggt ggaagtgtcc ttattgtatt atgggggtcct      180
tatcaagcta agcaagacac ttttattaaa cagcaaaaaa tgagattggg tgactggggg      240
tatttagcat tattttgggt aatcatccgt gtgatagcta ttgtaggtac ccttggttaac      300
cagctatggg ctgggtcaaca agtgagtgtc aatgatgctg caatacatat cttagctaga      360
cttatcaaag gtgggtttccc gctttatact gccctatttg tacttgtgat agctttttatc      420
gctcctatta tggaagaact agtctttaga ggatttccta tgattgatct cttcaaagga      480
aaatcactta aggtggcagg tttagtgtacc tctcttgttt ttgctttacc acatgccacc      540
aatagtgttg aatttatcat gtacagctgt atgggcattt ttctctttgt tgcctatcaa      600
agacgaggaa acttaaaaga tgctatcttg ttacatatat ttaataactt gattgaagtc      660
attttggttaa tgtcaatagg cttaggagtc atataa                                696
  
```

<210> SEQ ID NO 298
 <211> LENGTH: 231
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 298

```

Met Lys Gly Phe Ile Asn Tyr Leu Lys Ile Ala Val Leu Ile Ile Leu
1      5      10      15
Ala Met Val Phe Asn Val Leu Pro Met Ile Leu Leu Gln Lys Gln His
20     25     30
Asp Ile Pro Met Val Leu Asn Trp Gly Ile Gly Ile Phe Tyr Leu Val
35     40     45
Ile Val Gly Ser Val Leu Ile Val Leu Trp Gly Leu Tyr Gln Ala Lys
50     55     60
Gln Asp Thr Phe Ile Lys Gln Gln Lys Met Arg Leu Val Asp Trp Gly
65     70     75     80
Tyr Leu Ala Leu Phe Trp Leu Ile Ile Arg Val Ile Ala Ile Val Gly
85     90     95
Thr Leu Val Asn Gln Leu Trp Ser Gly Gln Gln Val Ser Ala Asn Asp
100    105    110
Ala Ala Ile His Thr Leu Ala Arg Leu Ile Lys Gly Gly Phe Pro Leu
115    120    125
Tyr Thr Ala Leu Phe Val Leu Val Ile Ala Phe Ile Ala Pro Ile Met
130    135    140
Glu Glu Leu Val Phe Arg Gly Phe Pro Met Ile Asp Leu Phe Lys Gly
145    150    155    160
Lys Ser Leu Lys Val Ala Gly Leu Val Thr Ser Leu Val Phe Ala Leu
165    170    175
Pro His Ala Thr Asn Ser Val Glu Phe Ile Met Tyr Ser Cys Met Gly
180    185    190
Ile Phe Leu Phe Val Ala Tyr Gln Arg Arg Gly Asn Leu Lys Asp Ala
195    200    205
Ile Leu Leu His Ile Phe Asn Asn Leu Ile Glu Val Ile Leu Leu Met
210    215    220
Ser Ile Gly Leu Gly Val Ile
225    230
  
```

```

<210> SEQ ID NO 299
<211> LENGTH: 1314
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 299
  atgacgatta taattatgga ctctaatagt gctcacgaga ctgataatct atcagtctct      60
  tttcttaact tttgttataa tagtcttatg aaacgacact ttttactctt gaccttttac      120
  ctctttttta caggtttaac agctggcctt gttgctttta tcttaacaaa agccattcac      180
  ctgattcagt ccctcagttt tggattcagt caaggttctt ttagcactat gattgctagt      240
  gttccaccac aaagacgagc tctttcactc ctctttgctg gacttcttgc aggtcctggg      300
  tggcacctat tggctaaaaa aggaaaggac attcaatcta ttcagcaaat cattcaagat      360
  gacatctcat ttagtccctg gacacagttt tggcatggtt ggctccaatt aacgaccgta      420
  tctatgggag ctctgtcgcg ccgagaagga gcttcacggg aagtcgctgt taccttgacg      480
  tctctttgga gccaaagatg caacttgtca aaagccgatc aaaaactttt attagcctgc      540
  gcttctggcg ctgcccttgg tgctgtctac aatgctccct tagccactat tttatttatc      600
  ttagaagcta ttcttaaccg ttgggtccctt aaaaatatat acgctgcctg cctaacgagc      660
  tatgtggctg tggaaacagt tgctttatta caaggccgac atgagattca atacctaatg      720
  cctcagcaac attggacgct aggaaccctt attgggtccg tcttggtggg tcttatcctt      780
  tccctctttg ctacagctta caaacatctt ttgaaacacc ttcctaaggc tgatgccaaa      840
  agtcagtggg ttattccgaa agttctcatc gcttttagcc ttatcgcagg actcagcatt      900
  ttcttccag agattttagg aaatggcaaa gctggattac tcttttttct ccatgaagaa      960
  ccacatctga gctatattag ctggctactt gttgccaaag ctgtcgctat ctctttagtt     1020
  tttgcttctg gagcaaaagg gggtaaaatt gctccttcta tgatgcttgg aggtgctagt     1080
  ggcttactac tagctatcct tagtcagtac cttattccct tgtctctatc aaatacgta      1140
  gccattatgg ttggtgcaac aatcttttta ggtgtgatca ataagatacc cttggcggca      1200
  ccagtttttc tgggtgaaat tacaggccaa tcgttactaa tgattatccc tttagcatta      1260
  gctaacctca ttttttattt tagctatcag ttttatcggt tcatccttaa atga          1314

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<210> SEQ ID NO 300
<211> LENGTH: 437
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 300
  Met Thr Ile Ile Ile Met Asp Ser Asn Ser Ala His Glu Thr Asp Asn
  1              5              10              15
  Leu Ser Val Ser Phe Leu Asn Phe Cys Tyr Asn Ser Leu Met Lys Arg
              20              25              30
  His Phe Leu Leu Leu Thr Phe Tyr Leu Phe Leu Thr Gly Leu Thr Ala
              35              40              45
  Gly Leu Val Ala Phe Ile Leu Thr Lys Ala Ile His Leu Ile Gln Ser
              50              55              60
  Leu Ser Phe Gly Phe Ser Gln Gly Ser Phe Ser Thr Met Ile Ala Ser
  65              70              75              80
  Val Pro Pro Gln Arg Arg Ala Leu Ser Leu Leu Phe Ala Gly Leu Leu
              85              90              95
  Ala Gly Leu Gly Trp His Leu Leu Ala Lys Lys Gly Lys Asp Ile Gln
              100             105             110
  Ser Ile Gln Gln Ile Ile Gln Asp Asp Ile Ser Phe Ser Pro Trp Thr
              115             120             125
  Gln Phe Trp His Gly Trp Leu Gln Leu Thr Thr Val Ser Met Gly Ala
              130             135             140
  Pro Val Gly Arg Glu Gly Ala Ser Arg Glu Val Ala Val Thr Leu Thr
  145             150             155             160
  Ser Leu Trp Ser Gln Arg Cys Asn Leu Ser Lys Ala Asp Gln Lys Leu
              165             170             175
  Leu Leu Ala Cys Ala Ser Gly Ala Ala Leu Gly Ala Val Tyr Asn Ala
              180             185             190

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<400> SEQUENCE: 302

Met	Lys	Gln	Ile	Thr	Gln	Gln	Lys	Trp	Leu	Arg	Tyr	Gly	Leu	Phe	Ile
1				5					10					15	
Ala	Leu	Val	Leu	Asn	Gly	Ile	Glu	Leu	Glu	Leu	Leu	Gly	Leu	Thr	Ala
			20					25					30		
Asn	Asn	Leu	Ser	Phe	Lys	Glu	Ala	Phe	Ala	Leu	Ile	Leu	Thr	Ile	Ser
		35				40						45			
Leu	Leu	Gly	Ile	Tyr	Leu	Ile	Pro	Phe	Ala	Ala	Ala	Ile	Phe	Tyr	Leu
	50					55					60				
Ser	Lys	Lys	Phe	His	Met	Asn	Leu	Asn	Val	Ile	Ile	Val	Ser	Cys	Leu
65					70					75					80
Ser	Gly	Leu	Tyr	Ile	Ser	Gly	Phe	Leu	Ala	Ser	Cys	Gly	Asn	His	Leu
			85						90					95	
Val	Gly	Gln	Phe	Trp	Ser	Tyr	Ile	Ile	Pro	Ser	Lys	Asp	Ala	Leu	Lys
			100						105					110	
Leu	Trp	Gly	Asp	Ala	Leu	Thr	Ala	Pro	Ile	Val	Glu	Glu	Pro	Ile	Lys
		115					120					125			
Ala	Ser	Ser	Ala	Ile	Leu	Val	Ile	Thr	Leu	Phe	Pro	Arg	Leu	Thr	Leu
	130					135					140				
Lys	Glu	Lys	Leu	Val	Val	Ala	Leu	Leu	Ser	Gly	Met	Gly	Phe	Gln	Leu
145					150					155					160
Thr	Glu	Asp	Ile	Arg	Tyr	Leu	Ile	Gln	Ala	Lys	Ser	Ile	Asp	Ser	Leu
				165					170					175	
Val	Pro	Thr	Ala	Ile	Glu	Arg	Ile	Ser	Thr	Ala	Val	Thr	Ser	His	Trp
			180						185					190	
Val	His	Thr	Ala	Ile	Phe	Thr	Ile	Gly	Ala	Tyr	Leu	Leu	Leu	Lys	Gly
		195					200					205			
Ser	Asn	Leu	Phe	Ser	Lys	Gln	Gln	Gln	Ile	Phe	Trp	Leu	Leu	Ser	Pro
	210					215					220				
Leu	Val	Leu	His	Phe	Ile	Trp	Asn	Ser	Pro	Leu	Thr	Ser	Ile	Pro	Gly
225					230					235					240
Met	Thr	Val	Leu	Leu	Gly	Thr	Leu	Ile	Leu	Leu	Ile	Phe	Gly	Asp	Leu
				245					250					255	
Phe	Gln	Lys	Ile	Asn	Thr	Leu	Asp	Asp	Asp	Val	Leu	Phe			
			260					265							

<210> SEQ ID NO 303
 <211> LENGTH: 291
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 303

ttgggagaaa	aaccagcagc	tttactcata	atgttaccaa	acatatcatt	aagattat	60
cggctcatga	cttggtctgc	attaaaggca	gcctcgaaag	ccaaaatcgc	attctcacta	120
tttgctaaga	caggctcaga	gcccatcaat	aaggctctgt	cttgggcaga	aatgttatct	180
agaatttcat	tccaagcatt	ttttagagca	tctagatatt	gtcgagattg	ttggctat	240
cgaaccgttt	cttccatgat	tttcaaaatg	gtaaccgat	caaccctgta	g	291

<210> SEQ ID NO 304
 <211> LENGTH: 96
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 304

Met	Gly	Glu	Lys	Pro	Ala	Ala	Leu	Leu	Ile	Met	Leu	Pro	Asn	Ile	Ser
1				5					10					15	
Leu	Arg	Leu	Phe	Arg	Leu	Met	Thr	Cys	Ser	Ala	Leu	Lys	Ala	Ala	Ser
			20					25				30			
Lys	Ala	Lys	Ile	Ala	Phe	Ser	Leu	Phe	Ala	Lys	Thr	Gly	Ser	Glu	Pro


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<210> SEQ ID NO 307
<211> LENGTH: 966
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 307
```

atggcagaaa	aaaaatgggtt	tgataaggta	ctgtccaagt	ggcagtatga	accatttcaa	60
gtctttatga	ggcattttaca	aagtgcagaa	atggatttat	ctgccattgc	ggttgcgat	120
taccttatct	taacggcctt	tccattaatt	gttattgcag	ccaatatatt	tccttacctc	180
aatattgata	ttgctgattt	gttacgttta	atgaagcaaa	atttgacctaa	agatatatttt	240
agaccggctt	ctgcaattgt	agaaaaatatt	ttctctaaac	cgtctggaag	tgttttggga	300
gtagcgactt	tgacaggatt	atggacaatg	tctcgaagtt	tgacatcgct	acaaaaagct	360
attaataaag	cctatggcgc	ttctcagcat	cgaqatttct	ttatcggaca	cttqgttqgt	420

ttgttgacca	gtttaattat	tttatttttta	ttagcctttg	ccttaatcct	ttcaatatatt	480
tctaaagctg	ctattcaagt	gctggataag	cattaccatt	tgagtgataa	tatcacaaacg	540
atcttcttgc	tcctcattca	acctattaca	gttttgatta	tttttgttgg	cttgatgcta	600
ctatatTTTT	tattacccaa	tgTTAagatt	aaaaaaattc	gctacatttt	accaggaacc	660
ctattttacat	cttttTgtgat	gacatttttg	agTaatctgg	tTggcaatta	cgTgtgtat	720
aatgttgagc	ggatggTaga	tattaaaatg	tttggTtcag	Ttatgatttt	tatcatcatg	780
ctatggTtta	ttttcttagc	aagaatcctg	atTTtaggag	ctatatTTaa	Tgcgacctat	840
caagaaatgt	ccttggggaa	attagaaggt	cgtagtggtg	atatgatcgc	tatccttaaa	900
aaaacacttg	ggaatgattc	agatctatct	ccttcacagt	ctatcgaaga	tagtcacact	960
gattga						966

[illegible]


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<210> SEQ ID NO 309
<211> LENGTH: 1221
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 309
atgtcaacat tatcattgga caccacaaat aagcgagctt tagtggcagc tattgcagct      60
tcaggaacgg atgacttgaa tgtcatgttt cttgcctttt ccatgtcttc cattatgaca      120
gacttgggtc ttagtggcac tcaggggtggc tggattgcga ccattaccaa tttaggaatg      180
ttggtgggag gcctcttatt cgggttgctg gctgataggc accacaagtt taaggtcttt      240
aaatggacga ttttactgtt ttcagtagca acaggattaa tttattttac ccagtctttg      300
ccctacctgt acctgatgcg atttattgct ggcataggag ttggaggtga gtacggtgta      360
gccattgcca taatggcagg gattgtacca ccagaaaaaa tgggtcggat gtcttcttta      420
aatggtattg ctggccagct tggctctatt agttcggctc ttttagcagg gtggctggct      480
ccaagtctag gctggcgtgg cctttttctc tttggattac ttccgattct cttggtgatt      540
tggtgactt tagccataga tgacaaaaaa atttgggatac attatgggca agaggaggaa      600
gaatgcagtc aaccaattaa aatcaatgaa ctattcaaaa caaaatcctt aacagctcaa      660
acccttgctt taatggtcat gacgactgtg cagattgcgg gctatttttg aatgatgaat      720
tggttgccaa ccattattca aacaagctta aacctttcag taaaaagttc gtccttgtgg      780
atggtggcta ctattgtcgg catgtgtttg gggatgctgt attttggta gcttttagat      840
tgctttggtc cacgtctgat ttattccctc tttttattag catcatctat ttgtgtttac      900
ctttttcaat ttgccaattc catggcgagt atggttattg gaggtgctat tgtcggtttt      960
tttgtcaatg ggatgtttgc tggctacggg gctatgatta ccagacttta tccccatcac      1020
attcgatcca cggctaataa tgttattttg aatgttggcc gtgctctagg aggattttcg      1080
tccgttgcta ttggtagtat tttagatgcc tcaggatatt caatgggcat gattttccta      1140
gcttctctgt atgtgattag ttttgagacc atgtggtcta ttggtcagtt aaaagcagaa      1200
cgctaccaac aattgcgtta g                                     1221

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<210> SEQ ID NO 310
<211> LENGTH: 406
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 310
Met Ser Thr Leu Ser Leu Asp Thr Thr Asn Lys Arg Ala Leu Val Ala
1          5          10          15
Ala Ile Ala Ala Ser Gly Thr Asp Asp Leu Asn Val Met Phe Leu Ala
20          25          30
Phe Ser Met Ser Ser Ile Met Thr Asp Leu Gly Leu Ser Gly Thr Gln
35          40          45
Gly Gly Trp Ile Ala Thr Ile Thr Asn Leu Gly Met Leu Val Gly Gly
50          55          60
Leu Leu Phe Gly Leu Leu Ala Asp Arg His His Lys Phe Lys Val Phe
65          70          75          80
Lys Trp Thr Ile Leu Leu Phe Ser Val Ala Thr Gly Leu Ile Tyr Phe
85          90          95
Thr Gln Ser Leu Pro Tyr Leu Tyr Leu Met Arg Phe Ile Ala Gly Ile
100         105         110
Gly Val Gly Gly Glu Tyr Gly Val Ala Ile Ala Ile Met Ala Gly Ile
115         120         125
Val Pro Pro Glu Lys Met Gly Arg Met Ser Ser Leu Asn Gly Ile Ala
130         135         140
Gly Gln Leu Gly Ser Ile Ser Ser Ala Leu Leu Ala Gly Trp Leu Ala
145         150         155         160
Pro Ser Leu Gly Trp Arg Gly Leu Phe Leu Phe Gly Leu Leu Pro Ile
165         170         175
Leu Leu Val Ile Trp Met Thr Leu Ala Ile Asp Asp Gln Lys Ile Trp
180         185         190

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Asp	His	Tyr	Gly	Gln	Glu	Glu	Glu	Glu	Cys	Ser	Gln	Pro	Ile	Lys	Ile
		195					200					205			
Asn	Glu	Leu	Phe	Lys	Thr	Lys	Ser	Leu	Thr	Ala	Gln	Thr	Leu	Ala	Leu
	210					215					220				
Met	Val	Met	Thr	Thr	Val	Gln	Ile	Ala	Gly	Tyr	Phe	Gly	Met	Met	Asn
225					230					235					240
Trp	Leu	Pro	Thr	Ile	Ile	Gln	Thr	Ser	Leu	Asn	Leu	Ser	Val	Lys	Ser
				245					250					255	
Ser	Ser	Leu	Trp	Met	Val	Ala	Thr	Ile	Val	Gly	Met	Cys	Leu	Gly	Met
			260					265					270		
Leu	Tyr	Phe	Gly	Gln	Leu	Leu	Asp	Cys	Phe	Gly	Pro	Arg	Leu	Ile	Tyr
	275						280					285			
Ser	Leu	Phe	Leu	Leu	Ala	Ser	Ser	Ile	Cys	Val	Tyr	Leu	Phe	Gln	Phe
	290					295					300				
Ala	Asn	Ser	Met	Ala	Ser	Met	Val	Ile	Gly	Gly	Ala	Ile	Val	Gly	Phe
305					310					315					320
Phe	Val	Asn	Gly	Met	Phe	Ala	Gly	Tyr	Gly	Ala	Met	Ile	Thr	Arg	Leu
				325					330					335	
Tyr	Pro	His	His	Ile	Arg	Ser	Thr	Ala	Asn	Asn	Val	Ile	Leu	Asn	Val
			340					345					350		
Gly	Arg	Ala	Leu	Gly	Gly	Phe	Ser	Ser	Val	Ala	Ile	Gly	Ser	Ile	Leu
	355					360						365			
Asp	Ala	Ser	Gly	Ile	Ser	Met	Val	Met	Ile	Phe	Leu	Ala	Ser	Leu	Tyr
	370					375					380				
Val	Ile	Ser	Phe	Gly	Ala	Met	Trp	Ser	Ile	Gly	Gln	Leu	Lys	Ala	Glu
385					390					395					400
Arg	Tyr	Gln	Gln	Leu	Arg										
				405											

<210> SEQ ID NO 311

<211> LENGTH: 510

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 311

ttgaataggg	gtatggctta	tttaaactac	tttacaaaaa	ccgagtgggc	acttttggtta	60
agctctgtct	tggccatttt	aattagcgcc	cttttattcg	gtaagcaagc	tcccttagct	120
ttaatagctt	ctttgattgg	tgtgacctct	ctcattttta	gtgctaaagc	taatcctatt	180
ggtcaagggc	tcgtcattat	tttttccatt	atctatgcct	atcttttcatt	acgaaacagt	240
tactatggag	agttaatgac	ctatcttttt	atgaccctcc	ctatgactat	tttttcactt	300
tttacttggg	taaaccatcc	ttttgaaggg	aaaaaatcac	aagtgactat	ttcacgatta	360
acacccactg	atcgaagatg	tcttttcggt	tttactatac	tgatcactct	tattttctac	420
agcatcttgg	cttctatttc	aaacagccta	tttacttgtc	tccactttat	cgattgccac	480
ttctttctca	gcggtttatc	tcagctataa				510

<210> SEQ ID NO 312

<211> LENGTH: 169

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 312

Met	Asn	Arg	Gly	Met	Ala	Tyr	Leu	Asn	Tyr	Phe	Thr	Lys	Thr	Glu	Trp
1			5					10					15		
Ala	Leu	Trp	Leu	Ser	Ser	Val	Leu	Ala	Ile	Leu	Ile	Ser	Ala	Leu	Leu
			20					25					30		
Phe	Gly	Lys	Gln	Ala	Pro	Leu	Ala	Leu	Ile	Ala	Ser	Leu	Ile	Gly	Val
	35					40					45				
Thr	Ser	Leu	Ile	Phe	Ser	Ala	Lys	Ala	Asn	Pro	Ile	Gly	Gln	Gly	Leu
	50					55					60				

Val	Ile	Ile	Phe	Ser	Ile	Ile	Tyr	Ala	Tyr	Leu	Ser	Leu	Arg	Asn	Ser
65					70					75					80
Tyr	Tyr	Gly	Glu	Leu	Met	Thr	Tyr	Leu	Phe	Met	Thr	Leu	Pro	Met	Thr
				85					90					95	
Ile	Phe	Ser	Leu	Phe	Thr	Trp	Leu	Asn	His	Pro	Phe	Glu	Gly	Lys	Lys
			100					105					110		
Ser	Gln	Val	Thr	Ile	Ser	Arg	Leu	Thr	Pro	Thr	Asp	Arg	Arg	Cys	Leu
		115					120					125			
Phe	Val	Phe	Thr	Ile	Leu	Ile	Thr	Leu	Ile	Phe	Tyr	Ser	Ile	Leu	Ala
	130					135					140				
Ser	Ile	Ser	Asn	Ser	Leu	Phe	Thr	Cys	Leu	His	Phe	Ile	Asp	Cys	His
145					150					155					160
Phe	Phe	Leu	Ser	Gly	Leu	Ser	Gln	Leu							
					165										

<210> SEQ ID NO 313
 <211> LENGTH: 342
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 313

atgattaaaa	cgattaaaag	gagaaacctt	atgaaatcta	ttatgttagt	ttgtaatgcc	60
ggtatgtcaa	ctagtatggt	ggtgactaag	atgcaaaaag	cagcccaagc	gcgtgacctt	120
gaagtttcta	tttgggcagt	tcctgtgagt	gaagctgaca	acgaaatggc	tgctaatagc	180
attgacgttc	tcttggttagg	tccacaagtc	aaattcttac	taaaggattt	taaagataag	240
tttgaaccag	atattaaagt	agatgccatt	aacatggctg	attatggtct	tatgaacggt	300
gaaaaagtcc	ttgaaacagc	cctagcaatg	atggaggagt	ag		342

<210> SEQ ID NO 314
 <211> LENGTH: 113
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 314

Met	Ile	Lys	Thr	Ile	Lys	Arg	Arg	Asn	Leu	Met	Lys	Ser	Ile	Met	Leu
1				5					10					15	
Val	Cys	Asn	Ala	Gly	Met	Ser	Thr	Ser	Met	Leu	Val	Thr	Lys	Met	Gln
			20					25					30		
Lys	Ala	Ala	Gln	Ala	Arg	Asp	Leu	Glu	Val	Ser	Ile	Trp	Ala	Val	Pro
			35				40					45			
Val	Ser	Glu	Ala	Asp	Asn	Glu	Met	Ala	Ala	Asn	Ser	Ile	Asp	Val	Leu
	50					55					60				
Leu	Leu	Gly	Pro	Gln	Val	Lys	Phe	Leu	Leu	Lys	Asp	Phe	Lys	Asp	Lys
65				70						75					80
Phe	Glu	Pro	Asp	Ile	Lys	Val	Asp	Ala	Ile	Asn	Met	Ala	Asp	Tyr	Gly
				85					90					95	
Leu	Met	Asn	Gly	Glu	Lys	Val	Leu	Glu	Thr	Ala	Leu	Ala	Met	Met	Glu
			100					105					110		
Glu															

<210> SEQ ID NO 315
 <211> LENGTH: 816
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 315

ttgaccaaac	gtaatattac	cattaccta	ccagataatg	taccacctgc	ggttaataaa	60
gcctttgctg	ccattattcc	aggaacagtt	gcgatttacg	cttcggcaat	tttcgcctac	120
ctcattttcg	cattaacagg	ttcttccta	agtgatgtca	tttcaaccta	tatccaatta	180
ccattgctag	gcttatcaca	gggtattggt	tcagttatct	tgtaaacctt	cttagttcaa	240

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ctgctctggt tcttcggcctt gcatgggtcat aatgtcttag ccccagtgat ggatgggtatt 300
tatatggtag ctttaacaga aaatacagct gcttacaata cagcgcatag cgctgctaata 360
ttaccataacc tttggacacg cgggtccttt gatgcttatg ctcaaaggg tgggttcagga 420
gtaaccttgg cattgattat tgctatcttc atattctcaa aacgagaaga gcataaaacc 480
attgccaaat tgtccgcacc aatgggtggt ttcaatatca acgaaccaat tacatttggg 540
atgccaaattg ttttgaatcc aacctttgtg attccatggc taattgtgcc accaatttgt 600
gctagcatag cttattttgc tactgcaata ggtttgattc caccggtatt cttatcagta 660
ccttggatta cccctggttg actttatgct tacctagcta ctggaggtaa tattatggca 720
ggtttggttt cactgtttaa cctctttgtt gccttcctta tctgggcacc atttgtcatt 780
ttggccaata aagaaaaagc gagtgacctt gcatga 816

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<210> SEQ ID NO 316

<211> LENGTH: 271

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 316

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Met Thr Lys Arg Asn Ile Thr Ile Thr Leu Pro Asp Asn Val Pro Pro
1           5           10           15
Ala Val Asn Lys Ala Phe Ala Ala Ile Ile Pro Gly Thr Val Ala Ile
          20           25           30
Tyr Ala Ser Ala Ile Phe Ala Tyr Leu Ile Phe Ala Leu Thr Gly Ser
          35           40           45
Ser Leu Ser Asp Val Ile Ser Thr Tyr Ile Gln Leu Pro Leu Leu Gly
          50           55           60
Leu Ser Gln Gly Ile Gly Ser Val Ile Leu Leu Thr Phe Leu Val Gln
65           70           75           80
Leu Leu Trp Phe Phe Gly Leu His Gly His Asn Val Leu Ala Pro Val
          85           90           95
Met Asp Gly Ile Tyr Met Val Ala Leu Thr Glu Asn Thr Ala Ala Tyr
          100          105          110
Asn Thr Ala His Ser Ala Ala Asn Leu Pro Tyr Leu Trp Thr Arg Gly
          115          120          125
Ser Phe Asp Ala Tyr Ala Gln Met Gly Gly Ser Gly Val Thr Leu Ala
          130          135          140
Leu Ile Ile Ala Ile Phe Ile Phe Ser Lys Arg Glu Glu His Lys Thr
145          150          155          160
Ile Ala Lys Leu Ser Ala Pro Met Gly Val Phe Asn Ile Asn Glu Pro
          165          170          175
Ile Thr Phe Gly Met Pro Ile Val Leu Asn Pro Thr Phe Val Ile Pro
          180          185          190
Trp Leu Ile Val Pro Pro Ile Cys Ala Ser Ile Ala Tyr Phe Ala Thr
          195          200          205
Ala Ile Gly Leu Ile Pro Pro Val Phe Leu Ser Val Pro Trp Ile Thr
          210          215          220
Pro Val Gly Leu Tyr Ala Tyr Leu Ala Thr Gly Gly Asn Ile Met Ala
225          230          235          240
Gly Leu Val Ser Leu Phe Asn Leu Phe Val Ala Phe Leu Ile Trp Ala
          245          250          255
Pro Phe Val Ile Leu Ala Asn Lys Glu Lys Ala Ser Asp Leu Ala
          260          265          270

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<210> SEQ ID NO 317

<211> LENGTH: 2175

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 317

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atgacgcaca aaataaaagt attgctgctt gcgataatgt ctattttttt gacatgcaat 60

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attgcaagtg ctgaaactat tgctattggt tcagatacag cttatgcccc atttgaattt 120
aaagactcag atcaaattta caaaggaatt gacgttgata ttattaatga agtagccaaa 180
cgtcaatctt gggatttcag tatgagtttc ccgggttttg atgcagctgt aaatgctgtt 240
caatctgggtc aagcgagtgc tctaattggcc ggtacaacca ttacgaatgc tcgtaagaaa 300
gtcttttcatt tctcagagcc atattacgat accaaaattg tcattgcgac acgtaaagcc 360
aatgccatca aaaaatacag tgacttaaaa ggaaaaaacgg tcggtgttaa aaatggaaca 420
gcgggtcaag ccttttttgaa taactataaa aaaaagtatg attatactgt taaaacattt 480
gacacagggtg atcttatgta taatagttta tctgctgggt ctattgccgc tgttatggat 540
gatgaggcgg ttatccaata cgcaatcagc caaaaccaag atattgctat taacatgaaa 600
ggagagccca ttggaagctt tgggtttgct gtcaaaaagg gaagcggata tgattatcta 660
gttaatgatt tcaatacagc tcttaaagct atgaaagctg atggtacctt ccaagctatc 720
atgaccaagt ggtaggcac agatgataaa gctaccacca gtcaggcaac gggaaatcca 780
tctgccaaag ctacacctac aaaggacagt tataaaattg tctctgattc gtcttttgca 840
ccgtttggaat ttcaaaatgg taagggcaaa tacgttggtt ttgacataga attaatcaaa 900
gctattgcta aacaacaagg tttcaaaatt gaaatcgcta atccaggttt cgaatgctgcc 960
ttaaatgctg tgcaatctag ccaagcagat ggggtcattg ctggtgcaac tattactgac 1020
gctcgtaaag ctatctttga tttttctgat ccttattata cttctaatat catttttagct 1080
gttaaagctg gaaaaaacat caagaactat gaagacttag acagaaaaaac agtcggtgct 1140
aaaaacggca cttcatctta ctcttggtta aaagaaaacg ctcctaaata tgggtataat 1200
gtcaaggcat ttgatgatgg ttctagcatg tatgatagct taaattcagg ttctgtagat 1260
gctatcatgg atgatgaggc ggttcttaaa tacgctatct ctcaaggctg tcgctttgaa 1320
acacctcttg agggcatttc tactggtgaa gttgggtttg ctgtcaagaa aggaactaat 1380
ccagaattaa tcgaaatggt caacaatggc ttagctgctc tcaaaaaatc tggtcagtat 1440
gatgacatta tagataaata ccttgactct aagaaagctg caactccttc tgaaaaaggt 1500
gctgatgagt ctactatttc aggcctatta tcaaataact acaaacact attggcagga 1560
cttggaacca cgctcagttt aacccttatt tcatttgcta ttgctataat tatcgggatc 1620
atctttggga tgatggccgt gtcaccaact aaatcacttc gacttatttc aacggtcttt 1680
gtggacgttg ttcgagggat tcctttgatg attgtggctg ccttcatttt ctggggagta 1740
ccaaacctta tcgagagtat gaccggccac cagtcaccga ttaatgattt cttagctgct 1800
acaattgcac tgtcacttaa tggcggagcc tatattgctg aaattgttcg cgggtggtatc 1860
gaagctgttc cagcagggca aatggaagct agtcgaagtc ttggtttgtc ttacggaacc 1920
acgatgagaa aagtaattct cccacaagct gtgaaactaa tgttacctaa ctttatcaat 1980
cagtttgtaa tttcattgaa ggatacaaca atcgtctcag caattggttt agtggaaactc 2040
ttccaaacag gtaaaatcat tattgctaga aattaccagt cgttccgtat gtatgctatt 2100
ttagcaatta tttaccttat catgattata ctcttaacaa gacttgcaaa acgtttagaa 2160
aagaggctta actaa 2175

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<210> SEQ ID NO 318

<211> LENGTH: 724

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 318

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Met Thr His Lys Ile Lys Val Leu Leu Leu Ala Ile Met Ser Ile Phe
1           5           10           15
Leu Thr Cys Asn Ile Ala Ser Ala Glu Thr Ile Ala Ile Val Ser Asp
20          25          30
Thr Ala Tyr Ala Pro Phe Glu Phe Lys Asp Ser Asp Gln Ile Tyr Lys
35          40          45
Gly Ile Asp Val Asp Ile Ile Asn Glu Val Ala Lys Arg Gln Ser Trp
50          55          60
Asp Phe Ser Met Ser Phe Pro Gly Phe Asp Ala Val Asn Ala Val
65          70          75          80
Gln Ser Gly Gln Ala Ser Ala Leu Met Ala Gly Thr Thr Ile Thr Asn
85          90          95
Ala Arg Lys Lys Val Phe His Phe Ser Glu Pro Tyr Tyr Asp Thr Lys
100         105         110
Ile Val Ile Ala Thr Arg Lys Ala Asn Ala Ile Lys Lys Tyr Ser Asp

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		115					120				125						
Leu	Lys	Gly	Lys	Thr	Val	Gly	Val	Lys	Asn	Gly	Thr	Ala	Ala	Gln	Ala		
	130					135					140						
Phe	Leu	Asn	Asn	Tyr	Lys	Lys	Lys	Tyr	Asp	Tyr	Thr	Val	Lys	Thr	Phe		
145					150					155					160		
Asp	Thr	Gly	Asp	Leu	Met	Tyr	Asn	Ser	Leu	Ser	Ala	Gly	Ser	Ile	Ala		
			165						170					175			
Ala	Val	Met	Asp	Asp	Glu	Ala	Val	Ile	Gln	Tyr	Ala	Ile	Ser	Gln	Asn		
			180					185					190				
Gln	Asp	Ile	Ala	Ile	Asn	Met	Lys	Gly	Glu	Pro	Ile	Gly	Ser	Phe	Gly		
	195						200					205					
Phe	Ala	Val	Lys	Lys	Gly	Ser	Gly	Tyr	Asp	Tyr	Leu	Val	Asn	Asp	Phe		
210						215					220						
Asn	Thr	Ala	Leu	Lys	Ala	Met	Lys	Ala	Asp	Gly	Thr	Tyr	Gln	Ala	Ile		
225				230					235						240		
Met	Thr	Lys	Trp	Leu	Gly	Thr	Asp	Asp	Lys	Ala	Thr	Thr	Ser	Gln	Ala		
			245					250						255			
Thr	Gly	Asn	Pro	Ser	Ala	Lys	Ala	Thr	Pro	Thr	Lys	Asp	Ser	Tyr	Lys		
		260					265						270				
Ile	Val	Ser	Asp	Ser	Ser	Phe	Ala	Pro	Phe	Glu	Phe	Gln	Asn	Gly	Lys		
	275					280						285					
Gly	Lys	Tyr	Val	Gly	Ile	Asp	Ile	Glu	Leu	Ile	Lys	Ala	Ile	Ala	Lys		
290					295						300						
Gln	Gln	Gly	Phe	Lys	Ile	Glu	Ile	Ala	Asn	Pro	Gly	Phe	Asp	Ala	Ala		
305				310					315					320			
Leu	Asn	Ala	Val	Gln	Ser	Ser	Gln	Ala	Asp	Gly	Val	Ile	Ala	Gly	Ala		
			325					330						335			
Thr	Ile	Thr	Asp	Ala	Arg	Lys	Ala	Ile	Phe	Asp	Phe	Ser	Asp	Pro	Tyr		
	340						345					350					
Tyr	Thr	Ser	Asn	Ile	Ile	Leu	Ala	Val	Lys	Ala	Gly	Lys	Asn	Ile	Lys		
	355					360					365						
Asn	Tyr	Glu	Asp	Leu	Asp	Arg	Lys	Thr	Val	Gly	Ala	Lys	Asn	Gly	Thr		
370					375					380							
Ser	Ser	Tyr	Ser	Trp	Leu	Lys	Glu	Asn	Ala	Pro	Lys	Tyr	Gly	Tyr	Asn		
385				390					395					400			
Val	Lys	Ala	Phe	Asp	Asp	Gly	Ser	Ser	Met	Tyr	Asp	Ser	Leu	Asn	Ser		
			405					410						415			
Gly	Ser	Val	Asp	Ala	Ile	Met	Asp	Asp	Glu	Ala	Val	Leu	Lys	Tyr	Ala		
	420						425					430					
Ile	Ser	Gln	Gly	Arg	Arg	Phe	Glu	Thr	Pro	Leu	Glu	Gly	Ile	Ser	Thr		
	435					440					445						
Gly	Glu	Val	Gly	Phe	Ala	Val	Lys	Lys	Gly	Thr	Asn	Pro	Glu	Leu	Ile		
450					455				460								
Glu	Met	Phe	Asn	Asn	Gly	Leu	Ala	Ala	Leu	Lys	Lys	Ser	Gly	Gln	Tyr		
465				470					475					480			
Asp	Asp	Ile	Ile	Asp	Lys	Tyr	Leu	Asp	Ser	Lys	Lys	Ala	Ala	Thr	Pro		
			485					490						495			
Ser	Glu	Lys	Gly	Ala	Asp	Glu	Ser	Thr	Ile	Ser	Gly	Leu	Leu	Ser	Asn		
	500						505					510					
Asn	Tyr	Lys	Gln	Leu	Leu	Ala	Gly	Leu	Gly	Thr	Thr	Leu	Ser	Leu	Thr		
	515					520					525						
Leu	Ile	Ser	Phe	Ala	Ile	Ala	Ile	Ile	Ile	Gly	Ile	Ile	Phe	Gly	Met		
530					535						540						
Met	Ala	Val	Ser	Pro	Thr	Lys	Ser	Leu	Arg	Leu	Ile	Ser	Thr	Val	Phe		
545				550					555					560			
Val	Asp	Val	Val	Arg	Gly	Ile	Pro	Leu	Met	Ile	Val	Ala	Ala	Phe	Ile		
			565					570						575			

Phe	Trp	Gly	Val	Pro	Asn	Leu	Ile	Glu	Ser	Met	Thr	Gly	His	Gln	Ser
			580					585					590		
Pro	Ile	Asn	Asp	Phe	Leu	Ala	Ala	Thr	Ile	Ala	Leu	Ser	Leu	Asn	Gly
		595					600					605			
Gly	Ala	Tyr	Ile	Ala	Glu	Ile	Val	Arg	Gly	Gly	Ile	Glu	Ala	Val	Pro
	610					615					620				
Ala	Gly	Gln	Met	Glu	Ala	Ser	Arg	Ser	Leu	Gly	Leu	Ser	Tyr	Gly	Thr
625					630					635					640
Thr	Met	Arg	Lys	Val	Ile	Leu	Pro	Gln	Ala	Val	Lys	Leu	Met	Leu	Pro
			645						650					655	
Asn	Phe	Ile	Asn	Gln	Phe	Val	Ile	Ser	Leu	Lys	Asp	Thr	Thr	Ile	Val
		660						665					670		
Ser	Ala	Ile	Gly	Leu	Val	Glu	Leu	Phe	Gln	Thr	Gly	Lys	Ile	Ile	Ile
		675					680					685			
Ala	Arg	Asn	Tyr	Gln	Ser	Phe	Arg	Met	Tyr	Ala	Ile	Leu	Ala	Ile	Ile
	690					695					700				
Tyr	Leu	Ile	Met	Ile	Ile	Leu	Leu	Thr	Arg	Leu	Ala	Lys	Arg	Leu	Glu
705					710					715					720
Lys	Arg	Leu	Asn												

<210> SEQ ID NO 319

<211> LENGTH: 825

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 319

ttggtaactt	attataataa	ggatttagtg	cctcaagcac	ctaaaagctt	tactgaatta	60
gaagtcttac	aaaaagattc	taagtttgct	tttgccctctg	aaccaggaaa	atctgtaggt	120
ttcttggcga	aatggacaga	cttctattat	ggttatgggt	taattgccgg	ttatggcgg	180
tatatctttg	gtgataaagg	aaccaaacca	agtgatttag	gcctaggtaa	cgacggaact	240
gttgaagggt	taaactacgc	gaaacagtgg	tatggcactt	ggcctcaagg	aatgcaagac	300
actaaaaaag	ctggtgattt	tatcactgaa	caatttat	ctaaaaaagc	tgggtgtcatt	360
attgatggtc	catgggcagc	tagctccttt	aaagatgctg	gtgttaactt	tggggtaatg	420
gaaattccta	ctttgacaaa	tggtaaaaaa	taccaaccgt	tcgcaggtgg	taaagcttgg	480
gttatttcaa	actattctaa	aggaaaaacg	actgctcaaa	aattccttga	ttatgtgacc	540
aatgctgaaa	accaaaaacg	tttctatgat	aaaacacaag	aaattccagc	taacttaaca	600
gcacgtaact	atgcttctaa	agagggtaat	gagttaacga	aagctgtgat	tagtcagttt	660
gagagcgcac	aaccaatgcc	aaatattcca	gaaatggctg	aagtttggga	accaggtgca	720
aatatgttct	ttaacgtggc	ttctggtaag	gaagaagcat	ctaaagctgc	aaaagaagca	780
gcaaaaacta	ttaaggaagc	tattgaacaa	aaatacgctg	aataa		825

<210> SEQ ID NO 320

<211> LENGTH: 274

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 320

Met	Val	Thr	Tyr	Tyr	Asn	Lys	Asp	Leu	Val	Pro	Gln	Ala	Pro	Lys	Ser
1				5					10					15	
Phe	Thr	Glu	Leu	Glu	Val	Leu	Gln	Lys	Asp	Ser	Lys	Phe	Ala	Phe	Ala
		20					25					30			
Ser	Glu	Pro	Gly	Lys	Ser	Val	Gly	Phe	Leu	Ala	Lys	Trp	Thr	Asp	Phe
	35					40						45			
Tyr	Tyr	Gly	Tyr	Gly	Leu	Ile	Ala	Gly	Tyr	Gly	Gly	Tyr	Ile	Phe	Gly
	50					55					60				
Asp	Lys	Gly	Thr	Lys	Pro	Ser	Asp	Leu	Gly	Leu	Gly	Asn	Asp	Gly	Thr
65					70					75				80	
Val	Glu	Gly	Leu	Asn	Tyr	Ala	Lys	Gln	Trp	Tyr	Gly	Thr	Trp	Pro	Gln
				85					90					95	

Gly	Met	Gln	Asp	Thr	Lys	Lys	Ala	Gly	Asp	Phe	Ile	Thr	Glu	Gln	Phe	
			100					105					110			
Ile	Ser	Lys	Lys	Ala	Gly	Val	Ile	Ile	Asp	Gly	Pro	Trp	Ala	Ala	Ser	
		115					120					125				
Ser	Phe	Lys	Asp	Ala	Gly	Val	Asn	Phe	Gly	Val	Met	Glu	Ile	Pro	Thr	
		130				135					140					
Leu	Thr	Asn	Gly	Lys	Lys	Tyr	Gln	Pro	Phe	Ala	Gly	Gly	Lys	Ala	Trp	
					150					155					160	
Val	Ile	Ser	Asn	Tyr	Ser	Lys	Gly	Lys	Thr	Thr	Ala	Gln	Lys	Phe	Leu	
				165					170					175		
Asp	Tyr	Val	Thr	Asn	Ala	Glu	Asn	Gln	Lys	Arg	Phe	Tyr	Asp	Lys	Thr	
			180					185					190			
Gln	Glu	Ile	Pro	Ala	Asn	Leu	Thr	Ala	Arg	Asn	Tyr	Ala	Ser	Lys	Glu	
		195					200					205				
Gly	Asn	Glu	Leu	Thr	Lys	Ala	Val	Ile	Ser	Gln	Phe	Glu	Ser	Ala	Gln	
	210					215					220					
Pro	Met	Pro	Asn	Ile	Pro	Glu	Met	Ala	Glu	Val	Trp	Glu	Pro	Gly	Ala	
	225				230					235					240	
Asn	Met	Phe	Phe	Asn	Val	Ala	Ser	Gly	Lys	Glu	Glu	Ala	Ser	Lys	Ala	
				245					250					255		
Ala	Lys	Glu	Ala	Ala	Lys	Thr	Ile	Lys	Glu	Ala	Ile	Glu	Gln	Lys	Tyr	
			260					265					270			
Ala	Glu															

<210> SEQ ID NO 321

<211> LENGTH: 1308

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 321

atggtagaga	accaaagaca	acagaagcct	aataaagcca	tgtggctatc	tggtatccca	60
ggtttgggac	aactatacaa	taaacaaatc	gttaaagggg	gagtcttatt	agttgttttc	120
ttcctagagc	tactagaaat	tgtagttcta	ggaattcctg	ctttaacagg	tctttacagt	180
cttggaaagt	ttccaatgca	agatcactcc	ttatttatgt	taattaaggg	ggccatgcaa	240
ttaattactc	tagtcttatt	tggatttttt	catttggttg	ctatgagaga	tgctaaatta	300
gttgcacatc	aaatgaatga	aggcaagaag	gttccggtga	cggctaaaga	gacccttgaa	360
gcgatttatg	aaaaaggatt	tccttacttg	ctcatcattc	cggcttattt	agcaatggct	420
ttcgctatta	tttttccagt	tttagtgacc	ttgctgattg	cttttaccaa	ttacgatttt	480
aggcatattc	ctccgtatcg	tttattggat	tgggtagggt	tgaagaattt	tcttaatatc	540
ttagaattaa	gcaccttcaa	aacagcattt	acatctgttt	tgatcatggg	gctgatctgg	600
acattagcag	cgacaagtct	tcaaattggt	attggaattg	caacggctgt	tattgctaata	660
caatccttta	tcagaggaaa	acgtctcttt	ggtgtgatata	tcttggtacc	atgggctggt	720
ccagcattta	tctctattat	gagttttggt	aatttcttta	atgattccat	tggggccatg	780
aatgttcagg	ttcttctctt	catcgagaaa	ttccttctct	tcgttgactt	cgggaattgtg	840
tcctggaaga	cagacccctt	ctggacaaaa	gtggctgtta	ttatggtgca	aggttggcta	900
ggatttccct	atatctatat	tttggtatca	ggtattttac	aggcaattcc	agctgattta	960
tacgaagcag	caaccggtga	tgggtgcgaca	gtcttacaga	aattccgcca	tatcaccatg	1020
ccaatgattt	ttgcggttgc	agcaccaacc	tttatctctc	agtacacctt	taacttcaat	1080
aatttctcta	ttatttatct	gtttaataat	gggggccctg	gtactgtggg	gggcggagct	1140
gggacaactg	atattctgat	ttcttggatt	tacaagttga	ccacacaaac	ctcgccctcaa	1200
ttttcgatgg	cgtcggcaat	gaccttaatc	atctctgtaa	taatgatttc	ggtatcattg	1260
attaccttta	agaaatttaa	agcttttgat	atggaggaga	gatcatga		1308

<210> SEQ ID NO 322

<211> LENGTH: 435

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 322

Met	Val	Glu	Asn	Gln	Arg	Gln	Gln	Lys	Pro	Asn	Lys	Ala	Met	Trp	Leu
1				5					10					15	
Ser	Val	Ile	Pro	Gly	Leu	Gly	Gln	Leu	Tyr	Asn	Lys	Gln	Ile	Val	Lys
			20					25					30		
Gly	Gly	Val	Leu	Leu	Val	Val	Phe	Phe	Leu	Glu	Leu	Leu	Glu	Ile	Val
		35					40					45			
Val	Leu	Gly	Ile	Pro	Ala	Leu	Thr	Gly	Leu	Tyr	Ser	Leu	Gly	Ser	Val
	50					55					60				
Pro	Met	Gln	Asp	His	Ser	Leu	Phe	Met	Leu	Ile	Lys	Gly	Ala	Met	Gln
65				70					75					80	
Leu	Ile	Thr	Leu	Val	Leu	Phe	Gly	Ile	Phe	His	Leu	Val	Ala	Met	Arg
			85					90						95	
Asp	Ala	Lys	Leu	Val	Ala	His	Gln	Met	Asn	Glu	Gly	Lys	Lys	Val	Pro
			100					105					110		
Val	Thr	Ala	Lys	Glu	Thr	Leu	Glu	Ala	Ile	Tyr	Glu	Lys	Gly	Phe	Pro
		115					120					125			
Tyr	Leu	Leu	Ile	Ile	Pro	Ala	Tyr	Leu	Ala	Met	Ala	Phe	Ala	Ile	Ile
	130					135					140				
Phe	Pro	Val	Leu	Val	Thr	Leu	Leu	Ile	Ala	Phe	Thr	Asn	Tyr	Asp	Phe
145					150					155					160
Arg	His	Ile	Pro	Pro	Tyr	Arg	Leu	Leu	Asp	Trp	Val	Gly	Leu	Lys	Asn
			165						170					175	
Phe	Leu	Asn	Ile	Leu	Glu	Leu	Ser	Thr	Phe	Lys	Thr	Ala	Phe	Thr	Ser
		180						185					190		
Val	Leu	Ser	Trp	Thr	Leu	Ile	Trp	Thr	Leu	Ala	Ala	Thr	Ser	Leu	Gln
		195					200					205			
Ile	Val	Ile	Gly	Ile	Ala	Thr	Ala	Val	Ile	Ala	Asn	Gln	Ser	Phe	Ile
	210					215					220				
Arg	Gly	Lys	Arg	Leu	Phe	Gly	Val	Ile	Phe	Leu	Leu	Pro	Trp	Ala	Val
225				230						235					240
Pro	Ala	Phe	Ile	Ser	Ile	Met	Ser	Phe	Gly	Asn	Phe	Phe	Asn	Asp	Ser
			245						250					255	
Ile	Gly	Ala	Met	Asn	Val	Gln	Val	Leu	Pro	Phe	Ile	Glu	Lys	Phe	Leu
		260						265					270		
Pro	Phe	Val	Asp	Phe	Gly	Ile	Val	Ser	Trp	Lys	Thr	Asp	Pro	Phe	Trp
		275					280					285			
Thr	Lys	Val	Ala	Val	Ile	Met	Val	Gln	Gly	Trp	Leu	Gly	Phe	Pro	Tyr
	290					295					300				
Ile	Tyr	Ile	Leu	Val	Ser	Gly	Ile	Leu	Gln	Ala	Ile	Pro	Ala	Asp	Leu
305				310						315				320	
Tyr	Glu	Ala	Ala	Thr	Val	Asp	Gly	Ala	Thr	Val	Leu	Gln	Lys	Phe	Arg
			325						330					335	
His	Ile	Thr	Met	Pro	Met	Ile	Phe	Ala	Val	Ala	Ala	Pro	Thr	Phe	Ile
			340					345					350		
Ser	Gln	Tyr	Thr	Phe											

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<210> SEQ ID NO 323
<211> LENGTH: 861
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 323
atgagaaaga cttatgtttc aatatccatg aaacgcaaac gtttcttcac ccaattattg      60
acttatctct atctaatctc cttagtgatc gtgattttat tccaataact agtgacggtc      120
agttcagctt ttagaccagg aaataccaca gccttttagtt ttcattttga tgggccatgg      180
accttgtcta actttaaaac actctttcaa gataccttat acttaagatg gtattggaat      240
accttgatcg tggcattctt caccatgctc atacaagtaa cagtcacacac tttgacaggt      300
tatgcgtata gccgttacaa tttctttgga cgcaaaaaaa gtttaatctt tttcctagtc      360
gtacagatgg ttcctaccat ggcggcttta acggcttact ttgttatggc gtggctcttt      420
aatgccttaa accaatactg gttcttgatt ttgatttacg tcggtggtgg tattcctatg      480
aatgcctggg tgatgaaggg ttattttgac acggtacctt atgacttga cgaatctgct      540
aagttagatg gttctggaca ctttaggacc ttctaccaa ttgtccttcc tcttggtgca      600
ccaatgattg cagtacaatc cttatgggct tttatgggct ctttcggaga cttcatgttg      660
gctaaattcc ttttaagggc gcaagaaaat tatacggtag cagttggtct tcaatcgttt      720
attacgaatg atgctagaaa tccaaggtta accttatattg ctgcgggagc tattctgatt      780
gcagtgccta tttcagttct ctttttcttc ctacagaaaa atttcgtttc cggtttaaca      840
agtggtggtta ccaaagggtta a

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<210> SEQ ID NO 324
<211> LENGTH: 286
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 324
Met Arg Lys Thr Tyr Val Ser Ile Ser Met Lys Arg Lys Arg Phe Phe
1      5      10      15
Thr Gln Leu Leu Thr Tyr Leu Tyr Leu Ile Ser Leu Val Ile Val Ile
20     25     30
Leu Phe Pro Ile Leu Val Thr Val Ser Ser Ala Phe Arg Pro Gly Asn
35     40     45
Thr Thr Ala Phe Ser Phe His Phe Asp Gly Pro Trp Thr Leu Ser Asn
50     55     60
Phe Lys Thr Leu Phe Gln Asp Thr Leu Tyr Leu Arg Trp Tyr Trp Asn
65     70     75     80
Thr Leu Ile Val Ala Phe Phe Thr Met Leu Ile Gln Val Thr Val Ile
85     90     95
Thr Leu Thr Gly Tyr Ala Tyr Ser Arg Tyr Asn Phe Phe Gly Arg Lys
100    105    110
Lys Ser Leu Ile Phe Phe Leu Val Val Gln Met Val Pro Thr Met Ala
115    120    125
Ala Leu Thr Ala Tyr Phe Val Met Ala Trp Leu Phe Asn Ala Leu Asn
130    135    140
Gln Tyr Trp Phe Leu Ile Leu Ile Tyr Val Gly Gly Gly Ile Pro Met
145    150    155    160
Asn Ala Trp Leu Met Lys Gly Tyr Phe Asp Thr Val Pro Tyr Asp Leu
165    170    175
Asp Glu Ser Ala Lys Leu Asp Gly Ser Gly His Phe Arg Thr Phe Tyr
180    185    190
Gln Ile Val Leu Pro Leu Val Arg Pro Met Ile Ala Val Gln Ser Leu
195    200    205
Trp Ala Phe Met Gly Pro Phe Gly Asp Phe Met Leu Ala Lys Phe Leu
210    215    220
Leu Arg Ala Gln Glu Asn Tyr Thr Val Ala Val Gly Leu Gln Ser Phe
225    230    235    240
Ile Thr Asn Asp Ala Arg Asn Pro Lys Val Thr Leu Phe Ala Ala Gly

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				245					250					255			
Ala	Ile	Leu	Ile	Ala	Val	Pro	Ile	Ser	Val	Leu	Phe	Phe	Phe	Leu	Gln		
			260					265						270			
Lys	Asn	Phe	Val	Ser	Gly	Leu	Thr	Ser	Gly	Gly	Thr	Lys	Gly				
		275					280						285				

<210> SEQ ID NO 325
 <211> LENGTH: 816
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 325

atgccagata	aaaaacaatt	tcctatcttct	tacattttcac	attgcctttc	tcctagggca	60
atgtttgcca	gccgagctca	gtttacttgg	tggcaaaatc	ttcttattat	tgtttttttg	120
aacgccttaa	taatgattcc	agttacgtta	cactatgcta	acatgacaac	gtatcccttg	180
gaacggattg	taactaagag	tttgtcgctt	atcacagaca	aaacctatca	agcattgacc	240
caaggaaaga	ttgagaaaga	tacgttttcag	ggccaatctc	tgattcgacg	agatgggtgaa	300
ttggtttttg	ctgtttttacc	gacaaagggtc	gattttagagc	aattggcatc	agaatcaacc	360
agacaaatta	ttgtgacaaa	aaaagaatgg	cgttttgtta	cccctgatgg	caaggaaactc	420
cgtgctcacg	ttagaggcca	gcagcagtca	ctcgctgacc	tgacaacagt	taaagcagtg	480
aaggactttg	tcaatcagca	atggatatgac	agtaataaag	ccagtgtact	tggtttttctt	540
ttgctgacgt	ttgtttctcat	ggtgtgtgtg	ggtaccctta	ttgtgattgg	tctaggcgct	600
ttctttttga	ctctgactaa	acgatcacga	ctatttatga	ttcgaaactt	ctctgaagga	660
cttggattga	tggttaattg	tttggcttgg	ccgagtctac	tggcgattgc	tcttagtttc	720
tttattcagg	atccagtact	gattatgaat	tgccaagtat	ttggtacctt	attaatgctg	780
acctgggtgt	tctacaaaac	acagttttaga	gattga			816

<210> SEQ ID NO 326
 <211> LENGTH: 271
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 326

Met	Pro	Asp	Lys	Lys	Gln	Phe	Pro	Ile	Ser	Tyr	Ile	Ser	His	Cys	Leu
1			5						10					15	
Ser	Pro	Arg	Ala	Met	Phe	Ala	Ser	Arg	Ala	Gln	Phe	Thr	Trp	Trp	Gln
			20					25					30		
Asn	Leu	Leu	Ile	Ile	Val	Phe	Leu	Asn	Ala	Leu	Ile	Met	Ile	Pro	Val
			35				40					45			
Thr	Leu	His	Tyr	Ala	Asn	Met	Thr	Thr	Tyr	Pro	Leu	Glu	Arg	Ile	Val
			50			55					60				
Thr	Lys	Ser	Leu	Ser	Pro	Ile	Thr	Asp	Lys	Thr	Tyr	Gln	Ala	Leu	Thr
65					70				75					80	
Gln	Gly	Lys	Ile	Glu	Lys	Asp	Thr	Phe	Gln	Gly	Gln	Ser	Leu	Ile	Arg
				85					90					95	
Arg	Asp	Gly	Glu	Leu	Val	Leu	Ala	Val	Leu	Pro	Thr	Lys	Val	Asp	Leu
				100				105					110		
Glu	Gln	Leu	Ala	Ser	Glu	Ser	Thr	Arg	Gln	Ile	Ile	Val	Thr	Lys	Lys
				115			120					125			
Glu	Trp	Arg	Phe	Val	Thr	Pro	Asp	Gly	Lys	Glu	Leu	Arg	Ala	His	Val
				130			135				140				
Arg	Gly	Gln	Gln	Gln	Ser	Leu	Ala	Asp	Leu	Thr	Thr	Val	Lys	Ala	Val
145					150					155					160
Lys	Asp	Phe	Val	Asn	Gln	Gln	Trp	Tyr	Asp	Ser	Asn	Lys	Ala	Ser	Val
				165					170						175
Leu	Gly	Phe	Leu	Leu	Leu	Thr	Phe	Val	Leu	Met	Val	Cys	Val	Gly	Thr
				180				185					190		
Leu	Ile	Val	Ile	Gly	Leu	Gly	Ala	Phe	Phe	Leu	Thr	Leu	Thr	Lys	Arg
				195			200						205		

Ser	Arg	Leu	Phe	Met	Ile	Arg	Asn	Phe	Ser	Glu	Gly	Leu	Gly	Leu	Met
210						215					220				
Val	Asn	Cys	Leu	Ala	Trp	Pro	Ser	Leu	Leu	Ala	Ile	Ala	Leu	Ser	Phe
225					230					235					240
Phe	Ile	Gln	Asp	Pro	Val	Leu	Ile	Met	Asn	Cys	Gln	Val	Phe	Gly	Thr
				245					250					255	
Leu	Leu	Met	Leu	Thr	Trp	Val	Phe	Tyr	Lys	Thr	Gln	Phe	Arg	Asp	
			260					265						270	

<210> SEQ ID NO 327

<211> LENGTH: 837

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 327

atgaaaaaca	aacgtcgatt	tcaacttgga	cttgtttatg	ctactttaat	catcctctca	60
atcatttggc	tcttcccaat	cgcttggggt	attcttacta	gcttccgtag	cgaaggaact	120
gcttacgtca	attattttat	tcctaagact	tttacattaa	atcactacat	taatcttttt	180
actaatgaaa	ccttttcctt	tggaaaatgg	tttatgaata	ctcttattgt	agccactttt	240
acatgtatta	tttcaacctt	cataactggt	gccatagcct	actctcttag	ccgaattaag	300
tttaagtttc	gcaatggcct	tttaaaacta	gcccttat	ttaaatagtt	ccctgggttc	360
atgagcatga	ttgccatcta	ctatatctta	aaggccttag	gtttgacgca	aaccctaaca	420
gcacttgtcc	ttgtttattc	ctcaggtgca	gcccttgggt	tttacattgc	aaaaggattt	480
tttgatacca	ttccttattc	acttgatgaa	tcagctatga	ttgatggcgc	tactcgtatg	540
gatattttct	ttaaaataac	ccttccttta	gcaaaaccaa	tcattgtcta	tactgccctt	600
cttgctttta	tggggccttg	gattgacttt	atctttgcac	aagttatttt	aggtgatgct	660
acaagtaaat	ataccgttgc	tattggacta	ttttcaatgc	ttcagccaga	taccattaac	720
aactggttta	tggccttcac	tgtctggtct	gtcttaattg	ccgtcccaat	cactctcctc	780
ttcatgttta	tgcaaaaata	ctatgttgaa	ggcatcacag	gtggttctgt	taaataa	837

<210> SEQ ID NO 328

<211> LENGTH: 278

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 328

Met	Lys	Asn	Lys	Arg	Arg	Phe	Gln	Leu	Gly	Leu	Val	Tyr	Ala	Thr	Leu
1			5						10					15	
Ile	Ile	Leu	Ser	Ile	Ile	Trp	Leu	Phe	Pro	Ile	Ala	Trp	Val	Ile	Leu
			20					25					30		
Thr	Ser	Phe	Arg	Ser	Glu	Gly	Thr	Ala	Tyr	Val	Asn	Tyr	Phe	Ile	Pro
			35				40					45			
Lys	Thr	Phe	Thr	Leu	Asn	His	Tyr	Ile	Asn	Leu	Phe	Thr	Asn	Glu	Thr
			50			55					60				
Phe	Pro	Phe	Gly	Lys	Trp	Phe	Met	Asn	Thr	Leu	Ile	Val	Ala	Thr	Phe
65					70					75					80
Thr	Cys	Ile	Ile	Ser	Thr	Phe	Ile	Thr	Val	Ala	Ile	Ala	Tyr	Ser	Leu
				85					90					95	
Ser	Arg	Ile	Lys	Phe	Lys	Phe	Arg	Asn	Gly	Phe	Leu	Lys	Leu	Ala	Leu
			100					105					110		
Ile	Leu	Asn	Met	Phe	Pro	Gly	Phe	Met	Ser	Met	Ile	Ala	Ile	Tyr	Tyr
		115					120					125			
Ile	Leu	Lys	Ala	Leu	Gly	Leu	Thr	Gln	Thr	Leu	Thr	Ala	Leu	Val	Leu
		130				135					140				
Val	Tyr	Ser	Ser	Gly	Ala	Ala	Leu	Gly	Phe	Tyr	Ile	Ala	Lys	Gly	Phe
145					150					155					160
Phe	Asp	Thr	Ile	Pro	Tyr	Ser	Leu	Asp	Glu	Ser	Ala	Met	Ile	Asp	Gly
				165					170					175	
Ala	Thr	Arg	Met	Asp	Ile	Phe	Phe	Lys	Ile	Thr	Leu	Pro	Leu	Ala	Lys

			180					185				190					
Pro	Ile	Ile	Val	Tyr	Thr	Ala	Leu	Leu	Ala	Phe	Met	Gly	Pro	Trp	Ile		
		195					200					205					
Asp	Phe	Ile	Phe	Ala	Gln	Val	Ile	Leu	Gly	Asp	Ala	Thr	Ser	Lys	Tyr		
	210					215					220						
Thr	Val	Ala	Ile	Gly	Leu	Phe	Ser	Met	Leu	Gln	Pro	Asp	Thr	Ile	Asn		
225					230					235					240		
Asn	Trp	Phe	Met	Ala	Phe	Thr	Ala	Gly	Ser	Val	Leu	Ile	Ala	Val	Pro		
			245						250					255			
Ile	Thr	Leu	Leu	Phe	Met	Phe	Met	Gln	Lys	Tyr	Tyr	Val	Glu	Gly	Ile		
		260						265					270				
Thr	Gly	Gly	Ser	Val	Lys												
	275																

<210> SEQ ID NO 329

<211> LENGTH: 1362

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 329

atgactcagt	caaacttgac	accaaata	tctgtaata	aagccttaaa	aagaggcagt	60
tgggatatta	aactttcgag	tattatcatg	ggatttgcca	actttgctaa	caaacagttt	120
atcaaaggaa	tcttattttt	aataagtga	cttatctttc	tagtagcttt	tgtctcccaa	180
atcatccctg	ctatccgtgg	ccttgtcact	cttggtactc	aaactcaggg	aatgactaca	240
aaaactattg	atgggattaa	catccaagtt	gctggtgatg	gcgataactc	tatgttaatg	300
cttatttttg	gttttagcatc	actcattttc	tgccatagtct	ttgcttacat	ttactgggtgt	360
aatctcaaaa	gtgctcgtaa	cctttatctt	ttcaaacaaa	aagggtcagaa	gataccaagc	420
ttcaaagaag	atcttgccac	acttacaaat	ggtcgctttc	atatgacttt	aatggctatc	480
ccactgattg	gtgtgctttt	attcaccatt	cttcctttga	tttacatgat	ctgtttggcc	540
tttaccaatt	ttgatcataa	tcacttgctt	ccaaaatctt	tatttgattg	gggtgggactt	600
gctaactttg	gaaatgtttt	aagcggccgt	atggcaggaa	ccttttttcc	tatcttctca	660
tggactttga	tttgggctgt	ttttgccaca	gtaactaatt	tcttctttgg	tattattctt	720
gctttgttaa	tcaataccaa	aggattaaag	tggaaaaaaa	tgtggcgaac	catctttgtt	780
atcaccattg	cagttccaca	attcatctca	ttattgatta	tgcggaactt	actcaatgac	840
gaaggcccac	taaatgctct	tctcaataaa	atcggcttga	ttaatggctc	actgccattt	900
ttatctgata	ctctttgggc	aaaattctca	atcatttttg	tcaacatgtg	gatcggtatt	960
ccatttacca	tgctgattgc	gactgggtatt	atcatgaacc	ttccaagtga	acaaattgag	1020
gctgctgaaa	ttgatggcgc	tagcaaatct	caagtcttca	agtctatcac	gttccctcaa	1080
attctcttga	tcatgacacc	aaacttgatt	caacaattta	tcggaaaatat	caataacttt	1140
aacgtcattt	acctccttac	tggtgggtgt	ccaacaaatt	cagaatacta	tcaggcagga	1200
acaacagact	tgctggtcac	ttggctttat	aaattaaccg	tcacagctgc	tgactacaat	1260
ttagcttctg	ttatcggtat	cttaatcttt	acagtttcag	ctatctttag	cttacttgct	1320
tatacaagga	cagcatccta	caaggaagga	gcggctaaat	aa		1362

<210> SEQ ID NO 330

<211> LENGTH: 453

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 330

Met	Thr	Gln	Ser	Asn	Leu	Thr	Pro	Asn	Ile	Ser	Val	Ile	Glu	Ala	Leu
1			5						10					15	
Lys	Arg	Gly	Ser	Trp	Asp	Ile	Lys	Leu	Ser	Ser	Ile	Ile	Met	Gly	Phe
		20						25					30		
Ala	Asn	Phe	Ala	Asn	Lys	Gln	Phe	Ile	Lys	Gly	Ile	Leu	Phe	Leu	Ile
		35					40					45			
Ser	Glu	Leu	Ile	Phe	Leu	Val	Ala	Phe	Val	Ser	Gln	Ile	Ile	Pro	Ala
	50					55					60				
Ile	Arg	Gly	Leu	Val	Thr	Leu	Gly	Thr	Gln	Thr	Gln	Gly	Met	Thr	Thr

65					70					75					80
Lys	Thr	Ile	Asp	Gly	Ile	Asn	Ile	Gln	Val	Ala	Val	Asp	Gly	Asp	Asn
				85					90					95	
Ser	Met	Leu	Met	Leu	Ile	Phe	Gly	Leu	Ala	Ser	Leu	Ile	Phe	Cys	Leu
			100					105					110		
Val	Phe	Ala	Tyr	Ile	Tyr	Trp	Cys	Asn	Leu	Lys	Ser	Ala	Arg	Asn	Leu
	115						120					125			
Tyr	Leu	Phe	Lys	Gln	Lys	Gly	Gln	Lys	Ile	Pro	Ser	Phe	Lys	Glu	Asp
	130					135					140				
Leu	Ala	Thr	Leu	Thr	Asn	Gly	Arg	Phe	His	Met	Thr	Leu	Met	Ala	Ile
145					150					155					160
Pro	Leu	Ile	Gly	Val	Leu	Leu	Phe	Thr	Ile	Leu	Pro	Leu	Ile	Tyr	Met
			165						170					175	
Ile	Cys	Leu	Ala	Phe	Thr	Asn	Phe	Asp	His	Asn	His	Leu	Pro	Pro	Lys
			180					185					190		
Ser	Leu	Phe	Asp	Trp	Val	Gly	Leu	Ala	Asn	Phe	Gly	Asn	Val	Leu	Ser
		195				200						205			
Gly	Arg	Met	Ala	Gly	Thr	Phe	Phe	Pro	Ile	Phe	Ser	Trp	Thr	Leu	Ile
	210					215						220			
Trp	Ala	Val	Phe	Ala	Thr	Val	Thr	Asn	Phe	Phe	Phe	Gly	Ile	Ile	Leu
225					230					235					240
Ala	Leu	Leu	Ile	Asn	Thr	Lys	Gly	Leu	Lys	Trp	Lys	Lys	Met	Trp	Arg
			245						250					255	
Thr	Ile	Phe	Val	Ile	Thr	Ile	Ala	Val	Pro	Gln	Phe	Ile	Ser	Leu	Leu
			260					265					270		
Ile	Met	Arg	Asn	Leu	Leu	Asn	Asp	Glu	Gly	Pro	Leu	Asn	Ala	Leu	Leu
		275				280						285			
Asn	Lys	Ile	Gly	Leu	Ile	Asn	Gly	Ser	Leu	Pro	Phe	Leu	Ser	Asp	Pro
	290					295					300				
Leu	Trp	Ala	Lys	Phe	Ser	Ile	Ile	Phe	Val	Asn	Met	Trp	Ile	Gly	Ile
305					310					315					320
Pro	Phe	Thr	Met	Leu	Ile	Ala	Thr	Gly	Ile	Ile	Met	Asn	Leu	Pro	Ser
			325						330					335	
Glu	Gln	Ile	Glu	Ala	Ala	Glu	Ile	Asp	Gly	Ala	Ser	Lys	Phe	Gln	Val
			340					345					350		
Phe	Lys	Ser	Ile	Thr	Phe	Pro	Gln	Ile	Leu	Leu	Ile	Met	Thr	Pro	Asn
		355					360					365			
Leu	Ile	Gln	Gln	Phe	Ile	Gly	Asn	Ile	Asn	Asn	Phe	Asn	Val	Ile	Tyr
	370					375					380				
Leu	Leu	Thr	Gly	Gly	Gly	Pro	Thr	Asn	Ser	Glu	Tyr	Tyr	Gln	Ala	Gly
385					390					395					400
Thr	Thr	Asp	Leu	Leu	Val	Thr	Trp	Leu	Tyr	Lys	Leu	Thr	Val	Thr	Ala
			405						410					415	
Ala	Asp	Tyr	Asn	Leu	Ala	Ser	Val	Ile	Gly	Ile	Leu	Ile	Phe	Thr	Val
			420					425					430		
Ser	Ala	Ile	Phe	Ser	Leu	Leu	Ala	Tyr	Thr	Arg	Thr	Ala	Ser	Tyr	Lys
		435					440					445			
Glu	Gly	Ala	Ala	Lys											
	450														

<210> SEQ ID NO 331

<211> LENGTH: 786

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 331

atgttttgga	aattattaaa	atacgaattt	agatctattg	gaaaatggta	ctttgcgctt	60
aatgctttcg	ttattgccat	cgctgccatt	ttgtcattta	cgataaaact	gtttgctcaa	120

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agcaatagtg atggactatt tggagtacta accaataaga tgttgccctct gacattaggt 180
ttaacttttg gctccctgat cgctgggtcc ctcttatcaa cattacttat cattatcaaa 240
cgtttcagca aaagtgtttt tggatgggaa ggatacttaa cgttgacttt acccgtaaat 300
tcgcatcaaaa ttattttatc aaaactacta gcttctttta tttgcagtgt tttcaatact 360
atcatccttg catttgctat cgctattgta attgtaccaa tgtttaacat caacgaacta 420
ttagaaggat tctttaatag ttttaagatg gattatttca tcaatatgct aactgtacta 480
gcctatgtcc tattatcaac atttacgagt atcttattaa tttatctttc catttctata 540
gggtcaacttt tttccaatcg gcgaggcttg atggccttta ttgcatatth tatattagtt 600
attctgatta gcgttgctgc aacatatgtt cacagtcaca tctttaatat taatacaagt 660
gccgatagtt tcccattttac tgagcaaaaa acaattttatc ttcttattttt ggaacaattt 720
attgaaatga taatgtttta cctcgccact aattttatta tcaaaaataa actcaaccta 780
cagtaa 786

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<210> SEQ ID NO 332
<211> LENGTH: 261
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 332

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Met Phe Gly Lys Leu Leu Lys Tyr Glu Phe Arg Ser Ile Gly Lys Trp
1      5      10      15
Tyr Phe Ala Leu Asn Ala Phe Val Ile Ala Ile Ala Ala Ile Leu Ser
      20      25      30
Phe Thr Ile Lys Leu Phe Ala Gln Ser Asn Ser Asp Gly Leu Phe Gly
      35      40      45
Val Leu Thr Asn Lys Met Leu Pro Leu Thr Leu Gly Leu Thr Phe Gly
      50      55      60
Ser Leu Ile Ala Gly Ser Leu Leu Ser Thr Leu Leu Ile Ile Ile Lys
65      70      75      80
Arg Phe Ser Lys Ser Val Phe Gly Trp Glu Gly Tyr Leu Thr Leu Thr
      85      90      95
Leu Pro Val Asn Ser His Gln Ile Ile Leu Ser Lys Leu Leu Ala Ser
      100     105     110
Phe Ile Cys Ser Val Phe Asn Thr Ile Ile Leu Ala Phe Ala Ile Ala
      115     120     125
Ile Val Ile Val Pro Met Phe Asn Ile Asn Glu Leu Leu Glu Gly Phe
      130     135     140
Phe Asn Ser Phe Lys Met Asp Tyr Phe Ile Asn Met Leu Thr Val Leu
145     150     155     160
Ala Tyr Val Leu Leu Ser Thr Phe Thr Ser Ile Leu Leu Ile Tyr Leu
      165     170     175
Ser Ile Ser Ile Gly Gln Leu Phe Ser Asn Arg Arg Gly Leu Met Ala
      180     185     190
Phe Ile Ala Tyr Phe Ile Leu Val Ile Leu Ile Ser Val Ala Ala Thr
      195     200     205
Tyr Val His Ser His Ile Phe Asn Ile Asn Thr Ser Ala Asp Ser Phe
      210     215     220
Pro Phe Thr Glu Gln Lys Thr Ile Tyr Leu Leu Ile Leu Glu Gln Phe
225     230     235     240
Ile Glu Met Ile Met Phe Tyr Leu Ala Thr Asn Phe Ile Ile Lys Asn
      245     250     255
Lys Leu Asn Leu Gln
      260

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<210> SEQ ID NO 333
<211> LENGTH: 558
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes

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<400> SEQUENCE: 333
atggttaaagc gagattttat aagaaatata ttattgttat taattgtgat tattggggct      60
attttggtga gaatctttgt tttttcaact tttaaagttt ctccagaaac agctaatact      120
tatttaaaga gtggtgattt agtcacaatc aaaaaaataa ttcagcccaa atataaagat      180
tttgtgggtt atagagttgg aaaaaaagat tatgtcagtc gagtcattgc tgttgaaggc      240
gatagcgtga cttatatgga cgatatTTTTT tacctcaata atatggtaga gtcacaggct      300
taccttgaaa agatgaaagc acattacttg aatcatgcac cgtttggcac attgtataca      360
gatgatttta cagttgctac catcacagct gataagtatc aaaaagtcc taaggggaag      420
tatcttcttt tgaatgataa ccggaaaaat acgaatgaca gtcgtcgatt tgggttaata      480
aatgcctcgc agattaaagg tttagtgacc tttagagttt tgcctctcag cgattttgga      540
tttgtagaag tagagtag
558

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<210> SEQ ID NO 334
<211> LENGTH: 185
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 334

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Met Val Lys Arg Asp Phe Ile Arg Asn Ile Leu Leu Leu Ile Val
1           5           10          15
Ile Ile Gly Ala Ile Leu Leu Arg Ile Phe Val Phe Ser Thr Phe Lys
20          25          30
Val Ser Pro Glu Thr Ala Asn Thr Tyr Leu Lys Ser Gly Asp Leu Val
35          40          45
Thr Ile Lys Lys Asn Ile Gln Pro Lys Tyr Lys Asp Phe Val Val Tyr
50          55          60
Arg Val Gly Lys Lys Asp Tyr Val Ser Arg Val Ile Ala Val Glu Gly
65          70          75          80
Asp Ser Val Thr Tyr Met Asp Asp Ile Phe Tyr Leu Asn Asn Met Val
85          90          95
Glu Ser Gln Ala Tyr Leu Glu Lys Met Lys Ala His Tyr Leu Asn His
100         105         110
Ala Pro Phe Gly Thr Leu Tyr Thr Asp Asp Phe Thr Val Ala Thr Ile
115         120         125
Thr Ala Asp Lys Tyr Gln Lys Val Pro Lys Gly Lys Tyr Leu Leu Leu
130         135         140
Asn Asp Asn Arg Lys Asn Thr Asn Asp Ser Arg Arg Phe Gly Leu Ile
145         150         155         160
Asn Ala Ser Gln Ile Lys Gly Leu Val Thr Phe Arg Val Leu Pro Leu
165         170         175
Ser Asp Phe Gly Phe Val Glu Val Glu
180         185

```

```

<210> SEQ ID NO 335
<211> LENGTH: 642
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 335

```

```

atgacctata ttcagcaagt tttaccacgc ttattagatg gtgccttggt gactttacaa      60
gtattcttta ttgttatcat tctttctata cccttagggg ctatttttagc tttcttgatg      120
aagattccct ttaaaccgct acagtgggtt ttgaccctat acgtgtggat gatgcgaggg      180
acaccattac tacttcaatt gatttttttc tattatgttt tgccaagtgt ggggattagt      240
tttgatcgaa tgccagctgc tattttggcg tttactttga attatgctgc ctactttgct      300
gaaattttta gaggtgggat tgaggctatt ccaaaaggtc aatatgaagc agctaaaagta      360
ttaaagttaa aacctcttca aaccattcgt tatattattt tgcctcaagt gtttaaaatt      420
gtgttaccaa gtgttttcaa tgaagtcatt aatttgggtca aagattcttc cttgtctat      480
gtactcgggtg taggagatct tttattagca agtaagacgg cagccaatag ggatgcaacc      540
ttagccccta tgtttatcgc tggcttatc tatttgcttt taattggact ggtcacgatt      600

```


atttcaaaac aagttgaaaa acggtttaat tattatcagt aa

642

<210> SEQ ID NO 336

<211> LENGTH: 213

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 336

```
Met Thr Tyr Ile Gln Gln Val Leu Pro Ser Leu Leu Asp Gly Ala Leu
1      5      10      15
Val Thr Leu Gln Val Phe Phe Ile Val Ile Ile Leu Ser Ile Pro Leu
20     25     30
Gly Ala Ile Leu Ala Phe Leu Met Lys Ile Pro Phe Lys Pro Leu Gln
35     40     45
Trp Phe Leu Thr Leu Tyr Val Trp Met Met Arg Gly Thr Pro Leu Leu
50     55     60
Leu Gln Leu Ile Phe Phe Tyr Tyr Val Leu Pro Ser Val Gly Ile Ser
65     70     75     80
Phe Asp Arg Met Pro Ala Ala Ile Leu Ala Phe Thr Leu Asn Tyr Ala
85     90     95
Ala Tyr Phe Ala Glu Ile Phe Arg Gly Gly Ile Glu Ala Ile Pro Lys
100    105    110
Gly Gln Tyr Glu Ala Ala Lys Val Leu Lys Leu Lys Pro Leu Gln Thr
115    120    125
Ile Arg Tyr Ile Ile Leu Pro Gln Val Phe Lys Ile Val Leu Pro Ser
130    135    140
Val Phe Asn Glu Val Ile Asn Leu Val Lys Asp Ser Ser Leu Val Tyr
145    150    155    160
Val Leu Gly Val Gly Asp Leu Leu Leu Ala Ser Lys Thr Ala Ala Asn
165    170    175
Arg Asp Ala Thr Leu Ala Pro Met Phe Ile Ala Gly Leu Ile Tyr Leu
180    185    190
Leu Leu Ile Gly Leu Val Thr Ile Ser Lys Gln Val Glu Lys Arg
195    200    205
Phe Asn Tyr Tyr Gln
210
```

<210> SEQ ID NO 337

<211> LENGTH: 774

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 337

```
atgaaaccca aacaccttct ctgtctttca acagttgttg ctggattagc tttattttca 60
actatgacgc actcagtttt agctgatgat gcttcaaadc ccgatgctat tttaatgaat 120
aacaaccaag caaatTTTtca aagagatgct ctagtGcaaa agcttgatga gggacatcaa 180
caattagaag ctattaaaca tgaagctaaa ggtactgata ttgagactac tgTTaacaaa 240
gctatcgatg ctgttgatca catgaagagt tctatacgct tcaatactga aacgatctat 300
gatttttagtt caattggggc aagagtagaa gcattatcag atgctatcaa agcaatcgta 360
ttttccacaa cccaattaac tcataaagta gaaaaagcgc atactgatat ggggtttgct 420
attactaaat tagtcattcg tattatagat ccatttgcac ctgttgacgc tatcaaagct 480
caagtacaag aaattaaagc acttgaggaa aaagttatca attatcctga tttacagcca 540
acagaccgtg ctactatcta tactaaagct aaactaaata aagctatttg gaacactcgt 600
ttagaaagag ataaaaaggt tttgggaatc aaaccatttg acgtttacaa tagacttaac 660
aaagctatca cacatgcggt tgggtgtccaa ctaaatccga caaccactgt tcaacaagtt 720
gacgatgaag ttattgctgt gcaagatgct ttggaaacag ctcttaagtc atag 774
```

<210> SEQ ID NO 338

<211> LENGTH: 257

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 338

```
Met Lys Pro Lys His Leu Leu Cys Leu Ser Thr Val Val Ala Gly Leu
 1          5          10          15
Ala Leu Phe Ser Thr Met Thr His Ser Val Leu Ala Asp Asp Ala Ser
 20          25          30
Asn Pro Asp Ala Ile Leu Met Asn Asn Asn Gln Ala Asn Phe Gln Arg
 35          40          45
Asp Ala Leu Val Gln Lys Leu Asp Glu Gly His Gln Gln Leu Glu Ala
 50          55          60
Ile Lys His Glu Ala Lys Gly Thr Asp Ile Glu Thr Thr Val Asn Lys
 65          70          75          80
Ala Ile Asp Ala Val Asp His Met Lys Ser Ser Ile Arg Phe Asn Thr
 85          90          95
Glu Thr Ile Tyr Asp Phe Ser Ser Ile Gly Ala Arg Val Glu Ala Leu
100          105          110
Ser Asp Ala Ile Lys Ala Ile Val Phe Ser Thr Thr Gln Leu Thr His
115          120          125
Lys Val Glu Lys Ala His Thr Asp Met Gly Phe Ala Ile Thr Lys Leu
130          135          140
Val Ile Arg Ile Ile Asp Pro Phe Ala Ser Val Asp Ala Ile Lys Ala
145          150          155          160
Gln Val Gln Glu Ile Lys Ala Leu Glu Glu Lys Val Ile Asn Tyr Pro
165          170          175
Asp Leu Gln Pro Thr Asp Arg Ala Thr Ile Tyr Thr Lys Ala Lys Leu
180          185          190
Asn Lys Ala Ile Trp Asn Thr Arg Leu Glu Arg Asp Lys Lys Val Leu
195          200          205
Gly Ile Lys Pro Phe Asp Val Tyr Asn Arg Leu Asn Lys Ala Ile Thr
210          215          220
His Ala Val Gly Val Gln Leu Asn Pro Thr Thr Thr Val Gln Gln Val
225          230          235          240
Asp Asp Glu Val Ile Ala Val Gln Asp Ala Leu Glu Thr Ala Leu Lys
245          250          255
Ser
```

<210> SEQ ID NO 339

<211> LENGTH: 1236

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 339

```
atgacacagg atccgattgc aaatttaaaa ctagccagaa agggcccaat cgttagtatt      60
attgtctact tgtcgcttag tgttgccaaa ttattagctg gttatttggt aaatgcaagt      120
tcccttattg ctgatggatt taacaattta tcggatattg tgggaaatgt agccctgctt      180
attggtcttc acttagctag ccaaccagcc gatgccaatc ataaatttgg tcattggaaa      240
attgaagact tatccagcct tgtcacttct tttattatgt ttcttgtagg tttccaagta      300
ctgattcaca caattaaag tatcttttag ggtcagcaag ttgatattga ccctcttggg      360
gctattgtcg gtatcgtttc agcttttggt atggttagggg tttatgtctt taacaaacgt      420
ctttccaaac gtgtaaaatc cagtgcctta gtcgctgctt ctaaggataa tctagctgat      480
gctgttactt ctatcggaac atcaattgct attatagcag cttctttgca tttaccagtt      540
atcgatcata tagctgctat gatcattacg ttctttattc ttaaaacagc ttttgatata      600
tttatggaaa gttcgtttag tttatctgat ggatttgata gccgtcattt gaaaaaatat      660
gaaaaagcca ttttagaaat ccctaaaatt gtcgccgtta agtctcaacg agctaggacc      720
tatggtagca atgtctatct tgatattgta cttgaaatga atcctgatct ttcagtctat      780
gaaagtcact ctattacaga gaaagtggag cagttattga gtgaccaatt ttctatttat      840
gacattgaca ttcacgttga gcctgccatg attcccgaag aagagatttt tgataatgtc      900
```

gccaaaaagc tctaccgcta cgaaaaatta attttgagta aggttcctga ctatgaccac	960
tacattgcta agtctttcca actgattgat gcgaatggcc aaacagttaa ctatgaacaa	1020
tttttgaacc aagaaattta ttatccaagt aacttcaacc attttcagat tgaatccatt	1080
agtcaaaaaa cgatgttggt aacttaccaa ttaaattggca atcaacgtac cagtatttgg	1140
aggcgtcatg aatcttggtc cttactcttc caccaaatta cccctatcgc taagaaacaa	1200
ttacatcaca cacactatcg tattgtaaaa atgtaa	1236

<210> SEQ ID NO 340

<211> LENGTH: 411

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 340

Met Thr Gln Asp Pro Ile Ala Asn Leu Lys Leu Ala Arg Lys Gly Pro	
1 5 10 15	
Ile Val Ser Ile Ile Val Tyr Leu Ser Leu Ser Val Ala Lys Leu Leu	
20 25 30	
Ala Gly Tyr Leu Leu Asn Ala Ser Ser Leu Ile Ala Asp Gly Phe Asn	
35 40 45	
Asn Leu Ser Asp Ile Val Gly Asn Val Ala Leu Leu Ile Gly Leu His	
50 55 60	
Leu Ala Ser Gln Pro Ala Asp Ala Asn His Lys Phe Gly His Trp Lys	
65 70 75 80	
Ile Glu Asp Leu Ser Ser Leu Val Thr Ser Phe Ile Met Phe Leu Val	
85 90 95	
Gly Phe Gln Val Leu Ile His Thr Ile Lys Ser Ile Phe Ser Gly Gln	
100 105 110	
Gln Val Asp Ile Asp Pro Leu Gly Ala Ile Val Gly Ile Val Ser Ala	
115 120 125	
Phe Val Met Leu Gly Val Tyr Val Phe Asn Lys Arg Leu Ser Lys Arg	
130 135 140	
Val Lys Ser Ser Ala Leu Val Ala Ala Ser Lys Asp Asn Leu Ala Asp	
145 150 155 160	
Ala Val Thr Ser Ile Gly Thr Ser Ile Ala Ile Ile Ala Ala Ser Leu	
165 170 175	
His Leu Pro Val Ile Asp His Ile Ala Ala Met Ile Ile Thr Phe Phe	
180 185 190	
Ile Leu Lys Thr Ala Phe Asp Ile Phe Met Glu Ser Ser Phe Ser Leu	
195 200 205	
Ser Asp Gly Phe Asp Ser Arg His Leu Lys Lys Tyr Glu Lys Ala Ile	
210 215 220	
Leu Glu Ile Pro Lys Ile Val Ala Val Lys Ser Gln Arg Ala Arg Thr	
225 230 235 240	
Tyr Gly Ser Asn Val Tyr Leu Asp Ile Val Leu Glu Met Asn Pro Asp	
245 250 255	
Leu Ser Val Tyr Glu Ser His Ser Ile Thr Glu Lys Val Glu Gln Leu	
260 265 270	
Leu Ser Asp Gln Phe Ser Ile Tyr Asp Ile Asp Ile His Val Glu Pro	
275 280 285	
Ala Met Ile Pro Glu Glu Glu Ile Phe Asp Asn Val Ala Lys Lys Leu	
290 295 300	
Tyr Arg Tyr Glu Lys Leu Ile Leu Ser Lys Val Pro Asp Tyr Asp His	
305 310 315 320	
Tyr Ile Ala Lys Ser Phe Gln Leu Ile Asp Ala Asn Gly Gln Thr Val	
325 330 335	
Asn Tyr Glu Gln Phe Leu Asn Gln Glu Ile Tyr Tyr Pro Ser Asn Phe	
340 345 350	
Asn His Phe Gln Ile Glu Ser Ile Ser Gln Lys Thr Met Leu Val Thr	

		355					360					365				
Tyr	Gln	Leu	Asn	Gly	Asn	Gln	Arg	Thr	Ser	Ile	Trp	Arg	Arg	His	Glu	
	370					375					380					
Ser	Trp	Ser	Leu	Leu	Phe	His	Gln	Ile	Thr	Pro	Ile	Ala	Lys	Lys	Gln	
385					390					395					400	
Leu	His	His	Thr	His	Tyr	Arg	Ile	Val	Lys	Met						
				405					410							

```
<210> SEQ ID NO 341
<211> LENGTH: 957
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 341
```

atgggttcag	ttgaacgtac	attaaaaaatg	accttggtcta	ccattgtttgc	cattttaatt	60
gcttaccaac	ttcatctgga	ttatgcaatg	tcagcgggga	tcattgccct	gttaagtgtt	120
ttagacaccc	gtaagtccag	tttggtggtc	gctaggaatc	gcttgctatc	ttttttcctg	180
gcttttgga	ttgcgatgat	gtgctttagc	ttgtttggtt	ttacgacagt	agggtttatg	240
tgttatttgt	taattattat	tcctttgctc	tatcactttc	agatagaggc	aggactgggt	300
cctataacag	tacttgtgac	acatttgatt	gctaaaaaaa	gtattgcatt	acctatttta	360
tcgaatgagt	ttatgctctt	ttttgtaggg	actagtgtcg	ctttactatt	taatgcttat	420
atgggtccac	aagatcagca	aattcggtag	tatcaccaa	aagttgaatc	ggatctgaaa	480
ggtagcttat	accgttttga	aagctttcta	ctggaaggaa	aaggtcaaaa	tgaagggtc	540
ttgatcaaaa	accttgataa	aatattagat	gaagctctaa	aactagttta	tcgagaaagg	600
cataatcaac	tatttcagca	gaccaattat	caagttcatt	attttgagat	gcgacgacaa	660
caaaatagac	tatttggaca	aatggctatc	aacgtaaaca	cgttaatgag	acaaagtaag	720
gaaagtattc	ttttgtcaca	tctttttcac	gaaactgctt	gtcagctaag	cgaacaaaaa	780
ccggctttaa	ccttgattga	tgacatcgaa	caattgcttg	aaacctttcg	tcatggtgat	840
cttcctcaaa	ctcgggagga	at ttgagcga	cgtgcggttt	tatttcagct	cttacaagac	900
ttagagcgct	ttatcttatt	aaaggtagag	ttttatcagg	attatcaaaa	tgactaa	957

```
<210> SEQ ID NO 342
<211> LENGTH: 318
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 342
```

Met	Gly	Ser	Val	Glu	Arg	Thr	Leu	Lys	Met	Thr	Leu	Ala	Thr	Ile	Val
1				5					10					15	
Ala	Ile	Leu	Ile	Ala	Tyr	Gln	Leu	His	Leu	Asp	Tyr	Ala	Met	Ser	Ala
			20					25					30		
Gly	Ile	Ile	Ala	Leu	Leu	Ser	Val	Leu	Asp	Thr	Arg	Lys	Ser	Ser	Leu
		35					40					45			
Val	Val	Ala	Arg	Asn	Arg	Leu	Leu	Ser	Phe	Phe	Leu	Ala	Phe	Gly	Ile
	50					55					60				
Ala	Met	Met	Cys	Phe	Ser	Leu	Phe	Gly	Phe	Thr	Thr	Val	Gly	Phe	Met
65					70					75					80
Cys	Tyr	Leu	Leu	Ile	Ile	Ile	Pro	Leu	Leu	Tyr	His	Phe	Gln	Ile	Glu
			85						90				95		
Ala	Gly	Leu	Val	Pro	Ile	Thr	Val	Leu	Val	Thr	His	Leu	Ile	Ala	Lys
			100					105					110		
Lys	Ser	Ile	Ala	Leu	Pro	Ile	Leu	Ser	Asn	Glu	Phe	Met	Leu	Phe	Phe
		115					120					125			
Val	Gly	Thr	Ser	Val	Ala	Leu	Leu	Phe	Asn	Ala	Tyr	Met	Gly	Pro	Gln
	130					135					140				
Asp	Gln	Gln	Ile	Arg	Tyr	His	Gln	Lys	Val	Glu	Ser	Asp	Leu	Lys	
145					150				155					160	
Gly	Ile	Leu	Tyr	Arg	Phe	Glu	Ser	Phe	Leu	Leu	Glu	Gly	Lys	Gly	Gln
				165					170					175	

Asn	Glu	Gly	Leu	Leu	Ile	Lys	Asn	Leu	Asp	Lys	Ile	Leu	Asp	Glu	Ala
			180					185					190		
Leu	Lys	Leu	Val	Tyr	Arg	Glu	Arg	His	Asn	Gln	Leu	Phe	Gln	Gln	Thr
		195					200					205			
Asn	Tyr	Gln	Val	His	Tyr	Phe	Glu	Met	Arg	Arg	Gln	Gln	Asn	Arg	Leu
	210					215					220				
Leu	Gly	Gln	Met	Ala	Ile	Asn	Val	Asn	Thr	Leu	Met	Arg	Gln	Ser	Lys
225					230					235					240
Glu	Ser	Ile	Leu	Leu	Ser	His	Leu	Phe	His	Glu	Thr	Ala	Cys	Gln	Leu
			245						250					255	
Ser	Glu	Gln	Asn	Pro	Ala	Leu	Thr	Leu	Ile	Asp	Asp	Ile	Glu	Gln	Leu
		260						265					270		
Leu	Glu	Thr	Phe	Arg	His	Gly	Asp	Leu	Pro	Gln	Thr	Arg	Glu	Glu	Phe
		275				280						285			
Glu	Arg	Arg	Ala	Val	Leu	Phe	Gln	Leu	Leu	Gln	Asp	Leu	Glu	Arg	Phe
	290					295					300				
Ile	Leu	Leu	Lys	Val	Glu	Phe	Tyr	Gln	Asp	Tyr	Gln	Asn	Asp		
305					310					315					

<210> SEQ ID NO 343
 <211> LENGTH: 936
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 343

atggaaaatc	aggaattggc	taaaaaatta	gcctcaccat	caaagaattc	aaggcttgaa	60
acctttggcc	gcaccattac	gttttttgtgt	ctggctttga	ttgtttttat	cgttgcgatg	120
attctgatct	tcgttgctca	aaaaggggtg	tcaaccttct	ttgttgacaa	ggttaatcct	180
tttgatttct	tgtttgaaaa	ggagtggcaa	ccaagtgtaa	aaaatgcggc	cggcattcct	240
tatcttggtg	ctctgccaat	gattacagga	tccttttttg	ttaccatttt	atctgctatt	300
attgccaccc	catttgccat	tggcgcagcc	gtttttatga	ctgaaatctc	acctaaatat	360
ggcgctaaat	tattacagcc	tgcggttgag	cttttggttg	gaattccttc	ggttgtttat	420
gggtttatcg	gtttgcaagt	gattgttcct	tttatgcgct	ctatcttttg	tggcacaggt	480
tttgaatcc	tatctggggg	ctgtgtcttg	tttgttatga	ttttaccaac	agtgactttt	540
atgacaacag	acagtctgcg	ggcggtgcc	cgtcattacc	gcgaagcgtc	tatggctatg	600
ggagcaaac	gttggcaaac	catttggcgt	gtgtgcctta	atgcagctcg	tccaggaatt	660
tttaccgctg	ttatttttgg	aatggcaaga	gcttttgag	aagccttggc	tatccaaatg	720
gtagtgggta	actctgctgt	aatgccaaagt	tcactaacga	caccagccgc	aaccttaacg	780
tctgtcttga	caatgggtat	tggtaacacg	gttatgggaa	cgggtccaaa	taatgtgctt	840
tgggcccttg	ccctagtctt	attattaatg	agtctggcct	tcaattccct	tgtcaaatta	900
atcacgaaag	aaagaaagag	aaattatgaa	cgctaa			936

<210> SEQ ID NO 344
 <211> LENGTH: 311
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 344

Met	Glu	Asn	Gln	Glu	Leu	Ala	Lys	Lys	Leu	Ala	Ser	Pro	Ser	Lys	Asn
1				5					10					15	
Ser	Arg	Leu	Glu	Thr	Phe	Gly	Arg	Thr	Ile	Thr	Phe	Leu	Cys	Leu	Ala
		20						25				30			
Leu	Ile	Val	Phe	Ile	Val	Ala	Met	Ile	Leu	Ile	Phe	Val	Ala	Gln	Lys
	35					40					45				
Gly	Leu	Ser	Thr	Phe	Phe	Val	Asp	Lys	Val	Asn	Leu	Phe	Asp	Phe	Leu
	50					55				60					
Phe	Gly	Lys	Glu	Trp	Gln	Pro	Ser	Val	Lys	Asn	Ala	Ala	Gly	Ile	Pro
65				70					75					80	
Tyr	Leu	Gly	Ala	Leu	Pro	Met	Ile	Thr	Gly	Ser	Phe	Leu	Val	Thr	Ile

				85					90					95					
Leu	Ser	Ala	Ile	Ile	Ala	Thr	Pro	Phe	Ala	Ile	Gly	Ala	Ala	Val	Phe				
			100					105					110						
Met	Thr	Glu	Ile	Ser	Pro	Lys	Tyr	Gly	Ala	Lys	Leu	Leu	Gln	Pro	Ala				
		115					120					125							
Val	Glu	Leu	Leu	Val	Gly	Ile	Pro	Ser	Val	Val	Tyr	Gly	Phe	Ile	Gly				
	130					135					140								
Leu	Gln	Val	Ile	Val	Pro	Phe	Met	Arg	Ser	Ile	Phe	Gly	Gly	Thr	Gly				
145					150					155					160				
Phe	Gly	Ile	Leu	Ser	Gly	Val	Cys	Val	Leu	Phe	Val	Met	Ile	Leu	Pro				
			165					170					175						
Thr	Val	Thr	Phe	Met	Thr	Thr	Asp	Ser	Leu	Arg	Ala	Val	Pro	Arg	His				
		180					185					190							
Tyr	Arg	Glu	Ala	Ser	Met	Ala	Met	Gly	Ala	Thr	Arg	Trp	Gln	Thr	Ile				
	195					200					205								
Trp	Arg	Val	Val	Leu	Asn	Ala	Ala	Arg	Pro	Gly	Ile	Phe	Thr	Ala	Val				
	210				215					220									
Ile	Phe	Gly	Met	Ala	Arg	Ala	Phe	Gly	Glu	Ala	Leu	Ala	Ile	Gln	Met				
225				230				235						240					
Val	Val	Gly	Asn	Ser	Ala	Val	Met	Pro	Ser	Ser	Leu	Thr	Thr	Pro	Ala				
			245			250						255							
Ala	Thr	Leu	Thr	Ser	Val	Leu	Thr	Met	Gly	Ile	Gly	Asn	Thr	Val	Met				
		260				265					270								
Gly	Thr	Val	Gln	Asn	Asn	Val	Leu	Trp	Ser	Leu	Ala	Leu	Val	Leu	Leu				
	275					280					285								
Leu	Met	Ser	Leu	Ala	Phe	Asn	Ser	Leu	Val	Lys	Leu	Ile	Thr	Lys	Glu				
	290				295					300									
Arg	Lys	Arg	Asn	Tyr	Glu	Arg													
305				310															

<210> SEQ ID NO 345

<211> LENGTH: 888

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 345

atgaacgcta	aaaaagtcga	taaagtagca	actggtactc	tttataccat	tgctggaatt	60
attgtagcta	ttttagcttc	cttaattcta	tatatccttg	tccgtggcct	gccacacatc	120
agctggctct	ttttaacagg	aaaatcgtct	tcgtacgaag	ctggtggggg	aattgggtatc	180
cagttgtata	attccttctt	cctattgatt	gttactttta	ttattttccat	tccttttatca	240
actggagcgg	ggattttactt	ggctgaatat	gccaaaaaag	gacctgttac	caactttatt	300
agaacctgta	ttgagattct	gtcttcccta	ccatctgtgg	ttgtggggct	ctttggttac	360
ttgattttcg	ttgtgcagtt	tgaatatggc	ttttctatta	tttcaggggc	tcttgctttg	420
acggctctta	atcttctcta	aatgacccgt	aatgttgaag	atagtttact	gcatgttcat	480
catacccaaa	gagaagcagg	attagcttta	ggcctgtcac	gctgggaaac	ggttttttat	540
gtggttatcc	cagaagctct	cccgggaatg	gtaacaggta	ttgtcttagc	ttcaggtcgt	600
atTTTTggtg	aagcggcagc	gcttatctat	actgctggtc	aatcagcacc	agctctggat	660
tggtcaaatt	ggaatccact	tagtgttact	agtccaatct	ctattttccg	tcaatctgag	720
acccttgctg	ttcatatttg	gaaagtcaat	agcgaaggga	caattccaga	tgctactctt	780
gtatccgcag	gaagtgcagc	agtgtctatta	atttttatcc	ttattttcaa	cttttcagct	840
cactttattg	ggaagaaact	tcattctaaa	atgacagcag	cgaaataa		888

<210> SEQ ID NO 346

<211> LENGTH: 295

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 346

Met Asn Ala Lys Lys Val Asp Lys Val Ala Thr Gly Thr Leu Tyr Thr

1				5					10					15			
Ile	Ala	Gly	Ile	Ile	Val	Ala	Ile	Leu	Ala	Ser	Leu	Ile	Leu	Tyr	Ile		
			20					25					30				
Leu	Val	Arg	Gly	Leu	Pro	His	Ile	Ser	Trp	Ser	Phe	Leu	Thr	Gly	Lys		
		35					40					45					
Ser	Ser	Ser	Tyr	Glu	Ala	Gly	Gly	Gly	Ile	Gly	Ile	Gln	Leu	Tyr	Asn		
	50					55					60						
Ser	Phe	Phe	Leu	Leu	Ile	Val	Thr	Leu	Ile	Ile	Ser	Ile	Pro	Leu	Ser		
65					70					75				80			
Thr	Gly	Ala	Gly	Ile	Tyr	Leu	Ala	Glu	Tyr	Ala	Lys	Lys	Gly	Pro	Val		
			85					90					95				
Thr	Asn	Phe	Ile	Arg	Thr	Cys	Ile	Glu	Ile	Leu	Ser	Ser	Leu	Pro	Ser		
		100						105					110				
Val	Val	Val	Gly	Leu	Phe	Gly	Tyr	Leu	Ile	Phe	Val	Val	Gln	Phe	Glu		
		115				120						125					
Tyr	Gly	Phe	Ser	Ile	Ile	Ser	Gly	Ala	Leu	Ala	Leu	Thr	Val	Phe	Asn		
	130					135					140						
Leu	Pro	Gln	Met	Thr	Arg	Asn	Val	Glu	Asp	Ser	Leu	Leu	His	Val	His		
145				150					155					160			
His	Thr	Gln	Arg	Glu	Ala	Gly	Leu	Ala	Leu	Gly	Leu	Ser	Arg	Trp	Glu		
		165				170							175				
Thr	Val	Phe	Tyr	Val	Val	Ile	Pro	Glu	Ala	Leu	Pro	Gly	Met	Val	Thr		
		180				185						190					
Gly	Ile	Val	Leu	Ala	Ser	Gly	Arg	Ile	Phe	Gly	Glu	Ala	Ala	Ala	Leu		
	195					200					205						
Ile	Tyr	Thr	Ala	Gly	Gln	Ser	Ala	Pro	Ala	Leu	Asp	Trp	Ser	Asn	Trp		
	210				215						220						
Asn	Pro	Leu	Ser	Val	Thr	Ser	Pro	Ile	Ser	Ile	Phe	Arg	Gln	Ser	Glu		
225				230					235					240			
Thr	Leu	Ala	Val	His	Ile	Trp	Lys	Val	Asn	Ser	Glu	Gly	Thr	Ile	Pro		
		245				250						255					
Asp	Ala	Thr	Leu	Val	Ser	Ala	Gly	Ser	Ala	Ala	Val	Leu	Leu	Ile	Phe		
		260				265						270					
Ile	Leu	Ile	Phe	Asn	Phe	Ser	Ala	His	Phe	Ile	Gly	Lys	Lys	Leu	His		
	275					280						285					
Ser	Lys	Met	Thr	Ala	Ala	Lys											
	290					295											

<210> SEQ ID NO 347

<211> LENGTH: 312

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 347

ttgatatatg	cattaagggc	ttcttctacc	atctgtttca	cagcttttcc	cataaggttg	60
atttggttctt	caaccactgg	aatacgtcc	tcacctttca	tacgaatagt	ggccttggca	120
atcgaagcag	catggtcacc	catacgttca	atatcacttg	atgcctttaa	aacagtaata	180
accattctaa	gatcattcga	aactggctgt	tgtagggcaa	taatttccag	cgatttcttt	240
tcaagctttg	tctcaaaatt	attaatagt	tcattcttctt	cgataacttc	tttggccaat	300
tcacgatcat	ga					312

<210> SEQ ID NO 348

<211> LENGTH: 103

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 348

Met	Ile	Tyr	Ala	Leu	Arg	Ala	Ser	Ser	Thr	Ile	Cys	Phe	Thr	Ala	Phe
1				5					10					15	

Pro	Ile	Arg	Leu	Ile	Cys	Ser	Ser	Thr	Thr	Gly	Ile	Arg	Ser	Ser	Pro
			20					25					30		
Phe	Ile	Arg	Ile	Val	Ala	Leu	Ala	Ile	Glu	Ala	Ala	Trp	Ser	Pro	Ile
		35					40					45			
Arg	Ser	Ile	Ser	Leu	Asp	Ala	Phe	Lys	Thr	Val	Ile	Thr	Ile	Leu	Arg
	50					55					60				
Ser	Phe	Glu	Thr	Gly	Cys	Cys	Arg	Ala	Ile	Ile	Ser	Ser	Asp	Phe	Phe
65					70					75				80	
Ser	Ser	Phe	Val	Ser	Lys	Leu	Leu	Ile	Val	Ser	Ser	Ser	Ser	Ile	Thr
				85					90					95	
Ser	Leu	Ala	Asn	Ser	Arg	Ser									
				100											

<210> SEQ ID NO 349

<211> LENGTH: 1311

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 349

atgaataaat	taaaaaaaga	gattttatca	gataactata	accacttttt	tcattttttt	60
gcggttttta	cagggtatttt	tgtcattatg	actattatta	tcttacagat	tatgcggttt	120
ggcgtttatt	cgtcagttga	cagtagttta	gtttctgtta	gtaataatgc	aagtagctat	180
gctaatacgt	cgatggctag	aatatcttct	ttttactttg	atactgaaaa	taacattatt	240
aaggcgctgc	ctgattcaga	tagttctaag	ttattaggaa	cgctgcagc	taatacagat	300
atcattttgt	ttagtgctaa	tggaacaatt	ttaaatgctt	ttgatgcgtt	ttctaactat	360
caaaattttc	atttagataa	acgccggttg	gggagtattg	aaaccaccag	tttaatgaat	420
ttttatggac	aagaagaaaa	ataccatacg	ataactgtag	gggttcatat	caaaaattat	480
cctgcagttg	cctatatgat	ggcagtagta	aatgtggaac	aattagaccg	cgtaaatgaa	540
cgttatgagc	gcattattat	tatagttatg	agtgtttttt	ggctaatttc	tatttttagca	600
agtattttatt	tagccaagtg	gagcagaaaa	cctatttttag	aaagctatga	aaaacaaaaa	660
atgtttgttg	aaaatgctag	tcatgaatta	aggacccttt	tggcggctct	acagaatcgt	720
ctggaatcgc	tttttcgtaa	gccaacgaa	acgatattag	aaaatagtga	gcctctcgct	780
tctagtttag	acgaggttcg	caacatgcgc	atcttaacaa	ctaattttatt	aaatttagca	840
agacgagatg	atggcattaa	tccacagtgg	actcatttag	atacagattt	ttttaatgct	900
atttttgaga	attatgaact	agttgctaaa	gaatatggaa	aaatatttta	ttttcagaac	960
caagtcaata	gatcgttaag	aatggataag	gctttactaa	aacaattaat	aacgatttta	1020
tttgacaatg	ctattaaata	tacagataaa	aatgggtatta	ttgaaattat	agtgaaaaca	1080
acggacaaaa	atttattaat	ttctgttatt	gataatggtc	cagggataac	agatgaagaa	1140
aagaaaaaga	tttttgatcg	tttttatcga	gttgacaaa	ctagaacacg	gcaaacaggt	1200
ggatttggtc	tggggttggc	tttagctcag	caaatcgtga	tgtcttttaa	aggaaatatt	1260
acagtaaagg	ataatgatcc	taaaggtagt	atttttgaag	tcaaactata	a	1311

<210> SEQ ID NO 350

<211> LENGTH: 436

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 350

Met	Asn	Lys	Leu	Lys	Lys	Glu	Ile	Leu	Ser	Asp	Asn	Tyr	Asn	His	Phe
1				5					10					15	
Phe	His	Phe	Phe	Ala	Val	Phe	Thr	Gly	Ile	Phe	Val	Ile	Met	Thr	Ile
		20						25				30			
Ile	Ile	Leu	Gln	Ile	Met	Arg	Phe	Gly	Val	Tyr	Ser	Ser	Val	Asp	Ser
	35					40					45				
Ser	Leu	Val	Ser	Val	Ser	Asn	Asn	Ala	Ser	Ser	Tyr	Ala	Asn	Arg	Thr
	50					55				60					
Met	Ala	Arg	Ile	Ser	Ser	Phe	Tyr	Phe	Asp	Thr	Glu	Asn	Asn	Ile	Ile
65					70					75				80	
Lys	Ala	Leu	Pro	Asp	Ser	Asp	Ser	Ser	Lys	Leu	Leu	Gly	Thr	Pro	Ala

				85					90					95			
Ala	Asn	Thr	Asp	Ile	Ile	Leu	Phe	Ser	Ala	Asn	Gly	Thr	Ile	Leu	Asn		
			100					105					110				
Ala	Phe	Asp	Ala	Phe	Ser	Asn	Tyr	Gln	Asn	Phe	His	Leu	Asp	Lys	Arg		
		115					120					125					
Arg	Leu	Gly	Ser	Ile	Glu	Thr	Thr	Ser	Leu	Met	Asn	Phe	Tyr	Gly	Gln		
	130					135					140						
Glu	Glu	Lys	Tyr	His	Thr	Ile	Thr	Val	Gly	Val	His	Ile	Lys	Asn	Tyr		
145					150					155				160			
Pro	Ala	Val	Ala	Tyr	Met	Met	Ala	Val	Val	Asn	Val	Glu	Gln	Leu	Asp		
			165					170						175			
Arg	Ala	Asn	Glu	Arg	Tyr	Glu	Arg	Ile	Ile	Ile	Ile	Val	Met	Ser	Val		
		180						185					190				
Phe	Trp	Leu	Ile	Ser	Ile	Leu	Ala	Ser	Ile	Tyr	Leu	Ala	Lys	Trp	Ser		
	195					200					205						
Arg	Lys	Pro	Ile	Leu	Glu	Ser	Tyr	Glu	Lys	Gln	Lys	Met	Phe	Val	Glu		
210					215					220							
Asn	Ala	Ser	His	Glu	Leu	Arg	Thr	Pro	Leu	Ala	Val	Leu	Gln	Asn	Arg		
225				230					235					240			
Leu	Glu	Ser	Leu	Phe	Arg	Lys	Pro	Asn	Glu	Thr	Ile	Leu	Glu	Asn	Ser		
			245					250					255				
Glu	His	Leu	Ala	Ser	Ser	Leu	Asp	Glu	Val	Arg	Asn	Met	Arg	Ile	Leu		
		260					265					270					
Thr	Thr	Asn	Leu	Leu	Asn	Leu	Ala	Arg	Arg	Asp	Asp	Gly	Ile	Asn	Pro		
	275					280						285					
Gln	Trp	Thr	His	Leu	Asp	Thr	Asp	Phe	Phe	Asn	Ala	Ile	Phe	Glu	Asn		
290					295					300							
Tyr	Glu	Leu	Val	Ala	Lys	Glu	Tyr	Gly	Lys	Ile	Phe	Tyr	Phe	Gln	Asn		
305				310					315					320			
Gln	Val	Asn	Arg	Ser	Leu	Arg	Met	Asp	Lys	Ala	Leu	Leu	Lys	Gln	Leu		
			325					330					335				
Ile	Thr	Ile	Leu	Phe	Asp	Asn	Ala	Ile	Lys	Tyr	Thr	Asp	Lys	Asn	Gly		
		340					345					350					
Ile	Ile	Glu	Ile	Ile	Val	Lys	Thr	Asp	Lys	Asn	Leu	Leu	Ile	Ser			
	355					360				365							
Val	Ile	Asp	Asn	Gly	Pro	Gly	Ile	Thr	Asp	Glu	Glu	Lys	Lys	Lys	Ile		
	370					375				380							
Phe	Asp	Arg	Phe	Tyr	Arg	Val	Asp	Lys	Ala	Arg	Thr	Arg	Gln	Thr	Gly		
385				390					395					400			
Gly	Phe	Gly	Leu	Gly	Leu	Ala	Leu	Ala	Gln	Gln	Ile	Val	Met	Ser	Leu		
			405					410					415				
Lys	Gly	Asn	Ile	Thr	Val	Lys	Asp	Asn	Asp	Pro	Lys	Gly	Ser	Ile	Phe		
		420					425					430					
Glu	Val	Lys	Leu														
		435															

<210> SEQ ID NO 351

<211> LENGTH: 969

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 351

gtggtaaata	agatgagttt	agtaacaatt	tttgccttat	tgatgtcatc	tatgcttatt	60
tatgcaacac	cactcatttt	cacaagtatt	ggaggaactt	tctcagagcg	ctcaggcggt	120
gtaaatggtg	gtttagaagg	tatcatgggtc	atgggagcgt	tctctgggat	tgttttcaac	180
ttagagtttg	tgaaaacatt	tggaaaagca	acgccttgga	tagccgtttt	agtcggtggt	240
attggttggt	tgattttttc	tttgattcac	gctgtagcaa	ccatcaactt	tcgagctgac	300
cacattgtca	gtggtacagt	gttgaacttg	ttagcacctt	cttttgctgt	cttcttggtt	360

aaagctatgt	acggtaaggg	acaaacagac	aacattcaac	aatcttttgg	gaagtttgat	420
ttcccagggt	tatcacaaat	tcctgtgatt	ggatgatatt	tcttttaaaa	tactagcctt	480
attgggtact	tcgccattgc	tttttcgttc	tttgcttggg	ttttgcttta	taaaaccagg	540
tttggctctgc	gtttacgatc	agttggggaa	caccctcagg	cagctgacac	acttggtatt	600
aacgtctatt	tgatgaaata	ctatgggtgtg	atgatctcag	gttttcttgg	tggaataggt	660
ggagctgttt	atgctcagtc	aatctccgtt	aactttgctg	taacaactat	cttaggtcct	720
ggattttattg	ctttggcagc	tatgatcttt	ggtaaatgga	atccagttgg	cgccatgcta	780
tctagtcttt	tctttggctt	atcgcaaaagt	ttagccgcta	ttggtgctca	attaccatta	840
ctagaaaaga	ttccaacggt	ttacttacag	attgcacctt	atatggtaac	gattattatt	900
ttagctgtct	tctttggtca	agcagttgca	ccaaaagctg	atggaatcaa	ctatatttaa	960
tctaaataa						969

<210> SEQ ID NO 352

<211> LENGTH: 322

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 352

Met	Val	Asn	Lys	Met	Ser	Leu	Val	Thr	Ile	Phe	Ala	Leu	Leu	Met	Ser	
1				5					10					15		
Ser	Met	Leu	Ile	Tyr	Ala	Thr	Pro	Leu	Ile	Phe	Thr	Ser	Ile	Gly	Gly	
			20					25					30			
Thr	Phe	Ser	Glu	Arg	Ser	Gly	Val	Val	Asn	Val	Gly	Leu	Glu	Gly	Ile	
			35				40					45				
Met	Val	Met	Gly	Ala	Phe	Ser	Gly	Ile	Val	Phe	Asn	Leu	Glu	Phe	Ala	
	50					55				60						
Glu	Thr	Phe	Gly	Lys	Ala	Thr	Pro	Trp	Ile	Ala	Val	Leu	Val	Gly	Gly	
65				70					75					80		
Ile	Val	Gly	Leu	Ile	Phe	Ser	Leu	Ile	His	Ala	Val	Ala	Thr	Ile	Asn	
			85					90						95		
Phe	Arg	Ala	Asp	His	Ile	Val	Ser	Gly	Thr	Val	Leu	Asn	Leu	Leu	Ala	
			100					105					110			
Pro	Ser	Phe	Ala	Val	Phe	Leu	Val	Lys	Ala	Met	Tyr	Gly	Lys	Gly	Gln	
			115				120					125				
Thr	Asp	Asn	Ile	Gln	Gln	Ser	Phe	Gly	Lys	Phe	Asp	Phe	Pro	Gly	Leu	
	130					135				140						
Ser	Gln	Ile	Pro	Val	Ile	Gly	Asp	Ile	Phe	Phe	Lys	Asn	Thr	Ser	Leu	
145				150					155						160	
Ile	Gly	Tyr	Phe	Ala	Ile	Ala	Phe	Ser	Phe	Phe	Ala	Trp	Phe	Leu	Leu	
			165					170						175		
Tyr	Lys	Thr	Arg	Phe	Gly	Leu	Arg	Leu	Arg	Ser	Val	Gly	Glu	His	Pro	
			180				185					190				
Gln	Ala	Ala	Asp	Thr	Leu	Gly	Ile	Asn	Val	Tyr	Leu	Met	Lys	Tyr	Tyr	
			195			200				205						
Gly	Val	Met	Ile	Ser	Gly	Phe	Leu	Gly	Gly	Ile	Gly	Gly	Ala	Val	Tyr	
	210				215					220						
Ala	Gln	Ser	Ile	Ser	Val	Asn	Phe	Ala	Val	Thr	Thr	Ile	Leu	Gly	Pro	
225				230					235					240		
Gly	Phe	Ile	Ala	Leu	Ala	Ala	Met	Ile	Phe	Gly	Lys	Trp	Asn	Pro	Val	
			245					250					255			
Gly	Ala	Met	Leu	Ser	Ser	Leu	Phe	Phe	Gly	Leu	Ser	Gln	Ser	Leu	Ala	
			260				265					270				
Val	Ile	Gly	Ala	Gln	Leu	Pro	Leu	Leu	Glu	Lys	Ile	Pro	Thr	Val	Tyr	
		275			280						285					
Leu	Gln	Ile	Ala	Pro	Tyr	Met	Val	Thr	Ile	Ile	Ile	Leu	Ala	Ala	Phe	
	290				295					300						
Phe	Gly	Gln	Ala	Val	Ala	Pro	Lys	Ala	Asp	Gly	Ile	Asn	Tyr	Ile	Lys	
305				310					315					320		

Ser Lys

<210> SEQ ID NO 353

<211> LENGTH: 1578

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 353

```
atgattatca aaaagaaaagc aaaagtaaaa tatttgctcc ataaaaggga acatggattt      60
ttaagaggaa ttttttagtag aacaacaatc attgtattat taattatttt gcaattagtt      120
ttcttatttc aatcttatgc ctggatggag cagtaccgtg tttggataac gattcttgaa      180
agtgtctttg ctattactat tgttttatat ttagttaata gtgatatgga tgctatttca      240
agaatgacgt ggtaattttt gattatgatt gctccattac cagtgtcact gtttttaatt      300
tatacaaaat tggattgggg ttacagaggg ctaaaacaaa gaataaatca tctttagat      360
ctgtctgcac cttacccttag cgatgatgac gctatattag aggtattaaa ggatagcaca      420
tcaaccacat atcattttagt acagtactta gaaagaagtc gtggcaactt tccgatttat      480
aataatacaa gggtaactta cttcccaaca ggtgaaactt tttttgatag tttaaaagaa      540
cagttattct tagctaaaaa gtacattttt cttgaatttt ttattattgc agaaggccaa      600
atgtggggag aaatccttag tattctagaa aaaaaagtca gtgaagggtg agaagttagg      660
gtgttggttg atggcatgaa cgaactatca acgctatcat cagattacgc caagagatta      720
gaacaaatag ggattaaagc taaatcattt ttaccgattt caccctttat ctctacctat      780
tacaattatc gagatcaccg aaaaattgtc gttattgatg gggaggtatc attcactgga      840
ggtattaatc tagcagatga gtacattaat gaagtagagc gttttggcca ctggaaagat      900
gctggtttaa tgcttgaggg tgaagcaaca gacagctttt taattttgtt tttacaaatg      960
tgggtctatca cagaaaaaga actgattatt gatccttatc tttcagatca ttctttaaaa      1020
cttccttcag atggctatgt tattccctac ggtgattccc cgcttgatac tgataaaaata      1080
ggtaaaaatg tttatataga catttttaaat catgctaaag agtacgttta tatcatgaca      1140
ccttacctta ttttagatag cgagatggaa cacgctttac ggtttgcatc agaacgtgga      1200
gtagatatcc gaattattat gccaggagtg ccagataaag gggtaaccata tgccttagct      1260
aaaacctatt ataaagcttt gatgtcttct ggagtaaaaa tttatgagta tcaaccaggg      1320
ttcgttcatt caaaggattt tatctctgat aatacaaaaag cagttgtcgg aacaattaac      1380
ttagactatc gtagccttta tcatcatttt gaatgcgcga cttatttata tcgtgtgtca      1440
gttattgctg atattgtgaa tgactttaat gaagctcaaa agcaatcact attgatgaca      1500
tcagatcatt tgacgcaacg tccttggtat caaaaattga taggattatt agtacgaata      1560
attgccccctc tcttgtaa                                     1578
```

<210> SEQ ID NO 354

<211> LENGTH: 525

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 354

```
Met Ile Ile Lys Lys Lys Ala Lys Val Lys Tyr Leu Leu His Lys Gly
 1             5             10             15
Lys His Gly Phe Leu Arg Gly Ile Phe Ser Arg Thr Thr Ile Ile Val
 20             25             30
Leu Leu Ile Ile Leu Gln Leu Val Phe Leu Phe Gln Ser Tyr Ala Trp
 35             40             45
Met Glu Gln Tyr Arg Val Trp Ile Thr Ile Leu Glu Ser Val Phe Ala
 50             55             60
Ile Thr Ile Val Leu Tyr Leu Val Asn Ser Asp Met Asp Ala Ile Ser
 65             70             75             80
Arg Met Thr Trp Leu Ile Leu Ile Met Ile Ala Pro Leu Pro Val Ser
 85             90             95
Leu Phe Leu Ile Tyr Thr Lys Leu Asp Trp Gly Tyr Arg Gly Leu Lys
100            105            110
Gln Arg Ile Asn His Leu Val Asp Leu Ser Ala Pro Tyr Leu Ser Asp
115            120            125
Asp Asp Ala Ile Leu Glu Val Leu Lys Asp Ser Thr Ser Thr Thr Tyr
```

130	135	140
His Leu Val Gln Tyr	Leu Glu Arg Ser Arg Gly Asn Phe Pro Ile Tyr	
145	150	155
Asn Asn Thr Arg Val Thr Tyr Phe Pro Thr Gly Glu Thr Phe Phe Asp		160
	165	170
Ser Leu Lys Glu Gln Leu Phe Leu Ala Lys Lys Tyr Ile Phe Leu Glu		175
	180	185
Phe Phe Ile Ile Ala Glu Gly Gln Met Trp Gly Glu Ile Leu Ser Ile		190
	195	200
Leu Glu Lys Lys Val Ser Glu Gly Val Glu Val Arg Val Leu Phe Asp		205
	210	215
Gly Met Asn Glu Leu Ser Thr Leu Ser Ser Asp Tyr Ala Lys Arg Leu		220
225	230	235
Glu Gln Ile Gly Ile Lys Ala Lys Ser Phe Leu Pro Ile Ser Pro Phe		240
	245	250
Ile Ser Thr Tyr Tyr Asn Tyr Arg Asp His Arg Lys Ile Val Val Ile		255
	260	265
Asp Gly Glu Val Ser Phe Thr Gly Gly Ile Asn Leu Ala Asp Glu Tyr		270
	275	280
Ile Asn Glu Val Glu Arg Phe Gly His Trp Lys Asp Ala Gly Leu Met		285
	290	295
Leu Glu Gly Glu Ala Thr Asp Ser Phe Leu Ile Leu Phe Leu Gln Met		300
305	310	315
Trp Ser Ile Thr Glu Lys Glu Leu Ile Ile Asp Pro Tyr Leu Ser Asp		320
	325	330
His Ser Leu Lys Leu Pro Ser Asp Gly Tyr Val Ile Pro Tyr Gly Asp		335
	340	345
Ser Pro Leu Asp Thr Asp Lys Ile Gly Lys Asn Val Tyr Ile Asp Ile		350
	355	360
Leu Asn His Ala Lys Glu Tyr Val Tyr Ile Met Thr Pro Tyr Leu Ile		365
	370	375
Leu Asp Ser Glu Met Glu His Ala Leu Arg Phe Ala Ser Glu Arg Gly		380
385	390	395
Val Asp Ile Arg Ile Ile Met Pro Gly Val Pro Asp Lys Gly Val Pro		400
	405	410
Tyr Ala Leu Ala Lys Thr Tyr Tyr Lys Ala Leu Met Ser Ser Gly Val		415
	420	425
Lys Ile Tyr Glu Tyr Gln Pro Gly Phe Val His Ser Lys Val Phe Ile		430
	435	440
Ser Asp Asn Thr Lys Ala Val Val Gly Thr Ile Asn Leu Asp Tyr Arg		445
	450	455
Ser Leu Tyr His His Phe Glu Cys Ala Thr Tyr Leu Tyr Arg Val Ser		460
465	470	475
Val Ile Ala Asp Ile Val Asn Asp Phe Asn Glu Ala Gln Lys Gln Ser		480
	485	490
Leu Leu Met Thr Ser Asp His Leu Thr Gln Arg Pro Trp Tyr Gln Lys		495
	500	505
Leu Ile Gly Leu Leu Val Arg Ile Ile Ala Pro Leu Leu		510
	515	520
		525

<210> SEQ ID NO 355

<211> LENGTH: 1224

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 355

atgacgaatt taacgtttta tgcaaaaatc ggtatttcag aagaagagca tgactctttt
gttaaagaac atcagcaa at tagcgtttta caaggtagtg attgggcaaa aatcaaaaat

60
120

```

caatggcaga atgagcgaat tggatatctat aaagaggaaa agcaggttgc ctctttatca 180
cttttgatta agctattgcc acttgggaaga agcattatct atattccaag agggccagtc 240
atggattatc ttgaccgtga tttggtggca ttaccatga aaacactaaa ggattatggt 300
aaaactaaaa aggccctctt tatcaaataat gatccagcta tcctgttaaa acaatacgca 360
ctggggacagg aagaagaaga aaaaccttta gctttagcag ctattaagaa tctccaagaa 420
gctggtgttc attggactgg ttttaacaatg gagattgcag atagtatcca acctcgtttc 480
caagctaata tttacactca agaaaacctt gagatgcaat ttcctaagca taccagacgt 540
ttaataaaaag atgctaagca gcgtggtgta aaaacatatc gtgtcagtca atcagaactt 600
cacaaatctt ccaagattgt ctccttaaca gaaaaacgta aaaatatttc tttgcgtaac 660
gaagcttact ttcaaaagtt gatgactact tatggggata aggcctactt acatctagca 720
aaagtgaata ttcctcaaaa actagatcaa taccgccagc aattaattct tattaaccaa 780
gatattactc gcacccaagc tcatcaaaag aagcgtttaa aaaaattaga agatcaaaaa 840
gcttcttttag aacgttatat aactgaattt gaaggcttta cagaccaata tcctgaggaa 900
gttggttagtag caggtatatt atctatttct tatggaaatg ttatggaaat gctttatgct 960
gggatgaatg atgattttta gaagttttat cctcagtatc tgctgtatcc taatgttttt 1020
caggatgctt atcaagatgg tattattttg gctaacatgg gaggagtaga aggtcgctt 1080
gatgatggac ttaccaaatt taaggccaac tttgctccga caatagaaga atttatagga 1140
gaatttaatc tccctgtcag cccactttat catattgcta ataccatgta caaaatacga 1200
aaacagttta agaataaaca ttaa 1224

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<210> SEQ ID NO 356

<211> LENGTH: 407

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 356

```

Met Thr Asn Leu Thr Phe Tyr Ala Lys Ile Gly Ile Ser Glu Glu Glu
1           5           10           15
His Asp Ser Phe Val Lys Glu His Gln Gln Ile Ser Val Leu Gln Gly
20          25          30
Ser Asp Trp Ala Lys Ile Lys Asn Gln Trp Gln Asn Glu Arg Ile Gly
35          40          45
Ile Tyr Lys Glu Glu Lys Gln Val Ala Ser Leu Ser Leu Leu Ile Lys
50          55          60
Leu Leu Pro Leu Gly Arg Ser Ile Ile Tyr Ile Pro Arg Gly Pro Val
65          70          75          80
Met Asp Tyr Leu Asp Arg Asp Leu Val Ala Phe Thr Met Lys Thr Leu
85          90          95
Lys Asp Tyr Gly Lys Thr Lys Lys Ala Leu Phe Ile Lys Tyr Asp Pro
100         105         110
Ala Ile Leu Leu Lys Gln Tyr Ala Leu Gly Gln Glu Glu Glu Glu Lys
115         120         125
Pro Leu Ala Leu Ala Ala Ile Lys Asn Leu Gln Glu Ala Gly Val His
130         135         140
Trp Thr Gly Leu Thr Met Glu Ile Ala Asp Ser Ile Gln Pro Arg Phe
145         150         155         160
Gln Ala Asn Ile Tyr Thr Gln Glu Asn Leu Glu Met Gln Phe Pro Lys
165         170         175
His Thr Arg Arg Leu Ile Lys Asp Ala Lys Gln Arg Gly Val Lys Thr
180         185         190
Tyr Arg Val Ser Gln Ser Glu Leu His Lys Phe Ser Lys Ile Val Ser
195         200         205
Leu Thr Glu Lys Arg Lys Asn Ile Ser Leu Arg Asn Glu Ala Tyr Phe
210         215         220
Gln Lys Leu Met Thr Thr Tyr Gly Asp Lys Ala Tyr Leu His Leu Ala
225         230         235         240
Lys Val Asn Ile Pro Gln Lys Leu Asp Gln Tyr Arg Gln Gln Leu Ile
245         250         255

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Leu	Ile	Asn	Gln	Asp	Ile	Thr	Arg	Thr	Gln	Ala	His	Gln	Lys	Lys	Arg
		260						265					270		
Leu	Lys	Lys	Leu	Glu	Asp	Gln	Lys	Ala	Ser	Leu	Glu	Arg	Tyr	Ile	Thr
	275						280					285			
Glu	Phe	Glu	Gly	Phe	Thr	Asp	Gln	Tyr	Pro	Glu	Glu	Val	Val	Val	Ala
	290					295					300				
Gly	Ile	Leu	Ser	Ile	Ser	Tyr	Gly	Asn	Val	Met	Glu	Met	Leu	Tyr	Ala
305					310					315					320
Gly	Met	Asn	Asp	Asp	Phe	Lys	Lys	Phe	Tyr	Pro	Gln	Tyr	Leu	Leu	Tyr
			325						330					335	
Pro	Asn	Val	Phe	Gln	Asp	Ala	Tyr	Gln	Asp	Gly	Ile	Ile	Trp	Ala	Asn
			340					345					350		
Met	Gly	Gly	Val	Glu	Gly	Ser	Leu	Asp	Asp	Gly	Leu	Thr	Lys	Phe	Lys
		355					360					365			
Ala	Asn	Phe	Ala	Pro	Thr	Ile	Glu	Glu	Phe	Ile	Gly	Glu	Phe	Asn	Leu
	370					375					380				
Pro	Val	Ser	Pro	Leu	Tyr	His	Ile	Ala	Asn	Thr	Met	Tyr	Lys	Ile	Arg
385					390					395					400
Lys	Gln	Leu	Lys	Asn	Lys	His									
					405										

<210> SEQ ID NO 357

<211> LENGTH: 1434

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 357

atgctaagaa	aaaagagaat	tttgggttta	tttcgacttg	ttgaattaat	tttcctagga	60
ttattgttga	gtttagtgtg	ttcgtacctt	gcgtagacca	atagttttgc	aacacttcat	120
aatatattag	caactgtcgg	aatagtggaa	cgaagcaaag	atcaacagcc	tcgctatcac	180
attggacaag	ctattcaagt	acaaaaaagt	ggtccatata	atcaatggat	tggaactatt	240
aataaacagg	tagaagatat	agccgaaaat	taccgagtga	gttatcatta	tgaagtggta	300
ttccaatag	gaaaagtcac	tgtttctttg	ccagaacata	acctgaaaga	gcctgataaa	360
ccgaggttta	aaaaaggaga	tatcggttaa	ttatcttcat	taactaaaaa	gccacatata	420
aaagtatatc	aagggtcaatt	agcgactatt	aaacaagtta	aaaaatgcta	tgactattcg	480
ttaggaggat	atcagtacga	tattaatctg	aaagataatc	taagattaga	tggaatttca	540
gagcaagatt	ttgttaaacc	ttattatatt	aggttcaata	aaggaaaattc	ccctgagcaa	600
aacaatcgtc	ttttgcgaaa	agctttcgct	tatgcaaagc	agcatccaaa	tagcgttata	660
tcttttccaa	aggggcaatt	tcacattggc	tctttgcctt	cacaaaaaga	ttattttgag	720
cttccatctg	atacagctat	tattgggtcat	cagacagagt	tcattattca	cggtaaaatg	780
ttgtggtttg	gattccctac	aggaccaaag	gctgaacaag	gtgttcgtaa	tctcgtgttg	840
actggagtg	atttcaaagc	aatgatttg	aaaaaaggag	accactttat	gattatggct	900
gatcatggta	ctgattggca	tatttacgat	aacaaattta	ctatggttca	taagcgtaat	960
agtcataatt	ttgatttagg	atctctacaa	aattcattgt	ttgagaaaaa	ccaatttatt	1020
ggctatgcgc	cagaattagt	acaagaccaa	cagctgctat	caaaggctca	agggcatgat	1080
tttttttcag	aagtcattca	gtttgatgct	gctgttcata	attttgcata	ggatggagg	1140
ctacttagta	atattgctcc	aaactatgaa	gcatttaacc	aaactcgaca	tctatgtcac	1200
aatattactg	taagccaaaa	tcaattttta	ccttatatag	atccgactgg	ttgcctgaga	1260
gcctatagt	gttctattgg	tcagcattcc	tcaaaagtag	gagttattag	ggttttaaat	1320
aatgttttta	cctcatccat	tgttactaaa	gcgaagctca	ctagttgggt	tatggaacct	1380
attcattttc	caccaaattc	accggttatt	gtcgcaggta	atatcattaa	ttga	1434

<210> SEQ ID NO 358

<211> LENGTH: 477

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 358

Met Leu Arg Lys Lys Arg Ile Leu Gly Leu Phe Arg Leu Val Glu Leu

1				5				10				15			
Ile	Phe	Leu	Gly	Leu	Leu	Leu	Ser	Leu	Val	Val	Ser	Tyr	Leu	Ala	Trp
			20					25					30		
Thr	Asn	Ser	Phe	Ala	Thr	Leu	His	Asn	Ile	Leu	Ala	Thr	Val	Gly	Ile
		35					40					45			
Val	Glu	Arg	Ser	Lys	Asp	Gln	Gln	Pro	Arg	Tyr	His	Ile	Gly	Gln	Ala
	50				55						60				
Ile	Gln	Val	Gln	Lys	Ser	Gly	Pro	Tyr	His	Gln	Trp	Ile	Gly	Thr	Ile
65				70					75					80	
Asn	Lys	Gln	Val	Glu	Asp	Ile	Ala	Glu	Asn	Tyr	Arg	Val	Ser	Tyr	His
			85						90				95		
Tyr	Glu	Val	Val	Phe	Pro	Ile	Gly	Lys	Val	Thr	Val	Ser	Leu	Pro	Glu
		100					105						110		
His	Asn	Leu	Lys	Glu	Pro	Asp	Lys	Pro	Arg	Phe	Lys	Lys	Gly	Asp	Ile
	115				120						125				
Val	Lys	Leu	Ser	Ser	Leu	Thr	Lys	Lys	Pro	His	Ile	Lys	Val	Tyr	Gln
	130				135						140				
Gly	Gln	Leu	Ala	Thr	Ile	Lys	Gln	Val	Lys	Lys	Cys	Tyr	Asp	Tyr	Ser
145				150					155						160
Leu	Gly	Gly	Tyr	Gln	Tyr	Asp	Ile	Asn	Leu	Lys	Asp	Asn	Leu	Arg	Leu
			165				170						175		
Asp	Gly	Ile	Ser	Glu	Gln	Asp	Phe	Val	Lys	Pro	Tyr	Tyr	Ile	Arg	Phe
	180				185							190			
Asn	Lys	Gly	Asn	Ser	Pro	Glu	Gln	Asn	Asn	Arg	Leu	Leu	Arg	Lys	Ala
	195				200						205				
Phe	Ala	Tyr	Ala	Lys	Gln	His	Pro	Asn	Ser	Val	Ile	Ser	Phe	Pro	Lys
	210				215						220				
Gly	Gln	Phe	His	Ile	Gly	Ser	Leu	Pro	Ser	Gln	Lys	Asp	Tyr	Phe	Glu
225				230					235						240
Leu	Pro	Ser	Asp	Thr	Ala	Ile	Ile	Gly	His	Gln	Thr	Glu	Phe	Ile	Ile
			245					250					255		
His	Gly	Lys	Met	Leu	Trp	Phe	Gly	Phe	Pro	Thr	Gly	Pro	Lys	Ala	Glu
	260				265							270			
Gln	Gly	Val	Arg	Asn	Leu	Val	Leu	Thr	Gly	Val	His	Phe	Lys	Ala	Asn
	275				280						285				
Asp	Leu	Lys	Lys	Gly	Asp	His	Phe	Met	Ile	Met	Ala	Asp	His	Gly	Thr
	290			295							300				
Asp	Trp	His	Ile	Tyr	Asp	Asn	Lys	Phe	Thr	Met	Val	His	Lys	Arg	Asn
305				310					315						320
Ser	His	Ile	Phe	Asp	Leu	Gly	Ser	Leu	Gln	Asn	Ser	Leu	Phe	Glu	Lys
			325				330						335		
Asn	Gln	Phe	Ile	Gly	Tyr	Ala	Pro	Glu	Leu	Val	Gln	Asp	Gln	Gln	Leu
		340					345					350			
Leu	Ser	Lys	Ala	Gln	Gly	His	Asp	Phe	Phe	Ser	Glu	Val	Ile	Gln	Phe
	355				360						365				
Asp	Ala	Ala	Val	His	His	Phe	Ala	Trp	Asp	Gly	Gly	Leu	Leu	Ser	Asn
	370				375						380				
Ile	Ala	Pro	Asn	Tyr	Glu	Ala	Phe	Asn	Gln	Thr	Arg	His	Leu	Cys	His
385				390					395						400
Asn	Ile	Thr	Val	Ser	Gln	Asn	Gln	Phe	Leu	Pro	Tyr	Ile	Asp	Pro	Thr
			405				410						415		
Gly	Cys	Leu	Arg	Ala	Tyr	Ser	Gly	Ser	Ile	Gly	Gln	His	Ser	Ser	Lys
		420					425					430			
Val	Gly	Val	Ile	Arg	Val	Leu	Asn	Val	Phe	Thr	Ser	Ser	Ile	Val	
	435					440					445				
Thr	Lys	Ala	Lys	Leu	Thr	Ser	Trp	Phe	Met	Glu	Pro	Ile	His	Phe	Pro
	450				455						460				

Pro Asn Ser Pro Val Ile Val Ala Gly Asn Ile Ile Asn
 465 470 475

<210> SEQ ID NO 359
 <211> LENGTH: 666
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 359
 ttggcacacc tgagcgtatt caatatgggtg ataaggttgt tgctcttatt gaataccgtg 60
 acggtagcct catggatgtg gtttacaatg tgtaaagaca cttatttttc aggcgaagct 120
 atccaactta gtgatatgtt aagagcccg cgaagaaagag ctctgcgtca gctgcattta 180
 ttaaaggagt acccagaagg tagcttatta tcggtcacca tgaatatccc tggaccaatt 240
 aaaacctctc ctaaacttct tgaagctttt gatatagtga ttaaggccat tcaaactgcc 300
 ttagctgacg ataagatttg ttaccagttg cgattactgc ctacaacggg ttatgagtat 360
 tacctcatca caagtctacc tagccgcgac ctgaagttaa aaatgatagc cttagagaca 420
 gagttgccaa taggtcgtct catggattta gatgtcttgg tcttgcaaaa tgatctgcct 480
 cattcaatta gcagaaccgt attaggaggc tcccctaggc aatgttttat ctgttctaaa 540
 gaggccaaag tctgcggtcg cctacgtaag cacagtgtcg aggagatgca gactgctatt 600
 tcaaaattac tccattcatt tttcaataaa gacaaccaat catcgtcatc agataagaca 660
 ggttga 666

<210> SEQ ID NO 360
 <211> LENGTH: 221
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 360
 Met Ala His Leu Ser Val Phe Asn Met Val Ile Arg Leu Leu Leu Leu
 1 5 10 15
 Leu Asn Thr Val Thr Val Ala Ser Trp Met Trp Phe Thr Met Cys Lys
 20 25 30
 Asp Thr Tyr Phe Ser Gly Glu Ala Ile Gln Leu Ser Asp Met Leu Arg
 35 40 45
 Ala Arg Glu Glu Arg Ala Leu Arg Gln Leu His Leu Leu Lys Glu Tyr
 50 55 60
 Pro Glu Gly Ser Leu Leu Ser Val Thr Met Asn Ile Pro Gly Pro Ile
 65 70 75 80
 Lys Thr Ser Pro Lys Leu Leu Glu Ala Phe Asp Ile Val Ile Lys Ala
 85 90 95
 Ile Gln Thr Ala Leu Ala Asp Asp Lys Ile Cys Tyr Gln Leu Arg Leu
 100 105 110
 Leu Pro Thr Thr Gly Tyr Glu Tyr Tyr Leu Ile Thr Ser Leu Pro Ser
 115 120 125
 Arg Asp Leu Lys Leu Lys Met Ile Ala Leu Glu Thr Glu Leu Pro Ile
 130 135 140
 Gly Arg Leu Met Asp Leu Asp Val Leu Val Leu Gln Asn Asp Leu Pro
 145 150 155 160
 His Ser Ile Ser Arg Thr Val Leu Gly Gly Ser Pro Arg Gln Cys Phe
 165 170 175
 Ile Cys Ser Lys Glu Ala Lys Val Cys Gly Arg Leu Arg Lys His Ser
 180 185 190
 Val Glu Glu Met Gln Thr Ala Ile Ser Lys Leu Leu His Ser Phe Phe
 195 200 205
 Asn Lys Asp Asn Gln Ser Ser Ser Asp Lys Thr Gly
 210 215 220

<210> SEQ ID NO 361
 <211> LENGTH: 1053

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 361

```
gtggacactt taatcgcagg aataacctcc atcaccattc ctcaaattgt tatgatggtc      60
attggtgccc tcttaatgta tctaggaatt aaaaaagaat acgaaccaac cttacttgtc      120
cccatgggac ttggaaccat tctcgtaaac ttccctgggt caggagtttt aacacaagtg      180
gttaacggag tcgagcaaga aggggttttt gaggctctct tcaattttgg gattggaaca      240
gaacttttcc cactgttgat tttcattggg ataggagcca tgattgactt tggccccttg      300
cttcaaaacc cattcatgct cttgtttggg gatgcagctc aattcgggaat tttctttggt      360
gtggttggtg ccgtactggc tggctttgac attaaagaag cagcttcaat cggcattatc      420
ggagcagcag acggaccgac ttctatcttt gttgcccaacc aactggccaa ggatttactg      480
ggtccaatta cggttgacgc ctattcttac atggctctgg ttcctattat ccaaccattt      540
gccattaaat tagtgacaac gaaaaaagag cgccgtatcc gtatgactta caaagctgag      600
aatgtatctc aaatgactaa aatcttattc ccaatcatca ttaccttagt agcagggttc      660
atcgcccaa tttctctacc tttagtggc tttttgatgt tcggtaaact attacgggag      720
tgtgggtgtg tcgatgcgct gtcacaaact gtcacaaatg aattggtaaa cattattagt      780
atcttgcttg gattgaccat ctctattaaa atgcaggcag acctgttctt aaatgtacag      840
acactcttaa tcatcgctct tggtttactt gcttttatca tggattctat cgggtggggtc      900
atgtttgcca aattttctca tctcttccga aaagagaaga ttaatccaat gattggcgct      960
gcgggtattt cagcttttcc aatgtcaagt cgtgtcattc aaaaaatggc acagatgaag     1020
accgcacaaa ctttatcctc atgtatgctg tag                                1053
```

<210> SEQ ID NO 362

<211> LENGTH: 350

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 362

```
Met Asp Thr Leu Ile Ala Gly Ile Thr Ser Ile Thr Ile Pro Gln Ile
1          5          10          15
Val Met Met Val Ile Gly Ala Leu Leu Met Tyr Leu Gly Ile Lys Lys
20        25        30
Glu Tyr Glu Pro Thr Leu Leu Val Pro Met Gly Leu Gly Thr Ile Leu
35        40        45
Val Asn Phe Pro Gly Ser Gly Val Leu Thr Gln Val Val Asn Gly Val
50        55        60
Glu Gln Glu Gly Val Phe Glu Ala Leu Phe Asn Phe Gly Ile Gly Thr
65        70        75        80
Glu Leu Phe Pro Leu Leu Ile Phe Ile Gly Ile Gly Ala Met Ile Asp
85        90        95
Phe Gly Pro Leu Leu Gln Asn Pro Phe Met Leu Leu Phe Gly Asp Ala
100       105       110
Ala Gln Phe Gly Ile Phe Phe Val Val Val Val Ala Val Leu Ala Gly
115       120       125
Phe Asp Ile Lys Glu Ala Ala Ser Ile Gly Ile Ile Gly Ala Ala Asp
130       135       140
Gly Pro Thr Ser Ile Phe Val Ala Asn Gln Leu Ala Lys Asp Leu Leu
145       150       155       160
Gly Pro Ile Thr Val Ala Ala Tyr Ser Tyr Met Ala Leu Val Pro Ile
165       170       175
Ile Gln Pro Phe Ala Ile Lys Leu Val Thr Thr Lys Lys Glu Arg Arg
180       185       190
Ile Arg Met Thr Tyr Lys Ala Glu Asn Val Ser Gln Met Thr Lys Ile
195       200       205
Leu Phe Pro Ile Ile Ile Thr Leu Val Ala Gly Phe Ile Ala Pro Ile
210       215       220
Ser Leu Pro Leu Val Gly Phe Leu Met Phe Gly Asn Leu Leu Arg Glu
225       230       235       240
```

Cys	Gly	Val	Leu	Asp	Arg	Leu	Ser	Gln	Thr	Ala	Gln	Asn	Glu	Leu	Val
				245					250					255	
Asn	Ile	Ile	Ser	Ile	Leu	Leu	Gly	Leu	Thr	Ile	Ser	Ile	Lys	Met	Gln
			260					265					270		
Ala	Asp	Leu	Phe	Leu	Asn	Val	Gln	Thr	Leu	Leu	Ile	Ile	Val	Phe	Gly
		275					280					285			
Leu	Leu	Ala	Phe	Ile	Met	Asp	Ser	Ile	Gly	Gly	Val	Met	Phe	Ala	Lys
	290				295						300				
Phe	Leu	Asn	Leu	Phe	Arg	Lys	Glu	Lys	Ile	Asn	Pro	Met	Ile	Gly	Ala
305					310				315						320
Ala	Gly	Ile	Ser	Ala	Phe	Pro	Met	Ser	Ser	Arg	Val	Ile	Gln	Lys	Met
			325					330					335		
Ala	Gln	Met	Lys	Thr	Arg	Lys	Thr	Leu	Ser	Ser	Cys	Met	Leu		
		340						345					350		

<210> SEQ ID NO 363

<211> LENGTH: 1425

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 363

ttgaaaaagg	agataacaat	gatgttatta	acaatgctgg	cttatgccat	gattattgtc	60
tttatgtacg	tggtaatgaa	gaaaaaaatg	acccttttta	ctgctttggg	catgattcca	120
ttaatcatga	cgattgctgt	tatactgact	ggttcagctg	acttcaatgc	agatgccaaa	180
tttgttgcct	ttgttggtga	cggtggaatt	gctaaagacc	taacagctat	cggaccaatg	240
gttatgtatg	gtatcaacaa	tactgctaaa	acaggatatca	tgttgctatt	tgccattttg	300
ttctttctctg	tcatgttaga	tgcaggattg	tttgatccga	ttactgaaaa	gatgattcgc	360
tttgctaaag	gtgatccaat	gaagggtgctt	atcgcaacag	ctgtcgttgc	tgctgcagta	420
tctcttaatg	gtgatggaac	aaccactact	ttaattttgtt	gctctgcttt	cttacctatc	480
tataaaaaat	tggacatgaa	aatcatgaac	ctagggtgtct	tgattattct	tcaaaatact	540
attatgaact	tactgccatg	gggtggccct	actgctcgtg	cgatgtctgt	tcttggtgtc	600
ggctctgaaa	ttcttggtga	tcttgaccg	ggatgatgtt	tatctcttct	ttatgtgatt	660
tgttggtgtg	ctccaagcat	ggggcgtaaa	gaacgtgcaa	gacttggtgt	tattgacttg	720
tctgaagaag	acatgcgtca	actcacagac	attactgacc	cagataccct	ttttattcgt	780
cgctctaaaa	actttgtttt	caatgctatc	ttaaccattg	gattaatcac	ttggttagtt	840
gctggctctt	tcaacaaatc	tattgctatg	gcaccgcttc	ttctttttgc	ggtagggaact	900
tgtatcgctt	tgatggtcaa	ttaccagctg	cttaaagatc	aatcaaaacg	cattggtgac	960
aatgctgggtg	atgcggttca	agtgggttatt	ctcgtctttg	ctgctggtat	ctttatgggt	1020
ctttttcaag	gttctgggtat	ggctagcgct	cttgacaaaa	gttttgcaac	cattattcca	1080
aaacaactgg	cagggtttctg	gggtctcggt	attgccttag	tttctgcacc	tggtaccttc	1140
tttatctcca	atgatgggtt	ttactatggt	atcttgcttg	ttcttgacaga	agctgggtgct	1200
gaatatgggt	tcagtaacat	ggctatggca	cttgcttccc	tcattgggaca	agccttccac	1260
ttacttagtc	cattagttgc	cttcatttat	cttcttcttc	gcttgacagg	tcttgacatg	1320
ggggaatggc	aaaaagaggc	tgctaaatat	gcccttatca	tctttgttat	ctttgtggta	1380
accattattg	ccatgggaca	aatgccactt	tacattccac	aataa		1425

<210> SEQ ID NO 364

<211> LENGTH: 474

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 364

Met	Lys	Lys	Glu	Ile	Thr	Met	Met	Leu	Leu	Thr	Met	Leu	Ala	Tyr	Ala
1			5					10					15		
Met	Ile	Ile	Val	Phe	Met	Tyr	Val	Val	Met	Lys	Lys	Lys	Met	Thr	Pro
			20					25				30			
Phe	Thr	Ala	Leu	Val	Met	Ile	Pro	Leu	Ile	Met	Thr	Ile	Ala	Val	Ile
		35				40					45				
Leu	Thr	Gly	Ser	Ala	Asp	Phe	Asn	Ala	Asp	Ala	Lys	Phe	Val	Ala	Phe

50	55	60													
Val Gly Asp Gly Gly Ile Ala Lys Asp Leu Thr Ala Ile Gly Pro Met															
65	70	75	80												
Val Met Tyr Gly Ile Asn Asn Thr Ala Lys Thr Gly Ile Met Leu Leu															
	85	90	95												
Phe Ala Ile Leu Phe Phe Ser Val Met Leu Asp Ala Gly Leu Phe Asp															
	100	105	110												
Pro Ile Thr Glu Lys Met Ile Arg Phe Ala Lys Gly Asp Pro Met Lys															
	115	120	125												
Val Leu Ile Ala Thr Ala Val Val Ala Ala Ala Val Ser Leu Asn Gly															
	130	135	140												
Asp Gly Thr Thr Thr Thr Leu Ile Cys Cys Ser Ala Phe Leu Pro Ile															
145	150	155	160												
Tyr Lys Lys Leu Asp Met Lys Ile Met Asn Leu Gly Val Leu Ile Ile															
	165	170	175												
Leu Gln Asn Thr Ile Met Asn Leu Leu Pro Trp Gly Gly Pro Thr Ala															
	180	185	190												
Arg Ala Met Ser Val Leu Gly Val Gly Pro Glu Ile Leu Gly Tyr Leu															
	195	200	205												
Ala Pro Gly Met Ile Leu Ser Leu Leu Tyr Val Ile Cys Trp Val Ala															
	210	215	220												
Pro Ser Met Gly Arg Lys Glu Arg Ala Arg Leu Gly Val Ile Asp Leu															
225	230	235	240												
Ser Glu Glu Asp Met Arg Gln Leu Thr Asp Ile Thr Asp Pro Asp Thr															
	245	250	255												
Leu Phe Ile Arg Arg Pro Lys Asn Phe Val Phe Asn Ala Ile Leu Thr															
	260	265	270												
Ile Gly Leu Ile Thr Trp Leu Val Ala Gly Ser Phe Asn Lys Ser Ile															
	275	280	285												
Ala Met Ala Pro Leu Leu Leu Phe Ala Val Gly Thr Cys Ile Ala Leu															
	290	295	300												
Met Val Asn Tyr Pro Val Leu Lys Asp Gln Ser Lys Arg Ile Gly Asp															
305	310	315	320												
Asn Ala Gly Asp Ala Val Gln Val Val Ile Leu Val Phe Ala Ala Gly															
	325	330	335												
Ile Phe Met Gly Leu Phe Gln Gly Ser Gly Met Ala Ser Ala Leu Ala															
	340	345	350												
Gln Ser Phe Ala Thr Ile Ile Pro Lys Gln Leu Ala Gly Phe Trp Gly															
	355	360	365												
Leu Val Ile Ala Leu Val Ser Ala Pro Gly Thr Phe Phe Ile Ser Asn															
	370	375	380												
Asp Gly Phe Tyr Tyr Gly Ile Leu Pro Val Leu Ala Glu Ala Gly Ala															
385	390	395	400												
Glu Tyr Gly Phe Ser Asn Met Ala Met Ala Leu Ala Ser Leu Met Gly															
	405	410	415												
Gln Ala Phe His Leu Leu Ser Pro Leu Val Ala Phe Ile Tyr Leu Leu															
	420	425	430												
Leu Arg Leu Thr Gly Leu Asp Met Gly Glu Trp Gln Lys Glu Ala Ala															
	435	440	445												
Lys Tyr Ala Leu Ile Ile Phe Val Ile Phe Val Val Thr Ile Ile Ala															
	450	455	460												
Met Gly Gln Met Pro Leu Tyr Ile Pro Gln															
465	470														

<210> SEQ ID NO 365

<211> LENGTH: 651

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 365

```
atgaacaaaa cctttaaaaca aagttttaccc ttatcttttta gtgaggaagt agcaaacagc      60
gtgacacacg ctatcggagc atttgctatg ctcattctac ttcctatttc agccagctat      120
gcttatcaaa cttatgacct taaagccgct attggatatct ccatctttgt catcagtctc      180
tttttgatgt ttttgtcctc tacgatttac cactccatgg cttatgggtc ggttcacaaa      240
tacattctac gcattattga tcacagtatg atttatattg ctatcgcagg aagttataca      300
cctgttgcc tttcccttgt ttctgggttg ctaggctata tcattattgt tttgcagtgg      360
ggcattacgc tttttgggat tttatacaaaa atttttgcca aacgtatcaa tgaaaaattc      420
agtttgatgc tttatatcgt tatgggctgg ctcgttggtg ttatcttgcc agtcatcatt      480
caaaaaacta gtcttgcttt tggctttctc atgttatattg gtggcttgtc ttataccatt      540
ggagcgggat tttatgccaa aaaaagaccc tacttccaca tgatttggca tctctttatt      600
ttattggcct ctgccctcca atttatcgct atcactttct ttatgcttta a                651
```

<210> SEQ ID NO 366

<211> LENGTH: 216

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 366

```
Met Asn Gln Thr Phe Lys Gln Ser Leu Pro Leu Ser Phe Ser Glu Glu
1      5      10      15
Val Ala Asn Ser Val Thr His Ala Ile Gly Ala Phe Ala Met Leu Ile
20     25     30
Leu Leu Pro Ile Ser Ala Ser Tyr Ala Tyr Gln Thr Tyr Asp Leu Lys
35     40     45
Ala Ala Ile Gly Ile Ser Ile Phe Val Ile Ser Leu Phe Leu Met Phe
50     55     60
Leu Ser Ser Thr Ile Tyr His Ser Met Ala Tyr Gly Ser Val His Lys
65     70     75     80
Tyr Ile Leu Arg Ile Ile Asp His Ser Met Ile Tyr Ile Ala Ile Ala
85     90     95
Gly Ser Tyr Thr Pro Val Ala Leu Ser Leu Val Ser Gly Trp Leu Gly
100    105    110
Tyr Ile Ile Ile Val Leu Gln Trp Gly Ile Thr Leu Phe Gly Ile Leu
115    120    125
Tyr Lys Ile Phe Ala Lys Arg Ile Asn Glu Lys Phe Ser Leu Met Leu
130    135    140
Tyr Ile Val Met Gly Trp Leu Val Val Phe Ile Leu Pro Val Ile Ile
145    150    155    160
Gln Lys Thr Ser Leu Ala Phe Gly Leu Leu Met Leu Phe Gly Gly Leu
165    170    175
Ser Tyr Thr Ile Gly Ala Val Phe Tyr Ala Lys Lys Arg Pro Tyr Phe
180    185    190
His Met Ile Trp His Leu Phe Ile Leu Leu Ala Ser Ala Leu Gln Phe
195    200    205
Ile Ala Ile Thr Phe Phe Met Leu
210    215
```

<210> SEQ ID NO 367

<211> LENGTH: 369

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 367

```
atgactaaaa aaaatcatgg cggttttttgg gggttggtgc ttggatcagc agcagctagc      60
attgcttact taagtttatc gtcttccaaa aaagatcaac tcttgaaaga tagtgctaaa      120
aaaatagatg atctcaacgc ttacttgcaa gataaaaagta agcaagttct ggatgcagta      180
tcggaaaaaag tccaagaatc caaagatgct gttgaagttt acggtggtat cgccgcagaa      240
```

```

acagttgaag aatctttggg acaggctaaa gaaaaggtag aaggaattgg cgaagctact 300
agccaaacta tccaatctaa aatggaaaaa ctactagcg ataagacaga tgctgatgat 360
gaaaaatag 369

<210> SEQ ID NO 368
<211> LENGTH: 122
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 368
Met Thr Lys Lys Asn His Gly Val Phe Trp Gly Leu Leu Leu Gly Ser
1      5      10      15
Ala Ala Ala Ser Ile Ala Tyr Leu Ser Leu Ser Ser Ser Lys Lys Asp
20     25     30
Gln Leu Leu Lys Asp Ser Ala Lys Lys Ile Asp Asp Leu Asn Ala Tyr
35     40     45
Leu Gln Asp Lys Ser Lys Gln Val Leu Asp Ala Val Ser Glu Lys Val
50     55     60
Gln Glu Ser Lys Asp Ala Val Glu Val Tyr Gly Gly Ile Ala Ala Glu
65     70     75     80
Thr Val Glu Glu Ser Leu Gly Gln Ala Lys Glu Lys Val Glu Gly Ile
85     90     95
Gly Glu Ala Thr Ser Gln Thr Ile Gln Ser Lys Met Glu Lys Leu Thr
100    105    110
Ser Asp Lys Thr Asp Ala Asp Asp Glu Lys
115    120

<210> SEQ ID NO 369
<211> LENGTH: 918
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 369
atggctggac ttttttccagt aggtcagcta accacttttt taaatgttgt tgtccaatat 60
accaaacctt tcaacgatat ttcactctgtc ttggcagaga tacagagttc tttagcttgt 120
gcgcaaaggc tttatgacct tttagatatt gaaataaaaag agcaagagca ctttctaaca 180
tttaaggcat cagcgggttaa ggggcaaatt gactttgaag aagtaagttt ttcttatcaa 240
aaagacaggc ccttactgaa agatattaat ttttctgttc ctgcgggttc caaggtagcg 300
attgtagggc ctacaggtgc aggtaaatca actttaatca atttactcat gcgcttttat 360
gaacttgatg ctggtagcat caagttagat aaagttccta ttaagtgtta tgctaaggaa 420
gaacttaggt ccattactgg catagtattg caagaaacct ggttgaaaga tgcgactgtt 480
catgagttga ttgcttacgg cagtgaagag gctagccgtg atgaagtagt ggcagcagcc 540
aaagcagctc atgcacactt ctttattatg caacttccta agacttatga tacttactta 600
agtgcttctg atgatgcttt gtccaaggg cagctccagt tattagctat tgccagaatg 660
tttttgaaaa aaccaaaggt cttggttcta gatgaagcca cctcctctat tgatattaga 720
acagaagctg ttattcaaga ggcactaaaa gaactcatga gaggaaggac cagctttatc 780
attgcccata gtttatcaac gattcaatca gctgatttga ttcttgttat ggatcaaggt 840
cgattggttg agtggggaac acatgccagc ttaatgtcaa aaaacgcctg ttatgctaga 900
ttacaaaaga tagaataa 918

<210> SEQ ID NO 370
<211> LENGTH: 305
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 370
Met Ala Gly Leu Phe Ser Val Gly Gln Leu Thr Thr Phe Leu Asn Val
1      5      10      15
Val Val Gln Tyr Thr Lys Pro Phe Asn Asp Ile Ser Ser Val Leu Ala
20     25     30

```

Glu	Ile	Gln	Ser	Ser	Leu	Ala	Cys	Ala	Gln	Arg	Leu	Tyr	Asp	Leu	Leu
		35					40					45			
Asp	Ile	Glu	Ile	Lys	Glu	Gln	Glu	His	Phe	Leu	Thr	Phe	Lys	Ala	Ser
	50					55					60				
Ala	Val	Lys	Gly	Gln	Ile	Asp	Phe	Glu	Glu	Val	Ser	Phe	Ser	Tyr	Gln
65					70					75				80	
Lys	Asp	Arg	Pro	Leu	Leu	Lys	Asp	Ile	Asn	Phe	Ser	Val	Pro	Ala	Gly
				85					90					95	
Ser	Lys	Val	Ala	Ile	Val	Gly	Pro	Thr	Gly	Ala	Gly	Lys	Ser	Thr	Leu
			100					105					110		
Ile	Asn	Leu	Leu	Met	Arg	Phe	Tyr	Glu	Leu	Asp	Ala	Gly	Ser	Ile	Lys
	115						120					125			
Leu	Asp	Lys	Val	Pro	Ile	Lys	Cys	Tyr	Ala	Lys	Glu	Glu	Leu	Arg	Ser
	130					135					140				
Ile	Thr	Gly	Ile	Val	Leu	Gln	Glu	Thr	Trp	Leu	Lys	Asp	Ala	Thr	Val
145					150					155				160	
His	Glu	Leu	Ile	Ala	Tyr	Gly	Ser	Glu	Glu	Ala	Ser	Arg	Asp	Glu	Val
				165						170				175	
Val	Ala	Ala	Ala	Lys	Ala	Ala	His	Ala	His	Phe	Phe	Ile	Met	Gln	Leu
			180					185					190		
Pro	Lys	Thr	Tyr	Asp	Thr	Tyr	Leu	Ser	Ala	Ser	Asp	Asp	Ala	Leu	Ser
	195						200				205				
Gln	Gly	Gln	Leu	Gln	Leu	Leu	Ala	Ile	Ala	Arg	Met	Phe	Leu	Lys	Lys
	210					215					220				
Pro	Lys	Val	Leu	Val	Leu	Asp	Glu	Ala	Thr	Ser	Ser	Ile	Asp	Ile	Arg
225					230					235				240	
Thr	Glu	Ala	Val	Ile	Gln	Glu	Ala	Leu	Lys	Glu	Leu	Met	Arg	Gly	Arg
				245						250				255	
Thr	Ser	Phe	Ile	Ile	Ala	His	Arg	Leu	Ser	Thr	Ile	Gln	Ser	Ala	Asp
			260					265					270		
Leu	Ile	Leu	Val	Met	Asp	Gln	Gly	Arg	Leu	Val	Glu	Trp	Gly	Thr	His
	275						280					285			
Ala	Ser	Leu	Met	Ser	Lys	Asn	Ala	Cys	Tyr	Ala	Arg	Leu	Gln	Lys	Ile
	290					295					300				
Glu															
305															

<210> SEQ ID NO 371

<211> LENGTH: 1725

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 371

atgaaacgat	tacgtccata	tgtgaaaggg	tacctaaaag	aaagtatctt	aggctcctctt	60
tttaaattat	tagaagcttt	atttgaatta	ttagtccctt	tgtaattgac	taacatgatt	120
gatatatcga	ttagtcaaca	caacagccag	ggaattttga	gggttggttt	aacattattt	180
ggtttagcaa	ccattggctt	attgctttcc	gttacagccc	agtatttttc	ttcgaaagca	240
gctgttggtt	ttacaagaca	aatgacagat	gacttggtta	aaaaaatcat	gtttttgagc	300
aaggaggacc	aagaccatct	tggttatgct	agtctgttat	cacgattgac	cagtgatagt	360
tttcaaattc	aaactgggat	caatcaattt	ttgcgtcttt	ttctaagggc	ccctattatc	420
gtatgtggtg	ctatggtaat	ggcttattgg	attagtccaa	gtctaaccct	atggtttggtg	480
atgatggtga	ttgtcttact	aacacttggt	tttgttatgt	cacatttatt	aggccccctt	540
tatctcttaa	tccgccgaga	aacagatcac	ttggttcggt	tgactagcca	acagttacaa	600
ggaatccgag	taattaaggc	ttttaatcaa	acccaaaaag	aactccaagc	atttaagcag	660
caaaatatgc	tcttaagtcg	ccaccaatat	caagctgcta	ccctagccaa	tgtcttgaat	720
cctatgactt	tttttagtgg	caatcttacc	ctgttaattc	tgatttggtg	aggaagttgg	780
caagtagctc	atagatcgct	tagtcagggc	atggttggtg	ctttaattaa	ttacctcttg	840
cagattttgg	cagaactttt	gaaaatgacc	atggtgatgg	gaaccatcaa	tcaaagtgtg	900

acagccgcaa	aacggattaa	tcaggtgttt	gttttagctg	atgaagcgcc	tttgcctta	960
cttaaagatg	gtcctatttc	aactcatctg	ttgaccatcc	ggcacttgac	ctttacttat	1020
ccaggagcag	cagagccaag	tctgtatgat	attcagttaa	gtgctgatca	gggagaatgg	1080
attggcatca	ttggtggtac	tggagcaggc	aaaacgactt	tgattgactt	gatctgccaa	1140
acttattcac	aatatagtg	tgagattagt	cttaattggc	aaggagaagt	gccaaaaaca	1200
ctaaccgagt	ggcgaaatgt	gattgctcct	gttcctcaaa	aagctcaatt	atttaaagga	1260
acgattagaa	gtaacctcct	actgggacaa	tcaatgccta	ttagtgatga	ggaactgtgg	1320
cgggctcttg	aattggctca	agcaaaagag	tttgtcgctg	ccttaccaga	acaattagag	1380
gcacctgttg	aagccttcgg	ccgtcatttt	tcaggagggc	aacggcaacg	tctagctatt	1440
gccagagcac	ttctgaagcc	aaaaccatt	ttgatttttg	atgatgccag	ttccgcctta	1500
gacaatgaga	ctcgaggacg	actttttaaa	gctctaaaag	aagagttatc	agatgtttta	1560
gtgattctag	tcacgcaatc	tattaagaat	ttgcagtttg	ctgataagat	tttagtgttg	1620
gaacagggcc	atcaattgga	ttttgccagt	catgaccagt	taaaagtaag	caatgcactt	1680
tatcaagaaa	tgctagcgct	ttacgtgaag	ggggagcaaa	aatga		1725

<210> SEQ ID NO 372

<211> LENGTH: 574

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 372

Met	Lys	Arg	Leu	Arg	Pro	Tyr	Val	Lys	Gly	Tyr	Leu	Lys	Glu	Ser	Ile
1				5					10					15	
Leu	Gly	Pro	Leu	Phe	Lys	Leu	Leu	Glu	Ala	Leu	Phe	Glu	Leu	Leu	Val
			20						25				30		
Pro	Leu	Leu	Ile	Ala	Asn	Met	Ile	Asp	Ile	Ser	Ile	Ser	Gln	His	Asn
			35				40					45			
Ser	Gln	Gly	Ile	Leu	Arg	Val	Val	Leu	Thr	Leu	Phe	Gly	Leu	Ala	Thr
	50					55					60				
Ile	Gly	Leu	Leu	Leu	Ser	Val	Thr	Ala	Gln	Tyr	Phe	Ser	Ser	Lys	Ala
65					70				75					80	
Ala	Val	Gly	Phe	Thr	Arg	Gln	Met	Thr	Asp	Asp	Leu	Phe	Lys	Lys	Ile
			85						90					95	
Met	Phe	Leu	Ser	Lys	Glu	Asp	Gln	Asp	His	Leu	Gly	Tyr	Ala	Ser	Leu
			100					105					110		
Leu	Ser	Arg	Leu	Thr	Ser	Asp	Ser	Phe	Gln	Ile	Gln	Thr	Gly	Ile	Asn
			115				120					125			
Gln	Phe	Leu	Arg	Leu	Phe	Leu	Arg	Ala	Pro	Ile	Ile	Val	Cys	Gly	Ala
	130					135					140				
Met	Val	Met	Ala	Tyr	Trp	Ile	Ser	Pro	Ser	Leu	Thr	Leu	Trp	Phe	Val
145				150					155					160	
Met	Met	Val	Ile	Val	Leu	Leu	Thr	Leu	Val	Phe	Val	Met	Ser	His	Leu
			165					170						175	
Leu	Gly	Pro	Leu	Tyr	Leu	Leu	Ile	Arg	Arg	Glu	Thr	Asp	His	Leu	Val
			180					185					190		
Arg	Leu	Thr	Ser	Gln	Gln	Leu	Gln	Gly	Ile	Arg	Val	Ile	Lys	Ala	Phe
		195				200						205			
Asn	Gln	Thr	Gln	Lys	Glu	Leu	Gln	Ala	Phe	Lys	Gln	Gln	Asn	Met	Leu
	210					215					220				
Leu	Ser	Arg	His	Gln	Tyr	Gln	Ala	Ala	Thr	Leu	Ala	Asn	Val	Leu	Asn
225				230					235					240	
Pro	Met	Thr	Phe	Leu	Val	Val	Asn	Leu	Thr	Leu	Leu	Ile	Leu	Ile	Trp
			245					250						255	
Gln	Gly	Ser	Trp	Gln	Val	Ala	His	Arg	Ser	Leu	Ser	Gln	Gly	Met	Leu
			260				265						270		
Val	Ala	Leu	Ile	Asn	Tyr	Leu	Leu	Gln	Ile	Leu	Ala	Glu	Leu	Leu	Lys
	275					280					285				
Met	Thr	Met	Leu	Met	Gly	Thr	Ile	Asn	Gln	Ser	Val	Thr	Ala	Ala	Lys

290	295	300
Arg Ile Asn Gln Val Phe Val Leu Ala Asp Glu Ala Pro Leu Pro Leu		
305	310	315
Leu Lys Asp Gly Pro Ile Ser Thr His Leu Leu Thr Ile Arg His Leu		
	325	330
Thr Phe Thr Tyr Pro Gly Ala Ala Glu Pro Ser Leu Tyr Asp Ile Gln		
	340	345
Leu Ser Ala Asp Gln Gly Glu Trp Ile Gly Ile Ile Gly Gly Thr Gly		
	355	360
Ala Gly Lys Thr Thr Leu Ile Asp Leu Ile Cys Gln Thr Tyr Ser Gln		
	370	375
Tyr Ser Gly Glu Ile Ser Leu Asn Trp Gln Gly Glu Val Pro Lys Thr		
385	390	395
Leu Thr Glu Trp Arg Asn Val Ile Ala Leu Val Pro Gln Lys Ala Gln		
	405	410
Leu Phe Lys Gly Thr Ile Arg Ser Asn Leu Leu Leu Gly Gln Ser Met		
	420	425
Pro Ile Ser Asp Glu Glu Leu Trp Arg Ala Leu Glu Leu Ala Gln Ala		
	435	440
Lys Glu Phe Val Ala Ala Leu Pro Glu Gln Leu Glu Ala Pro Val Glu		
	450	455
Ala Phe Gly Arg His Phe Ser Gly Gly Gln Arg Gln Arg Leu Ala Ile		
465	470	475
Ala Arg Ala Leu Leu Lys Pro Lys Pro Ile Leu Ile Leu Asp Asp Ala		
	485	490
Ser Ser Ala Leu Asp Asn Glu Thr Arg Gly Arg Leu Phe Lys Ala Leu		
	500	505
Lys Glu Glu Leu Ser Asp Val Leu Val Ile Leu Val Thr Gln Ser Ile		
	515	520
Lys Asn Leu Gln Phe Ala Asp Lys Ile Leu Val Leu Glu Gln Gly His		
	530	535
Gln Leu Asp Phe Ala Ser His Asp Gln Leu Lys Val Ser Asn Ala Leu		
545	550	555
Tyr Gln Glu Met Leu Ala Leu Tyr Val Lys Gly Glu Gln Lys		
	565	570

<210> SEQ ID NO 373

<211> LENGTH: 600

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 373

atgttttagac ttttaaagcg tgccctgcagt tttcttcttc tttttgtcat ttatcaatcc	60
tttgttattc atcacaatgt tcaacgtggt ttggcatata agcctatggt tgagaaaaca	120
ttagcagaaa atgatacaaa ggcaaagtga gacttagtct tagctatgat atacaccgag	180
acaaaaggag gagaagcaga tgtcatgcaa tccagtgaag gcagttcagg acaaaaaaac	240
tcgattacag atagtcaggc cagtattgag cacggggtga atttactgtc tcataatctt	300
gctctagctg aggaagcagg agtagattct tggacggctg ttcaggccta taatttttgg	360
acagcttata ttgattatat tgctgaacat ggagggtcaaa ataccgttga tttagcgact	420
acctattcca aaaccgttgt ggcgccaagc ctaggcaaca ctagtggtca aacctatttt	480
tattaccacc ccctcgctt gatttctgga ggtaagcttt ataagaatgg cggcaatatc	540
tattactcac gagaagttca tttcaatctt tatttaattg aactgatgag ccttttttag	600

<210> SEQ ID NO 374

<211> LENGTH: 199

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 374

Met	Phe	Arg	Leu	Leu	Lys	Arg	Ala	Cys	Ser	Phe	Leu	Leu	Leu	Phe	Val
1			5					10						15	
Ile	Tyr	Gln	Ser	Phe	Val	Ile	His	His	Asn	Val	Gln	Arg	Val	Leu	Ala
		20						25					30		
Tyr	Lys	Pro	Met	Val	Glu	Lys	Thr	Leu	Ala	Glu	Asn	Asp	Thr	Lys	Ala
		35					40					45			
Asn	Val	Asp	Leu	Val	Leu	Ala	Met	Ile	Tyr	Thr	Glu	Thr	Lys	Gly	Gly
	50					55					60				
Glu	Ala	Asp	Val	Met	Gln	Ser	Ser	Glu	Ser	Ser	Ser	Gly	Gln	Lys	Asn
65					70					75				80	
Ser	Ile	Thr	Asp	Ser	Gln	Ala	Ser	Ile	Glu	His	Gly	Val	Asn	Leu	Leu
			85						90				95		
Ser	His	Asn	Leu	Ala	Leu	Ala	Glu	Glu	Ala	Gly	Val	Asp	Ser	Trp	Thr
		100					105						110		
Ala	Val	Gln	Ala	Tyr	Asn	Phe	Gly	Thr	Ala	Tyr	Ile	Asp	Tyr	Ile	Ala
		115					120					125			
Glu	His	Gly	Gly	Gln	Asn	Thr	Val	Asp	Leu	Ala	Thr	Thr	Tyr	Ser	Lys
	130					135					140				
Thr	Val	Val	Ala	Pro	Ser	Leu	Gly	Asn	Thr	Ser	Gly	Gln	Thr	Tyr	Phe
145					150					155					160
Tyr	Tyr	His	Pro	Leu	Ala	Leu	Ile	Ser	Gly	Gly	Lys	Leu	Tyr	Lys	Asn
			165						170					175	
Gly	Gly	Asn	Ile	Tyr	Tyr	Ser	Arg	Glu	Val	His	Phe	Asn	Leu	Tyr	Leu
		180						185					190		
Ile	Glu	Leu	Met	Ser	Leu	Phe									
		195													

<210> SEQ ID NO 375

<211> LENGTH: 1284

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 375

atgacacatt	caacaaagca	ggaacattct	cactcgcaat	cagctgtcct	tggcttacag	60
catgtgcttt	cgatgtatgc	cggatctatt	ttagtaccaa	ttatgatcgc	aggtgcttta	120
ggttattccg	ctagagagtt	gacctacctg	atttcgacag	atattttcat	gtgtggtgtg	180
gctactttct	tacagttaaa	gttaaccaag	catacgggag	tgggattacc	agttgtttta	240
ggatgtgctt	ttcaatcagt	ggcacctcta	tccattattg	gagcgcaaca	aggttcaggt	300
gccatgtttg	gagccctcat	tgcgtcagga	atztatgtca	ttttagtggc	aggtattttt	360
tctaagattg	ctcgtttctt	cccaccaatt	gttacaggat	cggtcattac	cgttattggc	420
ttaagtctcg	taggtgttgc	tatggggaat	atgggagata	acgtcaaaga	gcctacggca	480
caaagcatga	tgttatcatt	gttgacgatt	gtcattattc	ttttagtcca	aaaatttacc	540
aaagggtttg	tgaaatccat	ttccattttg	attgggcttg	tagcgggaac	tttggtttca	600
gctatgatgg	gattagtaga	tacaactcct	gtttagagag	cttcttggat	tcatgtgcc	660
accccattht	atthtggcat	gccaacttht	gaaatcactt	ctattgtgat	gatgtgtatc	720
atcgcaacgg	tttctatgg	tgaatcaaca	ggtgtctact	tagcgctttc	agatttgact	780
aatgatcaat	tagatgaaaa	acgtttgcgc	aatgggtatc	gctcagaagg	gatcgagtc	840
tttctcggtg	ggttatttaa	caccttccct	tacactgggt	tttctcaaaa	cgttggactt	900
gtccaaatct	caggtattaa	aacccgctcg	ccgatttact	acgcagcagg	tatccttgtg	960
gtcattggcc	tactccctaa	atthtagagca	atggcacaaa	tgattccaag	cccagttctt	1020
ggtggagcca	tgcttgttct	ctttggatatg	gttgctcttc	aaggaatgca	aatgcttaat	1080
cgtgttgatt	tccaaaagaa	cgagtataat	tttattattg	ctgccgtttc	catctcagca	1140
ggtttaggct	ttaatggcac	taatcttttt	gccagcttac	cagagacagc	tcaaagtgtc	1200
ttaacgaatg	gtattgtgat	tgccactttg	acatctgttg	tcttaaatth	agttttaaat	1260
ggcaaaagaca	aacaagatga	ataa				1284

<210> SEQ ID NO 376

<211> LENGTH: 427

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 376

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Met Thr His Ser Thr Lys Gln Glu His Ser His Ser Gln Ser Ala Val
 1          5          10          15
Leu Gly Leu Gln His Val Leu Ser Met Tyr Ala Gly Ser Ile Leu Val
          20          25          30
Pro Ile Met Ile Ala Gly Ala Leu Gly Tyr Ser Ala Arg Glu Leu Thr
          35          40          45
Tyr Leu Ile Ser Thr Asp Ile Phe Met Cys Gly Val Ala Thr Phe Leu
          50          55          60
Gln Leu Lys Leu Thr Lys His Thr Gly Val Gly Leu Pro Val Val Leu
65          70          75          80
Gly Cys Ala Phe Gln Ser Val Ala Pro Leu Ser Ile Ile Gly Ala Gln
          85          90          95
Gln Gly Ser Gly Ala Met Phe Gly Ala Leu Ile Ala Ser Gly Ile Tyr
          100          105          110
Val Ile Leu Val Ala Gly Ile Phe Ser Lys Ile Ala Arg Phe Phe Pro
          115          120          125
Pro Ile Val Thr Gly Ser Val Ile Thr Val Ile Gly Leu Ser Leu Val
          130          135          140
Gly Val Ala Met Gly Asn Met Gly Asp Asn Val Lys Glu Pro Thr Ala
145          150          155          160
Gln Ser Met Met Leu Ser Leu Leu Thr Ile Val Ile Ile Leu Leu Val
          165          170          175
Gln Lys Phe Thr Lys Gly Phe Val Lys Ser Ile Ser Ile Leu Ile Gly
          180          185          190
Leu Val Ala Gly Thr Leu Val Ser Ala Met Met Gly Leu Val Asp Thr
          195          200          205
Thr Pro Val Val Glu Ala Ser Trp Ile His Val Pro Thr Pro Phe Tyr
          210          215          220
Phe Gly Met Pro Thr Phe Glu Ile Thr Ser Ile Val Met Met Cys Ile
225          230          235          240
Ile Ala Thr Val Ser Met Val Glu Ser Thr Gly Val Tyr Leu Ala Leu
          245          250          255
Ser Asp Leu Thr Asn Asp Gln Leu Asp Glu Lys Arg Leu Arg Asn Gly
          260          265          270
Tyr Arg Ser Glu Gly Ile Ala Val Phe Leu Gly Gly Leu Phe Asn Thr
          275          280          285
Phe Pro Tyr Thr Gly Phe Ser Gln Asn Val Gly Leu Val Gln Ile Ser
          290          295          300
Gly Ile Lys Thr Arg Arg Pro Ile Tyr Tyr Ala Ala Gly Ile Leu Val
305          310          315          320
Val Ile Gly Leu Leu Pro Lys Phe Arg Ala Met Ala Gln Met Ile Pro
          325          330          335
Ser Pro Val Leu Gly Gly Ala Met Leu Val Leu Phe Gly Met Val Ala
          340          345          350
Leu Gln Gly Met Gln Met Leu Asn Arg Val Asp Phe Gln Lys Asn Glu
          355          360          365
Tyr Asn Phe Ile Ile Ala Ala Val Ser Ile Ser Ala Gly Leu Gly Phe
          370          375          380
Asn Gly Thr Asn Leu Phe Ala Ser Leu Pro Glu Thr Ala Gln Met Phe
385          390          395          400
Leu Thr Asn Gly Ile Val Ile Ala Thr Leu Thr Ser Val Val Leu Asn
          405          410          415
Leu Val Leu Asn Gly Lys Asp Lys Gln Asp Glu
          420          425
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<210> SEQ ID NO 377
<211> LENGTH: 1563
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 377
atgcttttgt ggtcaattta tttggagggtg atgagcatgc ctagtttgtt tgtaactttc      60
caaaaccggt ttaatgaatg gctggcggct ctgggggaac acctgcaa at tccctttta      120
tctcttatga tcgccttgct aatagggtgtg ccttttagcag cccttctcag tcgcagcaaa      180
cgttgggtcag acattatggt acaggtaaca ggtgtttttc aaaccattcc ctcactggct      240
ttgcttggtc ttttcatccc tttaatggga attggaacgt tgctgcagt gacagcttta      300
gttatctatg cgatttttcc gattttacaa aacaccatca caggattaaa tgggtattgac      360
ccaagtctcg tggaagcagg aatagctttt gggatgacca aatgggagcg attgaaaaca      420
tttgagattc caattgccat gcctgttatt atgtcagggtg tgcggacgtc agcagtcagt      480
attatcggca cagctacttt agcttccttg ataggagccg gtggacttgg ctctttcatc      540
ttattaggga ttgatcgtaa taatgctaac ctgattctga taggggctat ttcttcagct      600
ctgctagcta ttattttcaa tagtttggtta cagtaccttg agaaaagcttc cttgcgacgg      660
attatgatta gttttggaat taccttactt gcactgctag catcgtatac tcctatggcg      720
cttagtcagt tttcaaaaagg aaaagataca gtggttattg ccggtaaatt gggagcagag      780
cccgatattc tgattaatct ctataaggaa ttaattgaag accaatcaga tataagtgtt      840
gagttgaaat ctaatttttg gaaaactagc ttcttatatg aagcccttaa atctggagat      900
attgatatgt atcctgaatt tacaggaacc ataacatcaa gtcttttacg cgacaaacca      960
cctttgtcta atgaccctaa gcaggctctat gaggatgcta aaaaaggcat tgctaagcaa      1020
gataaactga cccttctcaa gccatttgct taccaaaata cgtatgctgt tgctatgcca      1080
gaaaaattgg ctaaggaata tcagattgaa accatttctg atttaaaagc gcatgctgat      1140
actttaaagg ccggttttac tttggaattt aaggacagag cagatggcta taagggaatg      1200
caatctcaat atggattaca gctatctgtg gcgacgatgg agccagctct tcgttatcaa      1260
gcaattcaat caggagatat ccaagtaaca gatgcttact ctacggatgc tgaaattacg      1320
aaataccatt tgaaagtttt aaaggatgat aaacagttgt ttccacctta tcaggagct      1380
cctttgatga aaacttcctt attaacaaaa catccagaat taaaaggcat tcttaatcaa      1440
ttagcgggaa aaattactga aaaagagatg caggacatga actacgaggt atctgttaaa      1500
ggagcagatg ctaataaggt cgctcgagat tatctgttga aaacaggctt aatccagaaa      1560
taa

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<210> SEQ ID NO 378
<211> LENGTH: 520
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 378
Met Leu Leu Trp Ser Ile Tyr Leu Glu Val Met Ser Met Pro Ser Leu
1           5           10           15
Phe Val Thr Phe Gln Asn Arg Phe Asn Glu Trp Leu Ala Ala Leu Gly
20          25          30
Glu His Leu Gln Ile Ser Leu Leu Ser Leu Met Ile Ala Leu Leu Ile
35          40          45
Gly Val Pro Leu Ala Ala Leu Leu Ser Arg Ser Lys Arg Trp Ser Asp
50          55          60
Ile Met Leu Gln Val Thr Gly Val Phe Gln Thr Ile Pro Ser Leu Ala
65          70          75          80
Leu Leu Gly Leu Phe Ile Pro Leu Met Gly Ile Gly Thr Leu Pro Ala
85          90          95
Val Thr Ala Leu Val Ile Tyr Ala Ile Phe Pro Ile Leu Gln Asn Thr
100         105         110
Ile Thr Gly Leu Asn Gly Ile Asp Pro Ser Leu Val Glu Ala Gly Ile
115         120         125
Ala Phe Gly Met Thr Lys Trp Glu Arg Leu Lys Thr Phe Glu Ile Pro
130         135         140

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attgtaatga	gcgcttacga	aaaggtatat	gtttatatct	ttaaagactg	gtcacatgtc	240
ttaaaagtaa	aacgggggat	ttgtttactg	ttagcgtatt	tgacattttt	tattttaatt	300
acttggatta	tttccattgt	cattccagac	ttaattacaa	gtatttagtac	tctaacaaaa	360
tttgatacta	taacgataca	agaagttggt	aacaatcttg	agcacaataa	actgtttagca	420
cgtactattc	agtatattgg	tggcgatggc	aaacttacag	agacgattgc	taactatagt	480
caacagttat	taaagcaatt	tcttactggt	ttgacaaaata	ttttaacatc	tgtcacgggt	540
attgcttctg	caattattaa	tctttttatt	agttttgttt	tttcggtata	cgtttttagca	600
agtaaagaag	atctttgtcg	tcagggaaat	actttagtag	atacttatac	tggttaagtac	660
gctaaacgca	ttcattactt	gtagagttg	ttgcatcagc	gttttcacgg	attttttggt	720
agtcagacct	tagaagctat	gatttttaggt	tcgctgactg	ctagtggcat	gtttatatta	780
agattaccat	ttgcagggac	tattggcggt	ttagtagctt	ttacagcatt	gattccagtt	840
ataggtgctt	caattggagc	agctattgga	tttatttttaa	ttatgactca	gtccatgtca	900
caggccatta	tttttatcat	ttttttaatt	attttgcagc	agattgaagg	caatttttatt	960
tatccgaaag	tagttggtgg	atcgattgga	ttaccggcta	tgtgggtatt	aatggcaatt	1020
acaataggcg	cttcttttaa	gggaatagtt	ggtatgatta	ttgcagttcc	tttagcagcg	1080
acactttatc	aagtgattaa	agataatatt	caaaaaagac	aagctattca	aaaaaaacaa	1140
gtttcctaa						1149

<210> SEQ ID NO 380

<211> LENGTH: 382

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 380

Met	Ile	Ile	Lys	Gly	Val	Thr	Met	Lys	Phe	Glu	Lys	Lys	Gln	Val	Phe
1				5					10					15	
Tyr	Leu	Val	Leu	Thr	Phe	Ile	Leu	Cys	Tyr	Gly	Ile	Leu	Ala	Asn	Trp
			20					25					30		
Arg	Asn	Gly	Thr	Ala	Ile	Val	Thr	Thr	Ile	Tyr	Lys	Thr	Ser	Leu	Pro
		35				40					45				
Phe	Phe	Tyr	Gly	Ala	Ala	Gly	Ala	Tyr	Ile	Val	Asn	Ile	Val	Met	Ser
50						55					60				
Ala	Tyr	Glu	Lys	Val	Tyr	Val	Tyr	Ile	Phe	Lys	Asp	Trp	Ser	His	Val
65				70						75				80	
Leu	Lys	Val	Lys	Arg	Gly	Ile	Cys	Leu	Leu	Leu	Ala	Tyr	Leu	Thr	Phe
			85					90						95	
Phe	Ile	Leu	Ile	Thr	Trp	Ile	Ile	Ser	Ile	Val	Ile	Pro	Asp	Leu	Ile
		100						105					110		
Thr	Ser	Ile	Ser	Thr	Leu	Thr	Lys	Phe	Asp	Thr	Ile	Thr	Ile	Gln	Glu
		115					120						125		
Val	Val	Asn	Asn	Leu	Glu	His	Asn	Lys	Leu	Leu	Ala	Arg	Thr	Ile	Gln
		130				135					140				
Tyr	Ile	Gly	Gly	Asp	Gly	Lys	Leu	Thr	Glu	Thr	Ile	Ala	Asn	Tyr	Ser
145				150						155				160	
Gln	Gln	Leu	Leu	Lys	Gln	Phe	Leu	Thr	Val	Leu	Thr	Asn	Ile	Leu	Thr
			165						170					175	
Ser	Val	Thr	Val	Ile	Ala	Ser	Ala	Ile	Ile	Asn	Leu	Phe	Ile	Ser	Phe
		180						185					190		
Val	Phe	Ser	Leu	Tyr	Val	Leu	Ala	Ser	Lys	Glu	Asp	Leu	Cys	Arg	Gln
		195					200					205			
Gly	Asn	Thr	Leu	Val	Asp	Thr	Tyr	Thr	Gly	Lys	Tyr	Ala	Lys	Arg	Ile
	210					215					220				
His	Tyr	Leu	Leu	Glu	Leu	Leu	His	Gln	Arg	Phe	His	Gly	Phe	Phe	Val
225				230						235				240	
Ser	Gln	Thr	Leu	Glu	Ala	Met	Ile	Leu	Gly	Ser	Leu	Thr	Ala	Ser	Gly
			245						250					255	
Met	Phe	Ile	Leu	Arg	Leu	Pro	Phe	Ala	Gly	Thr	Ile	Gly	Val	Leu	Val
		260						265					270		

Ala	Phe	Thr	Ala	Leu	Ile	Pro	Val	Ile	Gly	Ala	Ser	Ile	Gly	Ala	Ala
		275					280					285			
Ile	Gly	Phe	Ile	Leu	Ile	Met	Thr	Gln	Ser	Met	Ser	Gln	Ala	Ile	Ile
	290					295					300				
Phe	Ile	Ile	Phe	Leu	Ile	Ile	Leu	Gln	Gln	Ile	Glu	Gly	Asn	Phe	Ile
305					310					315					320
Tyr	Pro	Lys	Val	Val	Gly	Gly	Ser	Ile	Gly	Leu	Pro	Ala	Met	Trp	Val
			325						330					335	
Leu	Met	Ala	Ile	Thr	Ile	Gly	Ala	Ser	Leu	Lys	Gly	Ile	Val	Gly	Met
		340						345					350		
Ile	Ile	Ala	Val	Pro	Leu	Ala	Ala	Thr	Leu	Tyr	Gln	Val	Ile	Lys	Asp
	355					360					365				
Asn	Ile	Gln	Lys	Arg	Gln	Ala	Ile	Gln	Lys	Lys	Gln	Val	Ser		
	370					375					380				

<210> SEQ ID NO 381

<211> LENGTH: 1074

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 381

atgcgtaa	ac	tttatt	cc	tt	tctagc	agga	gttttg	gggtg	ttattg	ttat	ttta	acaagt		60
ctttcttt	tca	tcttgc	agaa	aaaatc	gggt	tctggt	tagtc	aatcgg	ataa	attagt	tatt		120	
tataactg	ggg	gagatt	acat	tgatcc	agct	ttgctc	aaaa	aattca	ccaa	agaaac	gggc		180	
attgaagt	gc	agtatg	aaac	tttcgatt	cc	aatgaag	cca	tgtacac	ttaa	aatcaag	cag		240	
ggcggaac	ca	cttacg	acat	tgctgt	tcct	agtgatt	taca	ccattg	ataa	aatgat	caaa		300	
gaaaac	ctac	tcaata	agct	tgataagt	tca	aaattag	ttg	gcatgg	ataa	tatcgg	gaaa		360	
gaattttt	tag	ggaaaag	ctt	tgaccaca	aa	acgact	att	ctttgc	ctta	tttctg	ggga		420	
accgttgg	ga	ttgttt	tataa	tgatca	atta	gttgata	aagg	cgcctat	gca	ctggga	aagat		480	
ctgtggcg	tc	cagaata	tataa	aaatagt	tatt	atgctg	attg	atggag	cgcg	tgaaat	gcta		540	
ggggttgg	tt	taacaac	ttt	tggttat	agt	gtgaatt	tcta	aaaatc	taga	gcagtt	gcag		600	
gcagccga	gaga	gaaaact	gca	gcagtt	gacg	ccgaat	gtta	aagccatt	gt	agcagat	gag		660	
atgaaagg	ct	acatgatt	tca	aggtgac	gct	gctatt	ggaa	ttacct	tttc	tggtga	aagcc		720	
agtgaagt	gt	tagatagt	taa	cgaacac	ctt	cactacat	cg	tgccct	taca	aggttcta	ac		780	
ctttgg	tttg	ataatt	tggt	actacca	aaaa	accatg	aaac	acgaaaa	aaga	agcttat	gct		840	
tttttg	aact	ttatca	atcg	tcctg	aaaa	gctgcg	caaa	atgctg	cata	tattgg	ttat		900	
gcgacac	caa	ataaaaa	aagc	caaggc	ctta	cttccag	atg	agataaaa	aaaa	tgatcct	gct		960	
ttttat	ccaa	cagatg	acat	tatcaaaa	aaaa	ttggaag	ttt	atgaca	aattt	aggg	caaga		1020	
tggttgg	gga	tttata	atga	tttata	acctc	caattt	aaaa	tgtatc	gcaa	ataa			1074	

<210> SEQ ID NO 382

<211> LENGTH: 357

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 382

Met	Arg	Lys	Leu	Tyr	Ser	Phe	Leu	Ala	Gly	Val	Leu	Gly	Val	Ile	Val
1			5						10				15		
Ile	Leu	Thr	Ser	Leu	Ser	Phe	Ile	Leu	Gln	Lys	Lys	Ser	Gly	Ser	Gly
		20						25				30			
Ser	Gln	Ser	Asp	Lys	Leu	Val	Ile	Tyr	Asn	Trp	Gly	Asp	Tyr	Ile	Asp
	35					40					45				
Pro	Ala	Leu	Leu	Lys	Lys	Phe	Thr	Lys	Glu	Thr	Gly	Ile	Glu	Val	Gln
	50					55					60				
Tyr	Glu	Thr	Phe	Asp	Ser	Asn	Glu	Ala	Met	Tyr	Thr	Lys	Ile	Lys	Gln
65				70					75				80		
Gly	Gly	Thr	Thr	Tyr	Asp	Ile	Ala	Val	Pro	Ser	Asp	Tyr	Thr	Ile	Asp
				85				90					95		
Lys	Met	Ile	Lys	Glu	Asn	Leu	Leu	Asn	Lys	Leu	Asp	Lys	Ser	Lys	Leu

			100					105					110				
Val	Gly	Met	Asp	Asn	Ile	Gly	Lys	Glu	Phe	Leu	Gly	Lys	Ser	Phe	Asp		
		115					120					125					
Pro	Gln	Asn	Asp	Tyr	Ser	Leu	Pro	Tyr	Phe	Trp	Gly	Thr	Val	Gly	Ile		
	130					135					140						
Val	Tyr	Asn	Asp	Gln	Leu	Val	Asp	Lys	Ala	Pro	Met	His	Trp	Glu	Asp		
145				150					155					160			
Leu	Trp	Arg	Pro	Glu	Tyr	Lys	Asn	Ser	Ile	Met	Leu	Ile	Asp	Gly	Ala		
			165					170					175				
Arg	Glu	Met	Leu	Gly	Val	Gly	Leu	Thr	Thr	Phe	Gly	Tyr	Ser	Val	Asn		
		180					185						190				
Ser	Lys	Asn	Leu	Glu	Gln	Leu	Gln	Ala	Ala	Glu	Arg	Lys	Leu	Gln	Gln		
	195					200						205					
Leu	Thr	Pro	Asn	Val	Lys	Ala	Ile	Val	Ala	Asp	Glu	Met	Lys	Gly	Tyr		
	210				215						220						
Met	Ile	Gln	Gly	Asp	Ala	Ala	Ile	Gly	Ile	Thr	Phe	Ser	Gly	Glu	Ala		
225			230					235						240			
Ser	Glu	Met	Leu	Asp	Ser	Asn	Glu	His	Leu	His	Tyr	Ile	Val	Pro	Ser		
			245				250						255				
Glu	Gly	Ser	Asn	Leu	Trp	Phe	Asp	Asn	Leu	Val	Leu	Pro	Lys	Thr	Met		
		260				265						270					
Lys	His	Glu	Lys	Glu	Ala	Tyr	Ala	Phe	Leu	Asn	Phe	Ile	Asn	Arg	Pro		
	275				280						285						
Glu	Asn	Ala	Ala	Gln	Asn	Ala	Ala	Tyr	Ile	Gly	Tyr	Ala	Thr	Pro	Asn		
	290				295					300							
Lys	Lys	Ala	Lys	Ala	Leu	Leu	Pro	Asp	Glu	Ile	Lys	Asn	Asp	Pro	Ala		
305			310					315						320			
Phe	Tyr	Pro	Thr	Asp	Asp	Ile	Ile	Lys	Lys	Leu	Glu	Val	Tyr	Asp	Asn		
		325				330							335				
Leu	Gly	Ser	Arg	Trp	Leu	Gly	Ile	Tyr	Asn	Asp	Leu	Tyr	Leu	Gln	Phe		
		340				345							350				
Lys	Met	Tyr	Arg	Lys													
	355																

<210> SEQ ID NO 383

<211> LENGTH: 777

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 383

atgaaaaaat	ttgccaatct	ttattttagcg	agtgtctttg	ttttactcta	cattcctatt	60
ttttatttga	ttttctattc	tttcaacaaa	ggtggggata	tgaatggttt	tacaggattt	120
acccttgagc	attaccaaac	catgtttgag	gatagtcgtc	tcattgacaat	cttactgcaa	180
acctttgttc	ttgcttttag	tagcgtctta	ctagcaacga	ttattgggat	ctttggagct	240
atctttatcc	accatgttag	aggtaagtac	caaaatgcc	tgctatcagc	caataatgtc	300
ttgatgggat	caccagatgt	catgattggg	gcttcctttt	taattctttt	tacatcattg	360
aagtttcagc	tgggcatgtc	ttcagtttta	ttaagtcata	ttgctttttc	gattcctatt	420
gtggttttga	tgggtattgcc	gcgcttgaaa	gagatgaatc	aggacatggg	caacgccgct	480
tatgatttgg	gagctaatta	tttccaaatg	ctcaaagaag	tcattgctgcc	atactttaca	540
ccagggatta	ttgcagggtta	ttttatggcc	tttacctatt	ccttagatga	ttttgcagtg	600
actttctttt	tgactggaaa	tagtgttact	acattatctg	ttgagattta	ttcgcgggct	660
cgtcagggaa	tttccttgga	tatcaatgct	ttgtcaacca	tcgttttctt	tttctccatc	720
ctcttagtga	tcggttatta	ttatatgtca	caggacaagg	aggaaaaaca	tcggttaa	777

<210> SEQ ID NO 384

<211> LENGTH: 258

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 384

```
Met Lys Lys Phe Ala Asn Leu Tyr Leu Ala Ser Val Phe Val Leu Leu
1      5      10      15
Tyr Ile Pro Ile Phe Tyr Leu Ile Phe Tyr Ser Phe Asn Lys Gly Gly
20      25      30
Asp Met Asn Gly Phe Thr Gly Phe Thr Leu Glu His Tyr Gln Thr Met
35      40      45
Phe Glu Asp Ser Arg Leu Met Thr Ile Leu Leu Gln Thr Phe Val Leu
50      55      60
Ala Phe Ser Ser Ala Leu Leu Ala Thr Ile Ile Gly Ile Phe Gly Ala
65      70      75      80
Ile Phe Ile His His Val Arg Gly Lys Tyr Gln Asn Ala Met Leu Ser
85      90      95
Ala Asn Asn Val Leu Met Val Ser Pro Asp Val Met Ile Gly Ala Ser
100     105     110
Phe Leu Ile Leu Phe Thr Ser Leu Lys Phe Gln Leu Gly Met Ser Ser
115     120     125
Val Leu Leu Ser His Ile Ala Phe Ser Ile Pro Ile Val Val Leu Met
130     135     140
Val Leu Pro Arg Leu Lys Glu Met Asn Gln Asp Met Val Asn Ala Ala
145     150     155     160
Tyr Asp Leu Gly Ala Asn Tyr Phe Gln Met Leu Lys Glu Val Met Leu
165     170     175
Pro Tyr Phe Thr Pro Gly Ile Ile Ala Gly Tyr Phe Met Ala Phe Thr
180     185     190
Tyr Ser Leu Asp Asp Phe Ala Val Thr Phe Phe Leu Thr Gly Asn Ser
195     200     205
Val Thr Thr Leu Ser Val Glu Ile Tyr Ser Arg Ala Arg Gln Gly Ile
210     215     220
Ser Leu Asp Ile Asn Ala Leu Ser Thr Ile Val Phe Phe Phe Ser Ile
225     230     235     240
Leu Leu Val Ile Gly Tyr Tyr Tyr Met Ser Gln Asp Lys Glu Glu Lys
245     250     255
His Ala
```

<210> SEQ ID NO 385

<211> LENGTH: 816

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 385

```
atgccattga ggaggagcgt aatgaagaaa acctctagtc ttttttcgat tccttacttc      60
ttatggattc tcttttttgt tgtggcacca gtcactctct tgttttacaa gtcctttttt      120
gacatagaag ggcgcgtgac cttagccaat tatgaaacct ttttttagctc ttggacttat      180
ttgaggatga gtgtgaattc tattttatac gctgggatta tcacactcgt cagctcttg      240
atttcatatc ctacggctct ctttttaacg cgctaaagc acaagcagtt gtggcttatg      300
ctcattatct tgccaacctg ggtaaattta ttgctaaagg cctatgcctt tatgggaatc      360
tttgggtcaac aaggagggat taacagcttt ttaaccttta tggggattgg cccgcagcaa      420
atccttttca cagatttctc cttcattttt gtagcctctt acattgagct cccttttatg      480
atgttaccga tttttaacgc tttggatgat attgaccata atgtcatcaa tgccagtcgc      540
gacctaggag ctagtgaatt tcaggccttc tcaaaaagta tttttccctt ttctttaaat      600
ggggttaggg cagggtgttca gtctgtcttt atcccaagtt tgagtctctt tatgttaacc      660
cgtttgattg gtggaaaccg ggtgattaca cttggtacag ccattgaaca acattttttg      720
accacccaaa actggggaat gggatcaacc attggtgtcg tcttgatttt gaccatgggt      780
gctattatgt ggctcacaaa ggagaaaagt aaatga      816
```

<210> SEQ ID NO 386

<211> LENGTH: 271

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 386

```
Met Pro Leu Arg Arg Ser Val Met Lys Lys Thr Ser Ser Leu Phe Ser
1      5      10      15
Ile Pro Tyr Phe Leu Trp Ile Leu Phe Phe Val Val Ala Pro Val Thr
20      25      30
Leu Leu Phe Tyr Lys Ser Phe Phe Asp Ile Glu Gly Arg Val Thr Leu
35      40      45
Ala Asn Tyr Glu Thr Phe Phe Ser Ser Trp Thr Tyr Leu Arg Met Ser
50      55      60
Val Asn Ser Ile Leu Tyr Ala Gly Ile Ile Thr Leu Val Thr Leu Leu
65      70      75      80
Ile Ser Tyr Pro Thr Ala Leu Phe Leu Thr Arg Leu Lys His Lys Gln
85      90      95
Leu Trp Leu Met Leu Ile Ile Leu Pro Thr Trp Val Asn Leu Leu Leu
100     105     110
Lys Ala Tyr Ala Phe Met Gly Ile Phe Gly Gln Gln Gly Gly Ile Asn
115     120     125
Ser Phe Leu Thr Phe Met Gly Ile Gly Pro Gln Gln Ile Leu Phe Thr
130     135     140
Asp Phe Ser Phe Ile Phe Val Ala Ser Tyr Ile Glu Leu Pro Phe Met
145     150     155     160
Met Leu Pro Ile Phe Asn Ala Leu Asp Asp Ile Asp His Asn Val Ile
165     170     175
Asn Ala Ser Arg Asp Leu Gly Ala Ser Glu Phe Gln Ala Phe Ser Lys
180     185     190
Val Ile Phe Pro Leu Ser Leu Asn Gly Val Arg Ala Gly Val Gln Ser
195     200     205
Val Phe Ile Pro Ser Leu Ser Leu Phe Met Leu Thr Arg Leu Ile Gly
210     215     220
Gly Asn Arg Val Ile Thr Leu Gly Thr Ala Ile Glu Gln His Phe Leu
225     230     235     240
Thr Thr Gln Asn Trp Gly Met Gly Ser Thr Ile Gly Val Val Leu Ile
245     250     255
Leu Thr Met Val Ala Ile Met Trp Leu Thr Lys Glu Lys Ser Lys
260     265     270
```

<210> SEQ ID NO 387

<211> LENGTH: 963

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 387

```
atgaacaata gacataaacg gcgccaaaaa agaaaagcct tcactctcat taaccttata      60
ctattatttg cctgcattct tggtttgacc ctcattttct atttatatca agggctctaac      120
aaattcgggt tgtcagatgt ctctcgattt gtacctaaaa taagtctttt tcatcacaaa      180
aagacggcaa aaaaagaaac gacaaaactt aagaagactc atttcgattc ctcaaaatct      240
caaaaaaagg cccattctaa attgacttgg accaagcaag aaacacctgt caagatccca      300
attttaatgt atcatgctat tcatgtaatg tcccctgaag agacggctaa tgctaatttg      360
attgtcaacc cagatctctt tgatcaacaa cttcaaaaaa tgaaagacga gggctactat      420
tttttgagtc ctgaagaggt ctaccgcgct ctttcaaata atgaattgcc tgctaaaaaa      480
gttgatatggc taacatttga tgacagtatg attgatttct acaatgttgc ttaccaatc      540
ttaaaaaaat atgatgctaa agccaccaat aatgttatta caggactaac cgaaatggga      600
agcgctgcca atctgactct taagcagatg aaagaaatga aacaagtcgg tatgtctttc      660
caagatcata cagtgaatca tcctgatcta gagcaggcta gtcctgatgt tcaaacaact      720
gaaatgaaag attcaaagga ctatcttgat aagcaattaa accaaaaacac tattgccatt      780
gcttatccat ctggtagata taatgacact accttacaaa ttgcagctag acttaactat      840
```

aaattaggtg ttaccactaa cgaaggaata gctagcgcg	ctaattggact tctttctctt	900
aaccggattc gtatcctccc aaacatgagt cctgaaaatc	ttttacaaac aatggaacca	960
taa		963

<210> SEQ ID NO 388
 <211> LENGTH: 320
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 388

Met	Asn	Asn	Arg	His	Lys	Arg	Arg	Gln	Lys	Arg	Lys	Ala	Phe	Thr	Leu
1				5					10					15	
Ile	Asn	Leu	Ile	Leu	Leu	Phe	Ala	Cys	Ile	Leu	Gly	Leu	Thr	Leu	Ile
			20					25					30		
Phe	Tyr	Leu	Tyr	Gln	Gly	Ser	Asn	Lys	Phe	Gly	Leu	Ser	Asp	Val	Ser
		35					40					45			
Arg	Phe	Val	Pro	Lys	Ile	Ser	Leu	Phe	His	His	Lys	Lys	Thr	Ala	Lys
	50					55					60				
Lys	Glu	Thr	Thr	Lys	Leu	Lys	Lys	Thr	His	Phe	Asp	Ser	Ser	Lys	Ser
65					70					75					80
Gln	Lys	Lys	Ala	His	Ser	Lys	Leu	Thr	Trp	Thr	Lys	Gln	Glu	Thr	Pro
				85					90					95	
Val	Lys	Ile	Pro	Ile	Leu	Met	Tyr	His	Ala	Ile	His	Val	Met	Ser	Pro
			100					105					110		
Glu	Glu	Thr	Ala	Asn	Ala	Asn	Leu	Ile	Val	Asn	Pro	Asp	Leu	Phe	Asp
		115					120					125			
Gln	Gln	Leu	Gln	Lys	Met	Lys	Asp	Glu	Gly	Tyr	Tyr	Phe	Leu	Ser	Pro
	130					135						140			
Glu	Glu	Val	Tyr	Arg	Ala	Leu	Ser	Asn	Asn	Glu	Leu	Pro	Ala	Lys	Lys
145					150					155					160
Val	Val	Trp	Leu	Thr	Phe	Asp	Asp	Ser	Met	Ile	Asp	Phe	Tyr	Asn	Val
			165						170					175	
Ala	Tyr	Pro	Ile	Leu	Lys	Lys	Tyr	Asp	Ala	Lys	Ala	Thr	Asn	Asn	Val
			180					185					190		
Ile	Thr	Gly	Leu	Thr	Glu	Met	Gly	Ser	Ala	Ala	Asn	Leu	Thr	Leu	Lys
		195					200					205			
Gln	Met	Lys	Glu	Met	Lys	Gln	Val	Gly	Met	Ser	Phe	Gln	Asp	His	Thr
	210					215					220				
Val	Asn	His	Pro	Asp	Leu	Glu	Gln	Ala	Ser	Pro	Asp	Val	Gln	Thr	Thr
225					230					235					240
Glu	Met	Lys	Asp	Ser	Lys	Asp	Tyr	Leu	Asp	Lys	Gln	Leu	Asn	Gln	Asn
			245						250					255	
Thr	Ile	Ala	Ile	Ala	Tyr	Pro	Ser	Gly	Arg	Tyr	Asn	Asp	Thr	Thr	Leu
			260					265					270		
Gln	Ile	Ala	Ala	Arg	Leu	Asn	Tyr	Lys	Leu	Gly	Val	Thr	Thr	Asn	Glu
		275					280					285			
Gly	Ile	Ala	Ser	Ala	Ala	Asn	Gly	Leu	Leu	Ser	Leu	Asn	Arg	Ile	Arg
	290					295				300					
Ile	Leu	Pro	Asn	Met	Ser	Pro	Glu	Asn	Leu	Leu	Gln	Thr	Met	Glu	Pro
305					310					315					320

<210> SEQ ID NO 389
 <211> LENGTH: 1356
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 389

gtgttattgt tacagggtac ttgctttatg agcttggtta	agctactaaa ggtgtgtgcc	60
actatacttc cttccaaatt tctgagaatt tttgttataa	tagtaactat gaaagatata	120

atgataaaaa	ggtgggttat	cctttttttt	atggtattaa	cttggttcagg	gtttggtaaa	180
acagttctcg	cagctgattt	tcaagtggga	gcagaacatg	cgattgtcgt	agaggcagac	240
tctgggagag	ttctgtatga	gaaagacgct	aagacgccag	atgctattgc	ctctttgacc	300
aaattggtga	cggcttatct	ggttttagat	aaggttaaat	caggccagct	gcaattatca	360
gatcaagtta	atctctcaga	ttatgccttc	gagttaacaa	aagataggtc	tttaagtaat	420
gtaccttttg	acaaaaaaac	ttattcagtt	caagacctgt	tgacagctac	tttggttagca	480
agctcaaata	gcgctgctat	tgcgttagcc	gaaaaagtgg	cgggctcaga	gcttcatttt	540
gtaaatcaaa	tgagagaaca	gctatctcat	tgggggatta	cttctggtaa	aatcctcaac	600
gcttcaggac	tgccgaatga	ggtgctaaa	gaccatcggt	atcctgggtt	tgcggttgaa	660
gaagagaata	tggttgagtgc	tcaggatggt	gccattgtga	cgatgcattt	actggaagat	720
tttcttgaga	tttttagagat	cactaaacaa	acagaagttg	attttgctgg	taattctatt	780
aaaagtttta	atcaactctt	accaggtatg	gctaagggtg	gagcaggagt	ggatgggcta	840
aagacaggaa	cgacagattt	ggcaggtcac	tgccttggtg	taacttctat	tgaaaaatggt	900
atgaggctga	ttaccgttat	tctaaatgct	gatggatctg	ataaaaacca	aaacacgcgg	960
tttgagcaag	caaatcgctt	gttggactat	gtggctagaa	cttattgtcg	tcgtaagatt	1020
cttaaaaaag	gaagtcttgt	ctcggagcga	tcgctcccta	ttcaagatgg	ccaagtaaaa	1080
gaactaccga	tatctgttgc	cgaagatgta	accatcattt	tgcaacaggg	tgaacaagtt	1140
cccaaacctt	aacaatttat	gatatcagag	acttctttat	tagcaccgat	tactaaaggt	1200
gaagtgggtg	cttattttgac	gtctccaaga	ataacagatc	agtcagtgag	gtattttaag	1260
gaacctaaag	gtatttcctct	taaagctagc	caatctctaa	aaaaagcctc	tgacttacag	1320
ctgtggtggc	gagatttttct	tgaaaaaaga	cgtaa			1356

<210> SEQ ID NO 390
 <211> LENGTH: 451
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 390

Met	Leu	Leu	Leu	Gln	Gly	Thr	Cys	Phe	Met	Ser	Leu	Phe	Lys	Leu	Leu
1			5					10					15		
Lys	Val	Cys	Ala	Thr	Ile	Leu	Pro	Ser	Lys	Phe	Leu	Arg	Ile	Phe	Val
		20					25					30			
Ile	Ile	Val	Thr	Met	Lys	Asp	Ile	Met	Ile	Lys	Arg	Trp	Val	Ile	Leu
		35				40						45			
Phe	Phe	Met	Val	Leu	Thr	Cys	Ser	Gly	Phe	Gly	Lys	Thr	Val	Leu	Ala
	50					55					60				
Ala	Asp	Phe	Gln	Val	Gly	Ala	Glu	His	Ala	Ile	Val	Val	Glu	Ala	Asp
65				70					75					80	
Ser	Gly	Arg	Val	Leu	Tyr	Glu	Lys	Asp	Ala	Lys	Thr	Pro	Asp	Ala	Ile
			85				90						95		
Ala	Ser	Leu	Thr	Lys	Leu	Val	Thr	Ala	Tyr	Leu	Val	Leu	Asp	Lys	Val
		100					105						110		
Lys	Ser	Gly	Gln	Leu	Gln	Leu	Ser	Asp	Gln	Val	Asn	Leu	Ser	Asp	Tyr
		115				120					125				
Ala	Phe	Glu	Leu	Thr	Lys	Asp	Arg	Ser	Leu	Ser	Asn	Val	Pro	Phe	Asp
	130					135					140				
Lys	Lys	Thr	Tyr	Ser	Val	Gln	Asp	Leu	Leu	Thr	Ala	Thr	Leu	Val	Ala
145				150					155					160	
Ser	Ser	Asn	Ser	Ala	Ala	Ile	Ala	Leu	Ala	Glu	Lys	Val	Ala	Gly	Ser
			165				170							175	
Glu	Leu	His	Phe	Val	Asn	Gln	Met	Arg	Glu	Gln	Leu	Ser	His	Trp	Gly
		180				185						190			
Ile	Thr	Ser	Gly	Lys	Ile	Leu	Asn	Ala	Ser	Gly	Leu	Pro	Asn	Glu	Val
	195					200						205			
Leu	Lys	Asp	His	Arg	Tyr	Pro	Gly	Ser	Ala	Leu	Glu	Glu	Glu	Asn	Met
	210				215						220				
Leu	Ser	Ala	Gln	Asp	Val	Ala	Ile	Val	Thr	Met	His	Leu	Leu	Glu	Asp
225					230					235					240

Phe	Pro	Glu	Ile	Leu	Glu	Ile	Thr	Lys	Gln	Thr	Glu	Val	Asp	Phe	Ala		
				245					250					255			
Gly	Asn	Ser	Ile	Lys	Ser	Phe	Asn	Gln	Leu	Leu	Pro	Gly	Met	Ala	Lys		
			260					265					270				
Gly	Arg	Ala	Gly	Val	Asp	Gly	Leu	Lys	Thr	Gly	Thr	Thr	Asp	Leu	Ala		
		275					280					285					
Gly	His	Cys	Leu	Val	Val	Thr	Ser	Ile	Glu	Asn	Gly	Met	Arg	Leu	Ile		
	290					295					300						
Thr	Val	Ile	Leu	Asn	Ala	Asp	Gly	Ser	Asp	Lys	Asn	Gln	Asn	Thr	Arg		
305					310					315					320		
Phe	Glu	Gln	Ala	Asn	Arg	Leu	Leu	Asp	Tyr	Val	Ala	Arg	Thr	Tyr	Cys		
				325					330					335			
Arg	Arg	Lys	Ile	Leu	Lys	Lys	Gly	Ser	Leu	Val	Ser	Glu	Arg	Ser	Leu		
		340						345					350				
Pro	Ile	Gln	Asp	Gly	Gln	Val	Lys	Glu	Leu	Pro	Ile	Ser	Val	Ala	Glu		
		355					360					365					
Asp	Val	Thr	Ile	Ile	Leu	Gln	Gln	Gly	Glu	Gln	Val	Pro	Lys	Pro	Lys		
	370					375					380						
Gln	Phe	Met	Ile	Ser	Glu	Thr	Ser	Leu	Leu	Ala	Pro	Ile	Thr	Lys	Gly		
385					390					395				400			
Glu	Val	Val	Ala	Tyr	Leu	Thr	Ser	Pro	Arg	Ile	Thr	Asp	Gln	Ser	Val		
				405					410				415				
Arg	Tyr	Leu	Lys	Glu	Pro	Lys	Arg	Ile	Pro	Leu	Lys	Ala	Ser	Gln	Ser		
		420						425				430					
Leu	Lys	Lys	Ala	Ser	Asp	Leu	Gln	Leu	Trp	Trp	Arg	Asp	Phe	Leu	Glu		
		435					440					445					
Lys	Arg	Arg															
		450															

<210> SEQ ID NO 391

<211> LENGTH: 747

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 391

ttgttttgct	tactatacac	taaacgctca	gcaatatata	gaatgggagt	aactaatatg	60
ttgaaaatac	aaaatctaaa	aaaatcttat	ggtaagagaa	ccatattgaa	taatgtcaat	120
atgaatatcc	ctaaggga	agtgtatgct	ttaatcggtc	caaatgggtc	tggaaaatca	180
actattatga	aaattttgac	aggcttagtt	agtaagacaa	gtggttctat	tatttttgaa	240
ggtagagaat	ggtcacgtcg	ggatctgcga	aaaatcggga	gtattattga	agaaccacca	300
ctttataaaa	atttgagtgc	ttacgataat	atgaaggtag	ttacaacaat	gcttggtgtt	360
tcagaaagca	ctatacttcc	attattaaat	aaagttggtc	taggaaatat	tgacaagaga	420
ccagtaaaac	aattttctct	tggaatgaag	caacggttag	gtatagctat	ctctttaata	480
aattcaccta	aactacttat	attagacgaa	cctactaatg	gcttggaacc	aattggaatt	540
caagaattaa	gggaaattat	agagtcattt	aaatcagaag	gaatgacaat	tatgatttca	600
agccatatac	tgtcagaagt	tgaacatcta	gctgatttta	ttggatttat	ctatgaagga	660
aagattattc	tggaaaaaga	atatgacggc	tctgagaatc	ttgaagagtt	attcaataat	720
caaattttat	ttgaaaagag	gaggtag				747

<210> SEQ ID NO 392

<211> LENGTH: 248

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 392

Met	Phe	Cys	Leu	Leu	Tyr	Thr	Lys	Arg	Ser	Ala	Ile	Tyr	Arg	Met	Gly
1			5				10					15			
Val	Thr	Asn	Met	Leu	Lys	Ile	Gln	Asn	Leu	Lys	Lys	Ser	Tyr	Gly	Lys
		20					25					30			

Arg	Thr	Ile	Leu	Asn	Asn	Val	Asn	Met	Asn	Ile	Pro	Lys	Gly	Lys	Val
	35						40					45			
Tyr	Ala	Leu	Ile	Gly	Pro	Asn	Gly	Ala	Gly	Lys	Ser	Thr	Ile	Met	Lys
	50					55					60				
Ile	Leu	Thr	Gly	Leu	Val	Ser	Lys	Thr	Ser	Gly	Ser	Ile	Ile	Phe	Glu
65					70					75					80
Gly	Arg	Glu	Trp	Ser	Arg	Arg	Asp	Leu	Arg	Lys	Ile	Gly	Ser	Ile	Ile
				85					90					95	
Glu	Glu	Pro	Pro	Leu	Tyr	Lys	Asn	Leu	Ser	Ala	Tyr	Asp	Asn	Met	Lys
		100						105					110		
Val	Val	Thr	Thr	Met	Leu	Gly	Val	Ser	Glu	Ser	Thr	Ile	Leu	Pro	Leu
	115						120					125			
Leu	Asn	Lys	Val	Gly	Leu	Gly	Asn	Ile	Asp	Lys	Arg	Pro	Val	Lys	Gln
	130					135					140				
Phe	Ser	Leu	Gly	Met	Lys	Gln	Arg	Leu	Gly	Ile	Ala	Ile	Ser	Leu	Ile
145					150					155					160
Asn	Ser	Pro	Lys	Leu	Leu	Ile	Leu	Asp	Glu	Pro	Thr	Asn	Gly	Leu	Asp
			165						170					175	
Pro	Ile	Gly	Ile	Gln	Glu	Leu	Arg	Glu	Ile	Ile	Glu	Ser	Phe	Lys	Ser
		180						185					190		
Glu	Gly	Met	Thr	Ile	Met	Ile	Ser	Ser	His	Ile	Leu	Ser	Glu	Val	Glu
	195						200				205				
His	Leu	Ala	Asp	Phe	Ile	Gly	Phe	Ile	Tyr	Glu	Gly	Lys	Ile	Ile	Leu
	210					215					220				
Glu	Lys	Glu	Tyr	Asp	Gly	Ser	Glu	Asn	Leu	Glu	Glu	Leu	Phe	Asn	Asn
225					230					235					240
Gln	Ile	Leu	Phe	Glu	Lys	Arg	Arg								
				245											

<210> SEQ ID NO 393

<211> LENGTH: 1362

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 393

ttggttataa	atgggatgtt	taaaaaatat	tcaataaaaa	atcgtgtttg	gcgcgccgtc	60
gttgaaattg	tctttggagt	ttgtatcact	gttttaaatga	ttgcgataat	atcgctttct	120
ttttcaaagt	taaatatagt	gacatctcat	aatgtgggag	aagaatttta	tattaaagat	180
aaacagtcaa	tcaaacagtt	gaacaattat	atgaagacat	tgggattaga	ttatgttggt	240
tttgatagaa	aaacagataa	agctatggaa	ggaaaaatatt	tatctaaaga	attttcttta	300
tttaacgaag	ttgcagaaga	aaaaaataat	ctgactttta	attctgtaca	ttatgattta	360
tatactaata	tcaattataa	tattgttata	agatataatg	agataccgga	gttctctaac	420
cattacctta	gaaatgtttc	atataacatg	ttgacatttt	atattctggg	aataggaacg	480
agtatcagca	ttgtagttgc	tttaacacgg	tttgtaaaaag	aaatttcttt	gaatttcaag	540
gaaatcaaga	agttagcaaa	taaaatgggg	atagaagtcc	tttctgaaaa	tgaaaattat	600
tctaaaataa	tcgagtttga	tgatataact	agaactttac	atattaaagg	tgataatttg	660
aaaagtttga	ttgagcgaga	aatattggaa	aagcaagatc	tatcctttca	aattgcagca	720
ctttcgcagt	atattaaaaac	acctttaacg	gttttaaaaag	gaaatcttga	gttattagaa	780
ttgactactt	taaataaaaa	tcaggaaggt	tatattgtat	ctatgaacaa	tagtatttct	840
gtttttgaag	gctattttcaa	ttctttaata	tcttatacac	gcatgctttc	agaggataga	900
tcagtgaaac	taatttttagt	tgaggagcta	ttaagtga	tacattttga	agtcgatgac	960
ttattgaata	tcaataatat	tgaattttct	atttgtaata	gacttattat	cacttctttt	1020
tatggagatg	aggaaaatct	gataagagct	ctttctaacc	ttttagttaa	tgcaataaga	1080
tttatgcccg	tattagataa	aaaaatcgaa	gttatactgt	ctgagtcagg	agagcaaatt	1140
cattttgaaa	tatggaataa	tggtgagcgt	ttcagtgata	gtacactgaa	aaagggagat	1200
aaattatttt	acacggaaga	ttatagcaga	ggtaacaaac	attatggaat	cggtttggca	1260
tttgttaaaag	gcgttgctat	caaacacggt	gggaatcttc	aattgaataa	tccagctaga	1320
ggaggtgcta	gcgccataat	ctcgataaaa	aagaaaattt	aa		1362

<210> SEQ ID NO 394

<211> LENGTH: 453

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 394

Met	Val	Ile	Asn	Gly	Met	Phe	Lys	Lys	Tyr	Ser	Ile	Lys	Asn	Arg	Val
1			5						10					15	
Trp	Arg	Ala	Val	Val	Glu	Ile	Val	Phe	Gly	Val	Cys	Ile	Thr	Val	Leu
			20					25					30		
Met	Ile	Ala	Ile	Ile	Ser	Leu	Ser	Phe	Ser	Lys	Leu	Asn	Ile	Val	Thr
		35					40					45			
Ser	His	Asn	Val	Gly	Glu	Glu	Phe	Tyr	Ile	Lys	Asp	Lys	Gln	Ser	Ile
	50					55					60				
Lys	Gln	Leu	Asn	Asn	Tyr	Met	Lys	Thr	Leu	Gly	Leu	Asp	Tyr	Val	Val
65					70					75					80
Phe	Asp	Arg	Lys	Thr	Asp	Lys	Ala	Met	Glu	Gly	Lys	Tyr	Leu	Ser	Lys
				85						90					95
Glu	Phe	Ser	Leu	Phe	Asn	Glu	Val	Ala	Glu	Glu	Lys	Asn	Asn	Leu	Thr
			100					105						110	
Phe	Asn	Ser	Val	His	Tyr	Asp	Leu	Tyr	Thr	Asn	Ile	Asn	Tyr	Asn	Ile
		115					120					125			
Val	Ile	Arg	Tyr	Asn	Glu	Ile	Pro	Glu	Phe	Ser	Asn	His	Tyr	Leu	Arg
	130					135					140				
Asn	Val	Ser	Tyr	Asn	Met	Leu	Thr	Phe	Tyr	Ile	Leu	Gly	Ile	Gly	Thr
145				150						155					160
Ser	Ile	Ser	Ile	Val	Val	Ala	Leu	Thr	Arg	Phe	Val	Lys	Glu	Ile	Ser
				165					170						175
Leu	Asn	Phe	Lys	Glu	Ile	Lys	Lys	Leu	Ala	Asn	Lys	Met	Gly	Ile	Glu
		180					185						190		
Val	Leu	Ser	Glu	Asn	Glu	Asn	Tyr	Ser	Lys	Ile	Ile	Glu	Phe	Asp	Asp
		195					200					205			
Ile	Leu	Arg	Thr	Leu	His	Ile	Lys	Gly	Asp	Asn	Leu	Lys	Ser	Leu	Ile
	210					215					220				
Glu	Arg	Glu	Ile	Leu	Glu	Lys	Gln	Asp	Leu	Ser	Phe	Gln	Ile	Ala	Ala
225				230						235					240
Leu	Ser	His	Asp	Ile	Lys	Thr	Pro	Leu	Thr	Val	Leu	Lys	Gly	Asn	Leu
			245						250					255	
Glu	Leu	Leu	Glu	Leu	Thr	Thr	Leu	Asn	Lys	Asn	Gln	Glu	Gly	Tyr	Ile
		260					265					270			
Val	Ser	Met	Asn	Asn	Ser	Ile	Ser	Val	Phe	Glu	Gly	Tyr	Phe	Asn	Ser
		275				280						285			
Leu	Ile	Ser	Tyr	Thr	Arg	Met	Leu	Ser	Glu	Asp	Arg	Ser	Val	Lys	Leu
	290					295					300				
Ile	Leu	Val	Glu	Glu	Leu	Leu	Ser	Glu	Leu	His	Phe	Glu	Val	Asp	Asp
305				310						315					320
Leu	Leu	Asn	Ile	Asn	Asn	Ile	Glu	Phe	Ser	Ile	Cys	Asn	Arg	Leu	Ile
			325						330					335	
Ile	Thr	Ser	Phe	Tyr	Gly	Asp	Glu	Glu	Asn	Leu	Ile	Arg	Ala	Leu	Ser
		340					345					350			
Asn	Leu	Leu	Val	Asn	Ala	Ile	Arg	Phe	Met	Pro	Val	Leu	Asp	Lys	Lys
		355					360					365			
Ile	Glu	Val	Ile	Leu	Ser	Glu	Ser	Gly	Glu	Gln	Ile	His	Phe	Glu	Ile
	370					375					380				
Trp	Asn	Asn	Gly	Glu	Arg	Phe	Ser	Asp	Ser	Thr	Leu	Lys	Lys	Gly	Asp
385				390						395					400
Lys	Leu	Phe	Tyr	Thr	Glu	Asp	Tyr	Ser	Arg	Gly	Asn	Lys	His	Tyr	Gly

				405					410					415			
Ile	Gly	Leu	Ala	Phe	Val	Lys	Gly	Val	Ala	Ile	Lys	His	Gly	Gly	Asn		
			420					425					430				
Leu	Gln	Leu	Asn	Asn	Pro	Ala	Arg	Gly	Gly	Ala	Ser	Ala	Ile	Ile	Ser		
		435					440					445					
Ile	Lys	Lys	Lys	Ile													
	450																

<210> SEQ ID NO 395

<211> LENGTH: 687

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 395

atgtataaga	ttttagccat	agatgatgat	aaagaaattc	tgaagcttat	gaagactgct	60
ttggagattg	aaaattatca	tggtataacc	tgtaagaga	tagaattacc	aatagttttt	120
gatgatttta	aaggatatga	tttgatctta	ttggatatca	tgatgcctaa	tataagtggga	180
actgagtttt	gttataaaat	tcgggaagaa	gttcattctc	caattatttt	tgtttagcgct	240
ttagatggcg	ataatgaaat	tgtccaagct	ttaaatatag	ggggagacga	ttttattgtg	300
aaaccattta	gcttaaaaca	attcgtagct	aaagttaact	ctcatttgaa	gagagaagag	360
agagcaaaga	taaagaatga	ggctgaggag	agagtgaagc	gtagttttcc	acctatagaa	420
atctatctag	aggaacgtat	gttatatatt	gataaacagc	cgttattcct	gacttataga	480
gagtacgaaa	ttttagaatt	actgtcacgt	catccgtata	aagttttcac	aaaagaagag	540
atatatgaac	aagtatatag	cgatgaagct	tcagcattgt	ttcattctat	ttcagaatat	600
atctatcaga	ttagaatgaa	attttcaagt	tttggaatta	atccaataaa	aactattcgc	660
gggattgggt	ataaatggga	tggtttaa				687

<210> SEQ ID NO 396

<211> LENGTH: 228

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 396

Met	Tyr	Lys	Ile	Leu	Ala	Ile	Asp	Asp	Asp	Lys	Glu	Ile	Leu	Lys	Leu
1				5					10					15	
Met	Lys	Thr	Ala	Leu	Glu	Ile	Glu	Asn	Tyr	His	Val	Ile	Thr	Cys	Gln
			20					25					30		
Glu	Ile	Glu	Leu	Pro	Ile	Val	Phe	Asp	Asp	Phe	Lys	Gly	Tyr	Asp	Leu
		35					40					45			
Ile	Leu	Leu	Asp	Ile	Met	Met	Pro	Asn	Ile	Ser	Gly	Thr	Glu	Phe	Cys
	50				55					60					
Tyr	Lys	Ile	Arg	Glu	Glu	Val	His	Ser	Pro	Ile	Ile	Phe	Val	Ser	Ala
65				70					75					80	
Leu	Asp	Gly	Asp	Asn	Glu	Ile	Val	Gln	Ala	Leu	Asn	Ile	Gly	Gly	Asp
			85					90					95		
Asp	Phe	Ile	Val	Lys	Pro	Phe	Ser	Leu	Lys	Gln	Phe	Val	Ala	Lys	Val
			100					105					110		
Asn	Ser	His	Leu	Lys	Arg	Glu	Glu	Arg	Ala	Lys	Ile	Lys	Asn	Glu	Ala
		115				120						125			
Glu	Glu	Arg	Val	Lys	Arg	Ser	Phe	Pro	Pro	Ile	Glu	Ile	Tyr	Leu	Glu
	130					135					140				
Glu	Arg	Met	Leu	Tyr	Ile	Asp	Lys	Gln	Pro	Leu	Phe	Leu	Thr	Tyr	Arg
145				150					155					160	
Glu	Tyr	Glu	Ile	Leu	Glu	Leu	Leu	Ser	Arg	His	Pro	Tyr	Lys	Val	Phe
			165					170					175		
Thr	Lys	Glu	Glu	Ile	Tyr	Glu	Gln	Val	Tyr	Ser	Asp	Glu	Ala	Ser	Ala
			180					185					190		
Leu	Phe	His	Ser	Ile	Ser	Glu	Tyr	Ile	Tyr	Gln	Ile	Arg	Met	Lys	Phe
		195					200					205			

Ser Ser Phe Gly Ile Asn Pro Ile Lys Thr Ile Arg Gly Ile Gly Tyr
 210 215 220
 Lys Trp Asp Val
 225

<210> SEQ ID NO 397
 <211> LENGTH: 399
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 397
 ttgctatctg cttcttattt aagagtgatt gttgctccag cttcttcaag tttagctttg 60
 atttcttcag cttctgcagc agcaacgcct tctttaacgt tagcaggtgc tccatcaaca 120
 agacctttag cttctttaag accaagacct gtgatttcac gaacagcttt gataacgcca 180
 acttttttgt cgccagcaga tgtcaattca acgtcgaatg aatcttttagc agcttcttca 240
 gcaccaccag cagctgcagc agctacagga gcagctgcag ttacaccaaa ttcttcttcg 300
 atagctttta caagatcggt aagctcaagg attgaagctt ctttaatttc agcaataatg 360
 ttttcaatgt tcaatgccat tgtgatttcc tccaaataa 399

<210> SEQ ID NO 398
 <211> LENGTH: 132
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 398
 Met Leu Ser Ala Ser Tyr Leu Arg Val Ile Val Ala Pro Ala Ser Ser
 1 5 10 15
 Ser Leu Ala Leu Ile Ser Ser Ala Ser Ala Ala Thr Pro Ser Leu
 20 25 30
 Thr Leu Ala Gly Ala Pro Ser Thr Arg Pro Leu Ala Ser Leu Arg Pro
 35 40 45
 Arg Pro Val Ile Ser Arg Thr Ala Leu Ile Thr Pro Thr Phe Leu Ser
 50 55 60
 Pro Ala Asp Val Asn Ser Thr Ser Asn Glu Ser Leu Ala Ala Ser Ser
 65 70 75 80
 Ala Pro Pro Ala Ala Ala Ala Thr Gly Ala Ala Ala Val Thr Pro
 85 90 95
 Asn Ser Ser Ser Ile Ala Phe Thr Arg Ser Leu Ser Ser Arg Ile Glu
 100 105 110
 Ala Ser Leu Ile Ser Ala Ile Met Phe Ser Met Phe Asn Ala Ile Val
 115 120 125
 Ile Ser Ser Lys
 130

<210> SEQ ID NO 399
 <211> LENGTH: 1650
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 399
 atgcgaggtg aacaggtgga agaacatttt aaaaaacaat tacaagatga tatttctaga 60
 catttttcgt accaatcggt aatgttatca ttgttgctaa ttggtctttt tattattttt 120
 tcattagcgc cacaacaatt aggcctctat cgtgatatca atgccactgc aacccgttat 180
 caccgtttga ttagcaaaaca agaagccttg ctggatgact tagggaaaaa tagcttacta 240
 ccttttttaa ataaaaacct cagcactgct gatttaagca agcactattt tcatttgcgc 300
 catagcagcc aaacgtcacc agaactttta ctattttcac ctagtcaaga ccttttattt 360
 gctagtaacc cacatttagg aaatgttttt agtaaactctg tttatattca agaagtcttg 420
 agagcaactc attctccaaa aaccttggtt aaagatgcta tggatagtga agatgggtcac 480
 tacttgatga tcattatgcc aatgatagat caaaaccaac taaagggata tgctttttta 540
 gtgatgagtg gcaaagattt tcttcatcct aaaaaaacat tgacgtcaga gttgggtcatt 600

gctgataagc	tggacaatac	gtttacgttt	tccaatcgtg	agtttatagc	atctagtcta	660
gataagatca	atagccagta	tttacaccat	tattttgttt	ttcaagataa	tcgagccttt	720
atcacaagaa	agggtgcctt	acaaggaggt	ctttggcttt	acatgtatag	gcccttgatt	780
ccaatgggat	cgggtgatgtt	attttcactt	atttcacag	ctgttatctt	tgtgattttg	840
caacgtaaat	caagtgggtt	agctaaccga	attgcagcta	aaaattcaag	agcaatcaat	900
caaatgggta	gagatatgag	tgcgatctct	cggcaagaaa	aaagacgtat	tgaccttgag	960
agtcaagatg	aatttcaata	tttatctgat	caaatcaatc	aaatggtaga	gcgattgcaa	1020
cagttacatg	ataaaacggt	agattttggaa	actcaaaaaat	tattatttga	aaaacggatg	1080
ttagaagctc	aattcaatcc	gcatttcctc	tacaatacgc	tagaaaccat	tttgattacg	1140
agccattatg	attctgccct	aacagaaaaa	attgttatcc	aattgacaaa	attgttgccg	1200
tatagtctca	cggattctag	caaacctgtc	ttgctcaaag	atgatttaag	tgcatcagag	1260
tcttattttag	tgattaatca	gggtgcggtt	gaagaattgc	aatatagcat	taacctatcc	1320
ccagaccttg	atagtcttga	agtgccataa	ttgttcttgt	tacctttgat	agaaaaatgcc	1380
atcaaatatg	gcttgaaaga	acgacacgat	gtcaagatta	acattgcttg	ttattatcaa	1440
gatgaccaca	ttattttttc	tgtgagagat	aatggttcgg	gaattgatgc	tcatcaccaa	1500
aaagtgattc	gagagcaatt	ggaagctgga	gagtcacacc	atgggttaat	taactcttat	1560
cgtcggctta	agtatcat	ttcagaagta	tccttggttt	ttgatcaagg	tgataaacag	1620
tttaatgtta	gttaccatgt	taaggagtag				1650

<210> SEQ ID NO 400

<211> LENGTH: 549

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 400

Met	Arg	Gly	Glu	Gln	Val	Glu	Glu	His	Phe	Lys	Lys	Gln	Leu	Gln	Asp
1			5						10					15	
Asp	Ile	Ser	Arg	His	Phe	Ser	Tyr	Gln	Ser	Leu	Met	Leu	Ser	Leu	Leu
			20					25					30		
Leu	Ile	Gly	Leu	Phe	Ile	Ile	Phe	Ser	Leu	Ala	Pro	Gln	Gln	Leu	Gly
		35					40					45			
Leu	Tyr	Arg	Asp	Ile	Asn	Ala	Thr	Ala	Thr	Arg	Tyr	His	Arg	Leu	Ile
	50				55						60				
Ser	Lys	Gln	Glu	Ala	Leu	Leu	Asp	Asp	Leu	Gly	Lys	Asn	Ser	Leu	Leu
65					70					75				80	
Pro	Phe	Leu	Asn	Lys	Asn	Leu	Ser	Thr	Ala	Asp	Leu	Ser	Lys	His	Tyr
			85						90					95	
Phe	His	Leu	Arg	His	Ser	Ser	Gln	Thr	Ser	Pro	Glu	Leu	Leu	Leu	Phe
			100						105					110	
Ser	Pro	Ser	Gln	Asp	Leu	Leu	Phe	Ala	Ser	Asn	Pro	His	Leu	Gly	Asn
			115					120					125		
Val	Phe	Ser	Lys	Ser	Val	Tyr	Ile	Gln	Glu	Val	Leu	Arg	Ala	Thr	His
			130				135					140			
Ser	Pro	Lys	Thr	Leu	Phe	Lys	Asp	Ala	Met	Asp	Ser	Glu	Asp	Gly	His
145					150					155					160
Tyr	Leu	Met	Ile	Ile	Met	Pro	Met	Ile	Asp	Gln	Asn	Gln	Leu	Lys	Gly
			165						170					175	
Tyr	Ala	Phe	Leu	Val	Met	Ser	Gly	Lys	Asp	Phe	Leu	His	Pro	Thr	Lys
			180						185					190	
Thr	Leu	Thr	Ser	Glu	Leu	Val	Ile	Ala	Asp	Lys	Leu	Asp	Asn	Thr	Phe
			195					200						205	
Thr	Phe	Ser	Asn	Arg	Glu	Phe	Ile	Ala	Ser	Ser	Leu	Asp	Lys	Ile	Asn
			210				215					220			
Ser	Gln	Tyr	Leu	His	His	Tyr	Phe	Val	Phe	Gln	Asp	Asn	Arg	Ala	Phe
225					230					235					240
Ile	Thr	Arg	Lys	Val	Ala	Leu	Gln	Gly	Gly	Leu	Trp	Leu	Tyr	Met	Tyr
			245						250					255	
Arg	Pro	Leu	Ile	Pro	Met	Val	Ser	Val	Met	Leu	Phe	Ser	Leu	Ile	Ser

	260		265		270										
Ser	Ala	Val	Ile	Phe	Val	Ile	Leu	Gln	Arg	Lys	Ser	Ser	Gly	Leu	Ala
	275						280					285			
Asn	Arg	Ile	Ala	Ala	Lys	Asn	Ser	Arg	Ala	Ile	Asn	Gln	Met	Val	Arg
	290						295					300			
Asp	Met	Ser	Ala	Ile	Ser	Arg	Gln	Glu	Lys	Arg	Arg	Ile	Asp	Leu	Glu
305					310					315				320	
Ser	Gln	Asp	Glu	Phe	Gln	Tyr	Leu	Ser	Asp	Gln	Ile	Asn	Gln	Met	Val
			325						330					335	
Glu	Arg	Leu	Gln	Gln	Leu	His	Asp	Lys	Thr	Leu	Asp	Leu	Glu	Thr	Gln
		340						345					350		
Lys	Leu	Leu	Phe	Glu	Lys	Arg	Met	Leu	Glu	Ala	Gln	Phe	Asn	Pro	His
	355						360					365			
Phe	Leu	Tyr	Asn	Thr	Leu	Glu	Thr	Ile	Leu	Ile	Thr	Ser	His	Tyr	Asp
370					375						380				
Ser	Ala	Leu	Thr	Glu	Lys	Ile	Val	Ile	Gln	Leu	Thr	Lys	Leu	Leu	Arg
385				390						395					400
Tyr	Ser	Leu	Thr	Asp	Ser	Ser	Lys	Pro	Val	Leu	Leu	Lys	Asp	Asp	Leu
			405						410					415	
Ser	Val	Ile	Glu	Ser	Tyr	Leu	Val	Ile	Asn	Gln	Val	Arg	Phe	Glu	Glu
		420						425					430		
Leu	Gln	Tyr	Ser	Ile	Asn	Leu	Ser	Pro	Asp	Leu	Asp	Ser	Leu	Glu	Val
	435					440					445				
Pro	Lys	Leu	Phe	Leu	Leu	Pro	Leu	Ile	Glu	Asn	Ala	Ile	Lys	Tyr	Gly
450					455					460					
Leu	Lys	Glu	Arg	His	Asp	Val	Lys	Ile	Asn	Ile	Ala	Cys	Tyr	Tyr	Gln
465				470					475					480	
Asp	Asp	His	Ile	Ile	Phe	Ser	Val	Arg	Asp	Asn	Gly	Ser	Gly	Ile	Asp
			485					490						495	
Ala	His	His	Gln	Lys	Val	Ile	Arg	Glu	Gln	Leu	Glu	Ala	Gly	Glu	Ser
		500						505					510		
His	His	Gly	Leu	Ile	Asn	Ser	Tyr	Arg	Arg	Leu	Lys	Tyr	His	Phe	Ser
	515					520					525				
Glu	Val	Ser	Leu	Val	Phe	Asp	Gln	Gly	Asp	Lys	Gln	Phe	Asn	Val	Ser
	530				535						540				
Tyr	His	Val	Lys	Glu											
545															

<210> SEQ ID NO 401

<211> LENGTH: 1020

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 401

atgtcaactc	acttaagaaa	acttccaggg	ctgttacttt	gcttattggt	agctcttcca	60
gcctggtggt	tagggcgctt	atttcccatt	attggagcac	ctgtttttgc	tattctttta	120
ggaatggtgt	tagccttggt	ttatgaacat	cgtgacaaga	ctaaagaggg	aattagtttt	180
acatccaagt	atattttaca	aacagcagtg	gttttgcttg	gttttggtt	aaacctaacc	240
caagttatgg	cagtgggcat	gcagtcttta	ccgattatca	tttcaactat	tgcgacagct	300
cttttggtag	cttatggctt	acagaaatgg	ctgcgcttag	atgtcaatac	agccaccttg	360
gtaggtgtag	gatcttccat	ttgtgggggg	tctgctggtg	cagcgacagc	tcctgtcatt	420
aaggcaaagg	atgacgaggt	tgctaaggca	atttcagtca	tttttctctt	taatatgtta	480
gcagctttgc	tatttccaag	tttaggacaa	ttactaggct	tatctaata	aggttttgct	540
atttttgccg	ggacagctgt	taacgacact	tcttccgtga	ctgcaacggc	cacggcctgg	600
gatgcccttc	accattccaa	tacactagat	ggagcaacca	ttgttaaatt	gactcgacc	660
ttggctattc	tcccaattac	tttaggttta	tccctttacc	gagcgaaaaa	agagcacgac	720
atcgttacag	aagaaaactt	tagccttagg	aagtcattcc	ctcgtttcat	cctcttcttt	780
ttattagctt	ctctcatcac	aacattgatg	accagtttgg	gagtttctgc	cgatagtttc	840

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cattacctaa aaaccttatc aaaattcttt atcgtgatgg ctatggcagc gattgggtta 900
aacacaaacc tggttaaact gattaagacg ggcggtcagg ctatcctttt aggagctatt 960
tgctgggtag ctatcaccct tgtcagtta gccatgcaat taagtttggg catttggttaa 1020

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<210> SEQ ID NO 402
<211> LENGTH: 339
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 402

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Met Ser Thr His Leu Arg Lys Leu Pro Gly Leu Leu Leu Cys Leu Leu
1          5          10          15
Leu Ala Leu Pro Ala Trp Cys Leu Gly Arg Leu Phe Pro Ile Ile Gly
20        25        30
Ala Pro Val Phe Ala Ile Leu Leu Gly Met Leu Leu Ala Leu Phe Tyr
35        40        45
Glu His Arg Asp Lys Thr Lys Glu Gly Ile Ser Phe Thr Ser Lys Tyr
50        55        60
Ile Leu Gln Thr Ala Val Val Leu Leu Gly Phe Gly Leu Asn Leu Thr
65        70        75        80
Gln Val Met Ala Val Gly Met Gln Ser Leu Pro Ile Ile Ile Ser Thr
85        90        95
Ile Ala Thr Ala Leu Leu Val Ala Tyr Gly Leu Gln Lys Trp Leu Arg
100       105       110
Leu Asp Val Asn Thr Ala Thr Leu Val Gly Val Gly Ser Ser Ile Cys
115       120       125
Gly Gly Ser Ala Val Ala Ala Thr Ala Pro Val Ile Lys Ala Lys Asp
130       135       140
Asp Glu Val Ala Lys Ala Ile Ser Val Ile Phe Leu Phe Asn Met Leu
145       150       155       160
Ala Ala Leu Leu Phe Pro Ser Leu Gly Gln Leu Leu Gly Leu Ser Asn
165       170       175
Glu Gly Phe Ala Ile Phe Ala Gly Thr Ala Val Asn Asp Thr Ser Ser
180       185       190
Val Thr Ala Thr Ala Thr Ala Trp Asp Ala Leu His His Ser Asn Thr
195       200       205
Leu Asp Gly Ala Thr Ile Val Lys Leu Thr Arg Thr Leu Ala Ile Leu
210       215       220
Pro Ile Thr Leu Gly Leu Ser Leu Tyr Arg Ala Lys Lys Glu His Asp
225       230       235       240
Ile Val Thr Glu Glu Asn Phe Ser Leu Arg Lys Ser Phe Pro Arg Phe
245       250       255
Ile Leu Phe Phe Leu Leu Ala Ser Leu Ile Thr Thr Leu Met Thr Ser
260       265       270
Leu Gly Val Ser Ala Asp Ser Phe His Tyr Leu Lys Thr Leu Ser Lys
275       280       285
Phe Phe Ile Val Met Ala Met Ala Ala Ile Gly Leu Asn Thr Asn Leu
290       295       300
Val Lys Leu Ile Lys Thr Gly Gly Gln Ala Ile Leu Leu Gly Ala Ile
305       310       315       320
Cys Trp Val Ala Ile Thr Leu Val Ser Leu Ala Met Gln Leu Ser Leu
325       330       335
Gly Ile Trp

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<210> SEQ ID NO 403
<211> LENGTH: 645
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes

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<400> SEQUENCE: 403
gtggagggttg tgatggtaga aaacactaaa ttactatgta gctggggtatg gttattagcg      60
ttagctatttc tcataacgat ctattcaacg tggctgtggt atcctcttga ggtggaccat      120
ctaaagtttag aacaagttgt ttttatgagc aaggatgcta tcttgcataa ctataacgga      180
ctactcaatt acctcaccaa tctttttgtg acaagggttg aatttgctaa ttttctactca      240
tcggcagacg gactcaagca ttttgcagat gtgaagtggc tttttcacct aactcaagtc      300
gtttttcttg gccttcttta cccaaccctt aagactttca cacaaagggtt aaaaacccaaa      360
cgtttctggc tccttcaaaa acctttaata ctagcagctt tgtttcctct tatgattgggt      420
ctaattggcta gtttcattgg gtttgaacat ttttttactc tttttcatca ggtgcttttt      480
gtaggagata gcagctggct ctttgatccc ttgaaagatt ctgtgatttg gatccttcca      540
gaagtctttt tcttgcactg tttccttttc tttatgatag tttacgaaat catcctgtgg      600
agcttagtag gtttagcaag atggcagcgc ctaaagttag aatga                          645

```

<210> SEQ ID NO 404

<211> LENGTH: 214

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 404

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Met Glu Val Val Met Val Glu Asn Thr Lys Leu Leu Cys Ser Trp Val
1          5          10          15
Trp Leu Leu Ala Leu Ala Ile Leu Ile Thr Ile Tyr Ser Thr Trp Leu
20          25          30
Trp Tyr Pro Leu Glu Val Asp His Leu Lys Leu Glu Gln Val Val Phe
35          40          45
Met Ser Lys Asp Ala Ile Leu His Asn Tyr Asn Gly Leu Leu Asn Tyr
50          55          60
Leu Thr Asn Pro Phe Val Thr Arg Leu Glu Phe Ala Asn Phe His Ser
65          70          75          80
Ser Ala Asp Gly Leu Lys His Phe Ala Asp Val Lys Trp Leu Phe His
85          90          95
Leu Thr Gln Val Val Phe Leu Gly Leu Leu Tyr Pro Thr Leu Lys Thr
100         105         110
Phe Thr Gln Arg Leu Lys Thr Lys Arg Phe Trp Leu Leu Gln Lys Pro
115         120         125
Leu Ile Leu Ala Ala Leu Phe Pro Leu Met Ile Gly Leu Met Ala Ser
130         135         140
Phe Ile Gly Phe Glu His Phe Phe Thr Leu Phe His Gln Val Leu Phe
145         150         155         160
Val Gly Asp Ser Ser Trp Leu Phe Asp Pro Leu Lys Asp Ser Val Ile
165         170         175
Trp Ile Leu Pro Glu Val Phe Phe Leu His Cys Phe Leu Phe Phe Met
180         185         190
Ile Val Tyr Glu Ile Ile Leu Trp Ser Leu Val Gly Leu Ala Arg Trp
195         200         205
Gln Arg Leu Asn Val Glu
210

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<210> SEQ ID NO 405

<211> LENGTH: 957

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 405

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atgaaacgat ttttaaatag tcgtccttgg ttaggaatgg tatcagtctt ttttgcgatt      60
ctcctttttt taactgcagc atcgagcaat cataataact ctaactcgca aatttatagt      120
ccgattgaaa cctatacgca tagccttaaa gatgtaccaa ttgatatgaa gtatgatagt      180
gacaaatatt ttatcagtgg gtattcttat ggtgcggaag tttatctaac ctccactaat      240
cgtatcaaat tagattctga agtgaacaat gatacacgta attttaagat tgtggcggat      300

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ctaacacata	gtcatccagg	tacagtaagt	gtcaacctaa	gagtagaaaa	ccttccttct	360
ggggtgacag	ctaccgtatc	tccagataaa	atatcagtca	caattggcaa	aaaagaatct	420
aagggtatttc	ctggttagagg	aagcgttgat	gctaaacaaa	ttgcaaatgg	ttatgaaatt	480
agcaaaattg	aaacgggggt	taataagggt	gaagtgacca	gtgatgaatc	taccattgct	540
ttaattgatc	acgttggtggc	aaagttacct	gatgatcaag	tgtagatag	gaattatagt	600
agtcgagtga	ccttacaagc	tgtctcagct	gatggaacta	ttttagcaag	tgcaattgat	660
cctgcaaaaa	caaatttatc	agttgctgta	aaaaaaataa	cgaaatcagt	cccgattaga	720
gttgaggcag	tggggatgat	ggatgatagc	ttatcagata	ttcaatacaa	attgtcaaaa	780
caaacagctg	ttatctcagg	tagtcgagag	gtccttagaag	atattgatga	aattattgca	840
gaagttaaca	tttctgatgt	cactaaaaat	actagtaaga	ccgtgagttt	gtcttctagt	900
caggtgtcaa	ttgagccgtc	agtagtgacc	gttcagttga	caaccaccaa	aaaataa	957

<210> SEQ ID NO 406

<211> LENGTH: 318

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 406

Met	Lys	Arg	Phe	Leu	Asn	Ser	Arg	Pro	Trp	Leu	Gly	Met	Val	Ser	Val	
1				5					10					15		
Phe	Phe	Ala	Ile	Leu	Leu	Phe	Leu	Thr	Ala	Ala	Ser	Ser	Asn	His	Asn	
			20					25					30			
Asn	Ser	Asn	Ser	Gln	Ile	Tyr	Ser	Pro	Ile	Glu	Thr	Tyr	Thr	His	Ser	
		35				40					45					
Leu	Lys	Asp	Val	Pro	Ile	Asp	Met	Lys	Tyr	Asp	Ser	Asp	Lys	Tyr	Phe	
	50					55				60						
Ile	Ser	Gly	Tyr	Ser	Tyr	Gly	Ala	Glu	Val	Tyr	Leu	Thr	Ser	Thr	Asn	
65					70					75					80	
Arg	Ile	Lys	Leu	Asp	Ser	Glu	Val	Asn	Asn	Asp	Thr	Arg	Asn	Phe	Lys	
			85					90						95		
Ile	Val	Ala	Asp	Leu	Thr	His	Ser	His	Pro	Gly	Thr	Val	Ser	Val	Asn	
		100						105					110			
Leu	Arg	Val	Glu	Asn	Leu	Pro	Ser	Gly	Val	Thr	Ala	Thr	Val	Ser	Pro	
	115					120						125				
Asp	Lys	Ile	Ser	Val	Thr	Ile	Gly	Lys	Lys	Glu	Ser	Lys	Val	Phe	Pro	
	130					135				140						
Val	Arg	Gly	Ser	Val	Asp	Ala	Lys	Gln	Ile	Ala	Asn	Gly	Tyr	Glu	Ile	
145					150					155					160	
Ser	Lys	Ile	Glu	Thr	Gly	Val	Asn	Lys	Val	Glu	Val	Thr	Ser	Asp	Glu	
			165					170						175		
Ser	Thr	Ile	Ala	Leu	Ile	Asp	His	Val	Val	Ala	Lys	Leu	Pro	Asp	Asp	
		180						185					190			
Gln	Val	Leu	Asp	Arg	Asn	Tyr	Ser	Ser	Arg	Val	Thr	Leu	Gln	Ala	Val	
		195				200						205				
Ser	Ala	Asp	Gly	Thr	Ile	Leu	Ala	Ser	Ala	Ile	Asp	Pro	Ala	Lys	Thr	
	210					215					220					
Asn	Leu	Ser	Val	Ala	Val	Lys	Lys	Ile	Thr	Lys	Ser	Val	Pro	Ile	Arg	
225					230					235					240	
Val	Glu	Ala	Val	Gly	Met	Met	Asp	Asp	Ser	Leu	Ser	Asp	Ile	Gln	Tyr	
			245						250					255		
Lys	Leu	Ser	Lys	Gln	Thr	Ala	Val	Ile	Ser	Gly	Ser	Arg	Glu	Val	Leu	
		260						265					270			
Glu	Asp	Ile	Asp	Glu	Ile	Ile	Ala	Glu	Val	Asn	Ile	Ser	Asp	Val	Thr	
	275						280					285				
Lys	Asn	Thr	Ser	Lys	Thr	Val	Ser	Leu	Ser	Ser	Ser	Gln	Val	Ser	Ile	
	290					295						300				
Glu	Pro	Ser	Val	Val	Thr	Val	Gln	Leu	Thr	Thr	Thr	Lys	Lys			
305					310					315						

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<210> SEQ ID NO 407
<211> LENGTH: 2487
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 407
gtggtatatt tttacttagt aaatcaattt actttttatta tctcattttt atattggagg      60
aatttatcag tgaatactta tttttgcaca caccataaac aattactact ttattcaaac      120
ctattcctta gctttgctat gatgggccaa ggaactgcc a tttatgccga tacactgact      180
tcaaattcag aacctaataa tacttacttt caaacgcaaa cgctcactac tacagatagc      240
gaaaaaaagg tagtacagcc acaacaaaaa gactactata ctgaattgtt agaccaatgg      300
aacagtatta tcgcaggcaa cgatgcttat gataaaacca atcctgacat ggtcactttt      360
cataataaag ctgaaaagga tgctcaaaac attattaaaa gctatcaagg gcctgaccac      420
gaaaaatgaa cttacctttg ggaacatgca aaggattatt ccgcttctgc taatatcacg      480
aaaacttacc gcaatattga aaaaatagca aaacagatca ctaatcctga atcatgctat      540
tatcaagata gtaaagctat tgctattgta aaagacggta tggccttcac gtatgaacac      600
gcttataatc tagatcgtga aaatcatcaa acaactggaa aagaaaacaa agaaaaattgg      660
tggttttatg aaattggaac tcctcgtgct attaataata ccttatcctt gatgtatcct      720
tattttactc aagaagaaat tcttaaatac acagctccaa tcgaaaaatt tgtgcctgac      780
cctactcggt ttagggttcg cgctgccaat ttttcacctt ttgaagccaa tagcggaat      840
ttaattgata tggggcgtgt taaactcatt tccggtattc ttcgtaaaga tgatctcgaa      900
attagtgata caatcaaagc aattgagaaa gttttcacgc tagttgatga aggaaatggt      960
ttttaccaag acggttcttt aattgatcac gtggttacta acgctcaaag tccactttat     1020
aaaaaaggca ttgcttacac tggagcttac ggtaatgtgc ttatagatgg cttatcgcaa     1080
ttaattccta ttattcaaaa aacaaagtct cctataaaaag cggataaaaat ggctactatc     1140
tatcattgga ttaaccattc tttttccct atcatcggtc gtggagaaat gatggatatg     1200
actcgagggc gttctatcag tcgttttaat gcccaatctc atgttgctgg cattgaagca     1260
cttcgtgcta ttttacgtat tgctgacatg tctgaagagc ctcaccgttt ggcacttaaa     1320
acacgtataa aaacactcgt cacacaaggg aatgcttttt acaatgtcta tgataatttg     1380
aaaacctatc acgatatcaa acttatgaaa gaactactaa gtgatacttc tgttccagtc     1440
caaaaacttg atagttacgt agctagtttc aatagtatgg ataaattggc actatataat     1500
aataaacacg attttgcttt tggcctatca atgttttcga atcgaactca aaattatgaa     1560
gctatgaata atgaaaatct tcatggctgg tttacttctg atggaatgtt ttacctatac     1620
aataacgatt taggacacta cagtgaaaac tattgggcaa cggtaaatcc ctaccgctta     1680
cctggaacca cagaaactga gcaaaaacca ctagagggaa ctctgagaa tattaanaacg     1740
aactatcaac aagttggcat gactggcttc tctgatgacg cttttgttgc aagtaaaaaa     1800
cttaataaca caagtgtctc agctgctatg accctcacta attggaataa aagcctcacc     1860
ctcaataaag ggtggtttat cttaggaaac aaaataatct ttgttggtag caatatcaaa     1920
aaccaatcat ctcaacaggc gtatacaact attgaacaac gaaaagaaaa tcaaaaagta     1980
ccttactgtt cttatgttaa caatcaaccc gttgacttga ataatacagct agttgatttt     2040
acaaacacta aaagtatttt ccttgaaagt gatgatcccg ctcaaaaatat tggttactac     2100
ttcttcaagc caacaacact tagcataagt aaggcacttc aaacaggggaa atggcaaaac     2160
ataaaagctg atgacaaatc accagaagcc atcaaagaag tttcaaatac ctttatcact     2220
atcatgcaaa accatactca agatggcgat cgttatgcct atatgatgct tccaaatatg     2280
actcgtcaag aatttgaaac ctatattagc aagcttgata tcgacttatt agaaaacaat     2340
gacaaactgg ccgctgtcta cgatcatgat agtcaacaga tgcacgtcat tcactatgga     2400
aaaaaagcaa cgatgttttc aaatcataat ctttctcatc aaggctttta tagttttcct     2460
catcctgtca ggcaaaatca acaataa
2487

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<210> SEQ ID NO 408
<211> LENGTH: 828
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 408
Met Val Tyr Phe Tyr Leu Val Asn Gln Phe Thr Phe Ile Ile Ser Phe
1          5          10          15
Leu Tyr Trp Arg Asn Leu Ser Val Asn Thr Tyr Phe Cys Thr His His

```

			20					25					30			
Lys	Gln	Leu	Leu	Leu	Tyr	Ser	Asn	Leu	Phe	Leu	Ser	Phe	Ala	Met	Met	
		35					40					45				
Gly	Gln	Gly	Thr	Ala	Ile	Tyr	Ala	Asp	Thr	Leu	Thr	Ser	Asn	Ser	Glu	
	50					55					60					
Pro	Asn	Asn	Thr	Tyr	Phe	Gln	Thr	Gln	Thr	Leu	Thr	Thr	Thr	Asp	Ser	
65					70					75					80	
Glu	Lys	Lys	Val	Val	Gln	Pro	Gln	Gln	Lys	Asp	Tyr	Tyr	Thr	Glu	Leu	
			85						90					95		
Leu	Asp	Gln	Trp	Asn	Ser	Ile	Ile	Ala	Gly	Asn	Asp	Ala	Tyr	Asp	Lys	
			100					105						110		
Thr	Asn	Pro	Asp	Met	Val	Thr	Phe	His	Asn	Lys	Ala	Glu	Lys	Asp	Ala	
		115					120					125				
Gln	Asn	Ile	Ile	Lys	Ser	Tyr	Gln	Gly	Pro	Asp	His	Glu	Asn	Arg	Thr	
	130					135					140					
Tyr	Leu	Trp	Glu	His	Ala	Lys	Asp	Tyr	Ser	Ala	Ser	Ala	Asn	Ile	Thr	
145					150					155					160	
Lys	Thr	Tyr	Arg	Asn	Ile	Glu	Lys	Ile	Ala	Lys	Gln	Ile	Thr	Asn	Pro	
			165						170					175		
Glu	Ser	Cys	Tyr	Tyr	Gln	Asp	Ser	Lys	Ala	Ile	Ala	Ile	Val	Lys	Asp	
		180				185							190			
Gly	Met	Ala	Phe	Met	Tyr	Glu	His	Ala	Tyr	Asn	Leu	Asp	Arg	Glu	Asn	
	195					200						205				
His	Gln	Thr	Thr	Gly	Lys	Glu	Asn	Lys	Glu	Asn	Trp	Trp	Val	Tyr	Glu	
	210					215					220					
Ile	Gly	Thr	Pro	Arg	Ala	Ile	Asn	Asn	Thr	Leu	Ser	Leu	Met	Tyr	Pro	
225					230					235					240	
Tyr	Phe	Thr	Gln	Glu	Glu	Ile	Leu	Lys	Tyr	Thr	Ala	Pro	Ile	Glu	Lys	
			245						250					255		
Phe	Val	Pro	Asp	Pro	Thr	Arg	Phe	Arg	Val	Arg	Ala	Ala	Asn	Phe	Ser	
		260						265						270		
Pro	Phe	Glu	Ala	Asn	Ser	Gly	Asn	Leu	Ile	Asp	Met	Gly	Arg	Val	Lys	
	275					280						285				
Leu	Ile	Ser	Gly	Ile	Leu	Arg	Lys	Asp	Asp	Leu	Glu	Ile	Ser	Asp	Thr	
	290					295					300					
Ile	Lys	Ala	Ile	Glu	Lys	Val	Phe	Thr	Leu	Val	Asp	Glu	Gly	Asn	Gly	
305					310					315					320	
Phe	Tyr	Gln	Asp	Gly	Ser	Leu	Ile	Asp	His	Val	Val	Thr	Asn	Ala	Gln	
			325						330					335		
Ser	Pro	Leu	Tyr	Lys	Lys	Gly	Ile	Ala	Tyr	Thr	Gly	Ala	Tyr	Gly	Asn	
		340						345					350			
Val	Leu	Ile	Asp	Gly	Leu	Ser	Gln	Leu	Ile	Pro	Ile	Ile	Gln	Lys	Thr	
	355					360						365				
Lys	Ser	Pro	Ile	Lys	Ala	Asp	Lys	Met	Ala	Thr	Ile	Tyr	His	Trp	Ile	
	370					375					380					
Asn	His	Ser	Phe	Phe	Pro	Ile	Ile	Val	Arg	Gly	Glu	Met	Met	Asp	Met	
385					390					395					400	
Thr	Arg	Gly	Arg	Ser	Ile	Ser	Arg	Phe	Asn	Ala	Gln	Ser	His	Val	Ala	
			405					410						415		
Gly	Ile	Glu	Ala	Leu	Arg	Ala	Ile	Leu	Arg	Ile	Ala	Asp	Met	Ser	Glu	
		420						425					430			
Glu	Pro	His	Arg	Leu	Ala	Leu	Lys	Thr	Arg	Ile	Lys	Thr	Leu	Val	Thr	
		435					440					445				
Gln	Gly	Asn	Ala	Phe	Tyr	Asn	Val	Tyr	Asp	Asn	Leu	Lys	Thr	Tyr	His	
	450					455					460					
Asp	Ile	Lys	Leu	Met	Lys	Glu	Leu	Leu	Ser	Asp	Thr	Ser	Val	Pro	Val	
465					470					475					480	

caagaactaa	cagttaaaag	cttgcaacag	catttttcaag	gtttggggcg	agacaccgca	480
aaagagttgg	ccgagcttct	gaccacagac	aaattaaaaac	ggttccgtga	gttttttgc	540
agacctactc	aggcaaactct	gaccacagct	tctttttgcgc	ctgttctttt	ctcagatagt	600
catgcgacgt	ttgagacttt	gtctgacatg	cttgaccact	tttatcaaga	caaggctgag	660
cgtgaccgta	tcaatcagca	agccagtgat	ttgatccacc	gtgtgcaaac	tgaactggac	720
aaaaatcgca	acaagctaag	taagcaagaa	gctgagctgc	tagccactga	aaatgctgag	780
ttgttccgtc	aaaaaggaga	attattgacc	acctacctca	gtctggtccc	aaacaaccaa	840
gactctgtga	tttttagacaa	ttattatata	ggggaaaaaa	ttgagattgc	cttagacaag	900
gctctgacac	caaatcaaaa	tgctcaacgt	tatttttaaaa	aataccaaaa	gctaaaagaa	960
gctgtcaaac	acttatctgg	attgattgcc	gataccaagc	aaagtattac	ttactttgag	1020
agcgtagact	acaatttatc	tcaagcaagt	atcgacgaca	tccaagatat	tgcgcaagaa	1080
ttatatcagg	ctggcttttt	gaaaagtcgc	caaagagaca	aacgccataa	acgtaaaaag	1140
cctgagcagt	acctggcttc	agatggaaca	accattctct	tggtgggacg	caataacttg	1200
caaatgaag	aactcacctt	taaaatggct	aaaaaaggag	aactctggtt	ccatgctaag	1260
gatatccctg	gaagtcatgt	catcatcaaa	gacaatcttg	acccaagtga	cgaggttaaa	1320
actgatgctg	ccgaactagc	tgcttattat	tcgaaaagcta	ggttatcaaa	tctcgttcag	1380
gtcgaatatga	ttgaagctaa	aaaattacac	aaacctagtg	gcgccaagcc	aggatttgtg	1440
acttatactg	gtcaaaaaaac	tttacgggtt	actcctgacc	aagccaaaat	tctctctatg	1500
aaattatcct	ga					1512

<210> SEQ ID NO 410

<211> LENGTH: 503

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 410

Met	Leu	Leu	Ser	Ala	His	Pro	Val	Phe	Gly	Arg	Val	Gln	Ile	Thr	Gln
1			5						10					15	
Ala	Asp	Phe	Gln	Asn	Pro	Gln	Val	Pro	Asn	Thr	Phe	Thr	Met	Ile	Met
			20					25					30		
Arg	Lys	Tyr	Leu	Gln	Gly	Ala	Val	Ile	Glu	Gln	Leu	Glu	Gln	Ile	Asp
			35				40						45		
Asn	Asp	Arg	Ile	Ile	Glu	Ile	Lys	Val	Ser	Asn	Lys	Asn	Glu	Ile	Gly
			50			55					60				
Asp	Ala	Ile	Gln	Ala	Thr	Leu	Ile	Ile	Glu	Ile	Met	Gly	Lys	His	Ser
65					70					75					80
Asn	Ile	Ile	Leu	Val	Asp	Arg	Ala	Glu	Asn	Lys	Ile	Ile	Glu	Ser	Ile
				85					90					95	
Lys	His	Val	Gly	Phe	Ser	Gln	Asn	Ser	Tyr	Arg	Thr	Ile	Leu	Pro	Gly
			100					105					110		
Ser	Thr	Tyr	Ile	Glu	Pro	Pro	Lys	Thr	Ala	Ala	Val	Asn	Pro	Phe	Thr
			115				120					125			
Ile	Thr	Asp	Val	Pro	Leu	Phe	Glu	Ile	Leu	Gln	Thr	Gln	Glu	Leu	Thr
			130			135					140				
Val	Lys	Ser	Leu	Gln	Gln	His	Phe	Gln	Gly	Leu	Gly	Arg	Asp	Thr	Ala
145					150				155						160
Lys	Glu	Leu	Ala	Glu	Leu	Leu	Thr	Thr	Asp	Lys	Leu	Lys	Arg	Phe	Arg
				165					170					175	
Glu	Phe	Phe	Ala	Arg	Pro	Thr	Gln	Ala	Asn	Leu	Thr	Thr	Ala	Ser	Phe
			180					185					190		
Ala	Pro	Val	Leu	Phe	Ser	Asp	Ser	His	Ala	Thr	Phe	Glu	Thr	Leu	Ser
			195				200					205			
Asp	Met	Leu	Asp	His	Phe	Tyr	Gln	Asp	Lys	Ala	Glu	Arg	Asp	Arg	Ile
			210			215					220				
Asn	Gln	Gln	Ala	Ser	Asp	Leu	Ile	His	Arg	Val	Gln	Thr	Glu	Leu	Asp
225					230				235						240
Lys	Asn	Arg	Asn	Lys	Leu	Ser	Lys	Gln	Glu	Ala	Glu	Leu	Leu	Ala	Thr
				245					250					255	

Glu	Asn	Ala	Glu	Leu	Phe	Arg	Gln	Lys	Gly	Glu	Leu	Leu	Thr	Thr	Tyr
			260					265					270		
Leu	Ser	Leu	Val	Pro	Asn	Asn	Gln	Asp	Ser	Val	Ile	Leu	Asp	Asn	Tyr
			275				280					285			
Tyr	Thr	Gly	Glu	Lys	Ile	Glu	Ile	Ala	Leu	Asp	Lys	Ala	Leu	Thr	Pro
			290			295					300				
Asn	Gln	Asn	Ala	Gln	Arg	Tyr	Phe	Lys	Lys	Tyr	Gln	Lys	Leu	Lys	Glu
305					310					315					320
Ala	Val	Lys	His	Leu	Ser	Gly	Leu	Ile	Ala	Asp	Thr	Lys	Gln	Ser	Ile
			325						330					335	
Thr	Tyr	Phe	Glu	Ser	Val	Asp	Tyr	Asn	Leu	Ser	Gln	Ala	Ser	Ile	Asp
			340					345					350		
Asp	Ile	Glu	Asp	Ile	Arg	Glu	Glu	Leu	Tyr	Gln	Ala	Gly	Phe	Leu	Lys
		355				360						365			
Ser	Arg	Gln	Arg	Asp	Lys	Arg	His	Lys	Arg	Lys	Lys	Pro	Glu	Gln	Tyr
	370				375						380				
Leu	Ala	Ser	Asp	Gly	Thr	Thr	Ile	Leu	Met	Val	Gly	Arg	Asn	Asn	Leu
385					390					395					400
Gln	Asn	Glu	Glu	Leu	Thr	Phe	Lys	Met	Ala	Lys	Lys	Gly	Glu	Leu	Trp
			405					410					415		
Phe	His	Ala	Lys	Asp	Ile	Pro	Gly	Ser	His	Val	Ile	Ile	Lys	Asp	Asn
			420				425					430			
Leu	Asp	Pro	Ser	Asp	Glu	Val	Lys	Thr	Asp	Ala	Ala	Glu	Leu	Ala	Ala
		435				440					445				
Tyr	Tyr	Ser	Lys	Ala	Arg	Leu	Ser	Asn	Leu	Val	Gln	Val	Asp	Met	Ile
	450				455						460				
Glu	Ala	Lys	Lys	Leu	His	Lys	Pro	Ser	Gly	Ala	Lys	Pro	Gly	Phe	Val
465				470					475						480
Thr	Tyr	Thr	Gly	Gln	Lys	Thr	Leu	Arg	Val	Thr	Pro	Asp	Gln	Ala	Lys
			485					490					495		
Ile	Leu	Ser	Met	Lys	Leu	Ser									
			500												

<210> SEQ ID NO 411

<211> LENGTH: 1182

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 411

atgcccttaa	tacctgaaaa	gtctagaaca	gatagcttat	tttacaaatg	gtttttaaat	60
aatcaagcta	ccatggcttt	agtaataaca	cttttagcct	ttttaacgat	ttttgttttt	120
actaaaatct	cttttttatt	tatgccagtg	atctcttttt	ttgcggtcac	catgttgccc	180
ttgggtatttt	cgaccattct	gtattatctg	accaaaccct	tagttgacct	tattaatcac	240
ttggggccga	atcgtagcac	ctctattttt	attgtttttg	gtttgattac	cttacttttt	300
gtctggggcga	tttcaggctt	tggtcccatg	gtacagaccc	aacttaccag	ttttattgag	360
gatctgcccc	aatacgtggg	caaggtcaat	gaagaagcca	ataaacttct	tgaaaatgaa	420
tggttagtca	gctataagcc	ccaactccaa	gacatgctta	cccatacaag	tcaaaaggct	480
ttggattacg	cgcaaagttt	ttcaaaaaat	gctattgact	gggctggtaa	ttttgctggt	540
gccattgctc	ggattaccgt	ggctattatt	atttcgcctt	ttattctctt	ttatttttta	600
cgagacagta	gccacatgaa	aaatggcctt	gtgaatgtct	tacctctcaa	attacgggtg	660
cctatgggtc	gagtcctggg	agatattaac	aagcaattat	caggctatgt	gcaagggcag	720
gttacgggtg	caattgttgt	cggctttatg	ttttctatca	tgtttagcct	tgtagggactg	780
aaatatgccca	tcacttttgg	gattattgct	ggctttctta	acatgatacc	ttacttagga	840
agtttccttg	ccatgatacc	tggtgtgatt	atggctatgg	tacaaggccc	atztatgttg	900
gttaagggtgc	ttgttatctt	tatgattgag	caaaccatcg	aagggcggtt	tgtagcaccg	960
cttgttttgg	gaaataagct	gagcattcat	cctattacca	ttatgttctt	gttattgact	1020
gcaggctcta	tgtttggtgt	ctgggggtgt	ttccttgcca	tcccaatcta	cgcttctgtc	1080
aaagttgtga	ttaaagaatt	atgtgactgg	tacaaaaaag	ttagcggttt	gtatgacgaa	1140

1182

<400> SEQUENCE: 412

Met 1	Pro	Leu	Ile	Pro 5	Glu	Lys	Ser	Arg	Thr 10	Asp	Ser	Leu	Phe	Tyr 15	Lys
Trp	Phe	Leu	Asn 20	Asn	Gln	Ala	Thr	Met 25	Ala	Leu	Val	Ile	Thr 30	Leu	Leu
Ala	Phe	Leu	Thr	Ile	Phe	Val	Phe	Thr	Lys	Ile	Ser	Phe	Leu	Phe	Met
Pro	Val	Ile	Ser	Phe	Phe	Ala	Val	Ile	Met	Leu	Pro	Leu	Val	Ile	Ser
Thr 65	Ile	Leu	Tyr	Tyr	Leu 70	Thr	Lys	Pro	Leu	Val 75	Asp	Leu	Ile	Asn 80	His
Leu	Gly	Pro	Asn 85	Arg	Thr	Thr	Ser	Ile	Phe 90	Ile	Val	Phe	Gly	Leu 95	Ile
Thr	Leu	Leu	Phe 100	Val	Trp	Ala	Ile	Ser	Gly 105	Phe	Val	Pro	Met	Val	Gln
Thr	Gln	Leu	Thr	Ser	Phe	Ile	Glu	Asp	Leu	Pro	Lys	Tyr	Val	Gly	Lys
Val	Asn 130	Glu	Glu	Ala	Asn	Lys	Leu	Leu	Glu	Asn	Glu	Trp	Leu	Val	Ser
Tyr 145	Lys	Pro	Gln	Leu	Gln	Asp	Met	Leu	Thr	His	Thr	Ser	Gln	Lys	Ala
Leu	Asp	Tyr	Ala	Gln	Ser	Phe	Ser	Lys	Asn	Ala	Ile	Asp	Trp	Ala	Gly
Asn	Phe	Ala	Gly 180	Ala	Ile	Ala	Arg	Ile	Thr 185	Val	Ala	Ile	Ile	Ile	Ser
Pro	Phe	Ile	Leu	Phe	Tyr	Phe	Leu	Arg	Asp	Ser	Ser	His	Met	Lys	Asn
Gly	Leu	Val	Asn 210	Val	Leu	Pro	Leu	Lys	Leu	Arg	Val	Pro	Met	Val	Arg
Val	Leu	Gly	Asp	Ile	Asn	Lys	Gln	Leu	Ser	Gly	Tyr	Val	Gln	Gly	Gln
Val	Thr	Val	Ala	Ile	Val	Val	Gly	Phe	Met	Phe	Ser	Ile	Met	Phe	Ser
Leu	Val	Gly	Leu 260	Lys	Tyr	Ala	Ile	Thr 265	Phe	Gly	Ile	Ile	Ala	Gly	Phe
Leu	Asn	Met	Ile	Pro	Tyr	Leu	Gly	Ser	Phe	Leu	Ala	Met	Ile	Pro	Val
Val	Ile	Met	Ala	Met	Val	Gln	Gly	Pro	Phe	Met	Leu	Val	Lys	Val	Leu
Val	Ile	Phe	Met	Ile	Glu	Gln	Thr	Ile	Glu	Gly	Arg	Phe	Val	Ala	Pro
Leu	Val	Leu	Gly	Asn	Lys	Leu	Ser	Ile	His	Pro	Ile	Thr	Ile	Met	Phe
Leu	Leu	Leu	Thr 340	Ala	Gly	Ser	Met	Phe 345	Gly	Val	Trp	Gly	Val	Phe	Leu
Val	Ile	Pro	Ile	Tyr	Ala	Ser	Val	Lys	Val	Val	Ile	Lys	Glu	Leu	Phe
Asp	Trp	Tyr	Lys	Lys	Val	Ser	Gly	Leu	Tyr	Asp	Glu	Glu	Val	Leu	Val
Ile 385	Glu	Glu	Val	Lys	Asp	His	Val	Lys							

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<210> SEQ ID NO 413
<211> LENGTH: 711
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 413
atgagatata attgtcgcta ctcacatatt gataagaaaa tctacagcat gattatatgt      60
ttgtcatttc ttttatattc caatgttggt caagcaaat cttataatac aaccaataga      120
cataatctag aatcgcttta taagcatgat tctaacttga ttgaagccga tagtataaaa      180
aattctccag atattgtaac aagccatatg ttgaaatata gtgtcaagga taaaaatttg      240
tcagtttttt ttgagaaaga ttggatatca caggaattca aagataaaga agtagatatt      300
tatgtctctat ctgcacaaga ggtttgtgaa tgtccaggga aaagggtatga agcgtttggt      360
ggaattacat taactaattc agaaaaaaaa gaaattaaag ttctgtgtaa cgtgtgggat      420
aaaagtaaac aacagccgcc tatgtttatt acagtcaata aaccgaaagt aaccgctcag      480
gaagtggata taaaagttag aaagttattg attaagaaat acgatatcta taataaccgg      540
gaacaaaaat actctaaagg aactgttacc ttagatttaa attcaggtaa agatattggt      600
tttgatttgg attattttgg caatggagac tttaatagca tgctaaaaat atattccaat      660
aacgagagaa tagactcaac tcaatttcat gtagatgtgt caatcagcta a              711

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<210> SEQ ID NO 414
<211> LENGTH: 236
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 414
Met Arg Tyr Asn Cys Arg Tyr Ser His Ile Asp Lys Lys Ile Tyr Ser
1      5      10      15
Met Ile Ile Cys Leu Ser Phe Leu Leu Tyr Ser Asn Val Val Gln Ala
20      25      30
Asn Ser Tyr Asn Thr Thr Asn Arg His Asn Leu Glu Ser Leu Tyr Lys
35      40      45
His Asp Ser Asn Leu Ile Glu Ala Asp Ser Ile Lys Asn Ser Pro Asp
50      55      60
Ile Val Thr Ser His Met Leu Lys Tyr Ser Val Lys Asp Lys Asn Leu
65      70      75      80
Ser Val Phe Phe Glu Lys Asp Trp Ile Ser Gln Glu Phe Lys Asp Lys
85      90      95
Glu Val Asp Ile Tyr Ala Leu Ser Ala Gln Glu Val Cys Glu Cys Pro
100     105     110
Gly Lys Arg Tyr Glu Ala Phe Gly Gly Ile Thr Leu Thr Asn Ser Glu
115     120     125
Lys Lys Glu Ile Lys Val Pro Val Asn Val Trp Asp Lys Ser Lys Gln
130     135     140
Gln Pro Pro Met Phe Ile Thr Val Asn Lys Pro Lys Val Thr Ala Gln
145     150     155     160
Glu Val Asp Ile Lys Val Arg Lys Leu Leu Ile Lys Lys Tyr Asp Ile
165     170     175
Tyr Asn Asn Arg Glu Gln Lys Tyr Ser Lys Gly Thr Val Thr Leu Asp
180     185     190
Leu Asn Ser Gly Lys Asp Ile Val Phe Asp Leu Tyr Tyr Phe Gly Asn
195     200     205
Gly Asp Phe Asn Ser Met Leu Lys Ile Tyr Ser Asn Asn Glu Arg Ile
210     215     220
Asp Ser Thr Gln Phe His Val Asp Val Ser Ile Ser
225     230     235

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<210> SEQ ID NO 415
<211> LENGTH: 780

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<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 415

```
gtgagaaaaa ttgtaaatgt taatttttaa aagtttttaa cttcatcttt tctattgtgg      60
gtatttatat cagctataat tccaacgtgt tacgcgtatg agatgagtag tgtgggagtt      120
attaatttaa ggaatttata ctctacatat gatccaacag aagtaaaagg aaaaataaat      180
gaagggtccgc cattttcagg tagtttggtc tacaaaaata ttccttatgg caatagttcg      240
attgaattaa aagtagaact taatagcgta gaaaaagcta attttttttc tggtaaaagg      300
gtggatatat ttactttgga gtattctcct ccctgtaact ctaatataaa aaagaattca      360
tatggaggta ttactttaag cgacggtaat agaattgata aaaaaaatat acctgttaat      420
attttcatag acggcgttca acaaaaatat agctatacag atataagtac agtgagtact      480
gataagaaag aggttacgat tcaggaactt gatgtgaaat caagatatta tcttcaaaaa      540
cattttaata tatacggatt cggatgatgt aaagattttg gccgctcctc tagatttcaa      600
tctggccttg aggaaggaaa tattattttt catttgaata gtggagagag aatttcttat      660
aatctttttg atacaggaca tggtgacaga gagagtatgc taaaaaata cagtgataat      720
aagaccgctt attctgatca acttcatatt gatataact tagttaaatt taataaataa      780
```

<210> SEQ ID NO 416

<211> LENGTH: 259

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 416

```
Met Arg Lys Ile Val Asn Val Asn Phe Lys Lys Phe Leu Thr Ser Ser
1          5          10          15
Phe Leu Leu Trp Val Phe Ile Ser Ala Ile Ile Pro Thr Cys Tyr Ala
20          25          30
Tyr Glu Met Ser Ser Val Gly Val Ile Asn Leu Arg Asn Leu Tyr Ser
35          40          45
Thr Tyr Asp Pro Thr Glu Val Lys Gly Lys Ile Asn Glu Gly Pro Pro
50          55          60
Phe Ser Gly Ser Leu Phe Tyr Lys Asn Ile Pro Tyr Gly Asn Ser Ser
65          70          75          80
Ile Glu Leu Lys Val Glu Leu Asn Ser Val Glu Lys Ala Asn Phe Phe
85          90          95
Ser Gly Lys Arg Val Asp Ile Phe Thr Leu Glu Tyr Ser Pro Pro Cys
100         105         110
Asn Ser Asn Ile Lys Lys Asn Ser Tyr Gly Gly Ile Thr Leu Ser Asp
115         120         125
Gly Asn Arg Ile Asp Lys Lys Asn Ile Pro Val Asn Ile Phe Ile Asp
130         135         140
Gly Val Gln Gln Lys Tyr Ser Tyr Thr Asp Ile Ser Thr Val Ser Thr
145         150         155         160
Asp Lys Lys Glu Val Thr Ile Gln Glu Leu Asp Val Lys Ser Arg Tyr
165         170         175
Tyr Leu Gln Lys His Phe Asn Ile Tyr Gly Phe Gly Asp Val Lys Asp
180         185         190
Phe Gly Arg Ser Ser Arg Phe Gln Ser Gly Phe Glu Glu Gly Asn Ile
195         200         205
Ile Phe His Leu Asn Ser Gly Glu Arg Ile Ser Tyr Asn Leu Phe Asp
210         215         220
Thr Gly His Gly Asp Arg Glu Ser Met Leu Lys Lys Tyr Ser Asp Asn
225         230         235         240
Lys Thr Ala Tyr Ser Asp Gln Leu His Ile Asp Ile Tyr Leu Val Lys
245         250         255
Phe Asn Lys
```

<210> SEQ ID NO 417

```

<211> LENGTH: 333
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 417
    ttgataaaat tagcgtctaa accaacaata ctgctagctt tgagattaat cacattgatt      60
    ttgtttgcat cgattgtccc accgataatc tggtcggctc ttagcttgat aaactcccct      120
    aacttagccc caaaagctcc attaaccgtc gtattgccat caagagcgat gtttttacca      180
    gctatttgca caccgcggga attcaagtta atcgctgaga taatatcgct gccagacatt      240
    ttactttgcg ggattttgtc tttaatcgca agcatgatac tgtcgccaga ttgccgcaag      300
    agggaactgta tttttcctaa gggtcacagac tga                                  333

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<210> SEQ ID NO 418
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 418
    Met Ile Lys Leu Ala Ser Lys Pro Thr Ile Leu Leu Ala Leu Arg Leu
    1           5           10           15
    Ile Thr Leu Ile Leu Phe Ala Ser Ile Val Pro Pro Ile Ile Trp Ser
           20           25           30
    Ala Leu Ser Leu Ile Asn Ser Pro Asn Leu Ala Pro Lys Ala Pro Leu
           35           40           45
    Thr Val Val Leu Pro Ser Arg Ala Met Phe Leu Pro Ala Ile Cys Thr
           50           55           60
    Pro Arg Glu Phe Lys Leu Ile Ala Glu Ile Ile Ser Leu Pro Asp Ile
    65           70           75           80
    Leu Leu Cys Gly Ile Leu Ser Leu Ile Ala Ser Met Ile Leu Ser Pro
           85           90           95
    Asp Cys Arg Lys Arg Asp Cys Ile Phe Pro Lys Val Thr Asp
           100           105           110

```

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<210> SEQ ID NO 419
<211> LENGTH: 270
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 419
    gtgaataaac gaatcaagaa aaaacataaa ttggaaacag cagttgtggt gcttatcgca      60
    gaaaatgcta tgcaggctga agctattaag aatcaaaaaca gacaaattgc agagctgaga      120
    tcgattatac aacaaaacgc ccaagcaata aatagagagt ttgcagcagt taaaggtgtg      180
    tgtcttgata atcaagcagc tattacaaac attgcagttg atattaacta cgtcaagaaa      240
    aactacaaac ggaagtgggg gaagaaatag                                  270

```

```

<210> SEQ ID NO 420
<211> LENGTH: 89
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 420
    Met Asn Lys Arg Ile Lys Lys Lys His Lys Leu Glu Thr Ala Val Val
    1           5           10           15
    Leu Leu Ile Ala Glu Asn Ala Met Gln Ala Glu Ala Ile Lys Asn Gln
           20           25           30
    Asn Arg Gln Ile Ala Glu Leu Arg Ser Ile Ile Gln Gln Asn Ala Gln
           35           40           45
    Ala Ile Asn Arg Glu Phe Ala Ala Val Lys Gly Val Cys Leu Asp Asn
           50           55           60
    Gln Ala Ala Ile Thr Asn Ile Ala Val Asp Ile Asn Tyr Val Lys Lys
    65           70           75           80

```

Asn Tyr Lys Arg Lys Trp Gly Lys Lys
85

<210> SEQ ID NO 421

<211> LENGTH: 870

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 421

```
atgaaaggta ttattcttgc aggaggttca gggacacgct tgtatccact gacccgtgcc      60
gcatctaaac agttgatgcc catttatgac aaaccaatga tttattaccc attgtcaacc      120
ttgatgttgg cagggattaa agatgtttta atcatttcaa ctccccaaga tcttcctcgt      180
ttcgaagaat tgctaggaga cgggtcagaa tttggcatta gcttatccta taaggaacaa      240
ccaagcccag atggttttagc acaagctttc attattggag aggagtttat cggtgatgac      300
cgtgttgctc ttatttttagg agataatatt taccacggtta atggcctcac taaaatgctt      360
caaaaggcag ctgccaaaga aaaaggagcc accgtttttg gttatcaagt gaaagaccct      420
gagcgctttg gagtgggtgga atttgatgag aacatgaatg ctatctctat cgaagaaaaa      480
ccagaagtgc ctaagtctca ctttgcagtg actggacttt atttctatga caatgacgtg      540
gtagagattg ctaaaaacat taaaccaagc gcgcgtggtg agttggaaaat tacagacgtc      600
aacaaggctt acttgaacg tggtgacctc tccgttgaat tgatggggcg tggtttttgc      660
tggttagaca ctggaacgca tgaaagtcta cttgaagcgg ctcaatatat tgaaactgtt      720
caacgcttgc aaaacgctca agtggcaaat ctggaagaaa ttgcctatcg catgggctat      780
atcagtaaag aagatgtcca taaattggcg caatctttaa agaaaaacga atacgggcaa      840
tacttgcttc gtttgattgg agaagcttaa                                     870
```

<210> SEQ ID NO 422

<211> LENGTH: 289

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 422

```
Met Lys Gly Ile Ile Leu Ala Gly Gly Ser Gly Thr Arg Leu Tyr Pro
1      5      10      15
Leu Thr Arg Ala Ser Lys Gln Leu Met Pro Ile Tyr Asp Lys Pro
20     25     30
Met Ile Tyr Tyr Pro Leu Ser Thr Leu Met Leu Ala Gly Ile Lys Asp
35     40     45
Val Leu Ile Ile Ser Thr Pro Gln Asp Leu Pro Arg Phe Glu Glu Leu
50     55     60
Leu Gly Asp Gly Ser Glu Phe Gly Ile Ser Leu Ser Tyr Lys Glu Gln
65     70     75     80
Pro Ser Pro Asp Gly Leu Ala Gln Ala Phe Ile Ile Gly Glu Glu Phe
85     90     95
Ile Gly Asp Asp Arg Val Ala Leu Ile Leu Gly Asp Asn Ile Tyr His
100    105    110
Gly Asn Gly Leu Thr Lys Met Leu Gln Lys Ala Ala Lys Glu Lys
115    120    125
Gly Ala Thr Val Phe Gly Tyr Gln Val Lys Asp Pro Glu Arg Phe Gly
130    135    140
Val Val Glu Phe Asp Glu Asn Met Asn Ala Ile Ser Ile Glu Glu Lys
145    150    155    160
Pro Glu Val Pro Lys Ser His Phe Ala Val Thr Gly Leu Tyr Phe Tyr
165    170    175
Asp Asn Asp Val Val Glu Ile Ala Lys Asn Ile Lys Pro Ser Ala Arg
180    185    190
Gly Glu Leu Glu Ile Thr Asp Val Asn Lys Ala Tyr Leu Glu Arg Gly
195    200    205
Asp Leu Ser Val Glu Leu Met Gly Arg Gly Phe Ala Trp Leu Asp Thr
210    215    220
```

Gly	Thr	His	Glu	Ser	Leu	Leu	Glu	Ala	Ala	Gln	Tyr	Ile	Glu	Thr	Val
225					230					235					240
Gln	Arg	Leu	Gln	Asn	Ala	Gln	Val	Ala	Asn	Leu	Glu	Glu	Ile	Ala	Tyr
			245						250					255	
Arg	Met	Gly	Tyr	Ile	Ser	Lys	Glu	Asp	Val	His	Lys	Leu	Ala	Gln	Ser
		260						265					270		
Leu	Lys	Lys	Asn	Glu	Tyr	Gly	Gln	Tyr	Leu	Leu	Arg	Leu	Ile	Gly	Glu
		275					280						285		
Ala															

<210> SEQ ID NO 423
 <211> LENGTH: 900
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 423

atgacaaaaa	taaaaaatag	tgtgattg	ggtccgacag	cggttggaaa	aacagcactt	60
gggattagtt	tagccaaggc	ttttaatgga	gaaattat	caggagatag	ccagcaagtt	120
tatcgacagt	tggatattgg	aacagccaag	gccactcaag	aagagcaaga	agcagcgggt	180
catcacttaa	ttgatattcg	tgagggtgacg	gagtccttatt	cggcctacga	ttttgttcaa	240
gatgctcaaa	aatctatttc	agatattg	agtcgtggga	aattaccaat	tattgtaggt	300
ggaactggtc	tttacttaca	aagtttactc	gaagggtatc	atctaggagg	tcaagttgat	360
caagaggcgg	taaaagccta	tcggaatgag	ttggagcaat	tggaacgatca	cgacttgtat	420
gaacgcttgc	aagtcaataa	cattaccatt	gagcaggtga	atcgacagacg	ggcgatccga	480
gcccttgaat	tggctcagtt	tgctgatgaa	ttagagaatg	ccgagacggc	ttatgagccg	540
cttattatcg	gcttgaatga	tgaccgccaa	gtcatctatg	accgtatcaa	tcagcgcgtg	600
aatcgatga	ttgaaaacgg	cttattggaa	gaagcaaaat	ggttatatga	gcattaccgg	660
actgttcagg	ctagtcgtgg	cataggttat	aaggaattat	tcccctat	tgtaggtgaa	720
atgactttgg	cagaagctag	tgatcaatta	aaacaaaaca	cgagacgttt	tgccaagcga	780
cagctaactt	ggttccgcaa	tcgaatggct	gtagcttca	ctgccataac	ggctcctgat	840
taccacacag	tagtacatga	tagggtcagg	gattttcttg	gtcagaaaaga	gaagtcatga	900

<210> SEQ ID NO 424
 <211> LENGTH: 299
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 424

Met	Thr	Lys	Ile	Lys	Ile	Val	Val	Ile	Val	Gly	Pro	Thr	Ala	Val	Gly
1				5					10					15	
Lys	Thr	Ala	Leu	Gly	Ile	Ser	Leu	Ala	Lys	Ala	Phe	Asn	Gly	Glu	Ile
			20					25					30		
Ile	Ser	Gly	Asp	Ser	Gln	Gln	Val	Tyr	Arg	Gln	Leu	Asp	Ile	Gly	Thr
		35				40					45				
Ala	Lys	Ala	Thr	Gln	Glu	Glu	Gln	Glu	Ala	Ala	Val	His	His	Leu	Ile
	50				55					60					
Asp	Ile	Arg	Glu	Val	Thr	Glu	Ser	Tyr	Ser	Ala	Tyr	Asp	Phe	Val	Gln
65				70					75					80	
Asp	Ala	Gln	Lys	Ser	Ile	Ser	Asp	Ile	Val	Ser	Arg	Gly	Lys	Leu	Pro
			85					90					95		
Ile	Ile	Val	Gly	Gly	Thr	Gly	Leu	Tyr	Leu	Gln	Ser	Leu	Leu	Glu	Gly
		100					105					110			
Tyr	His	Leu	Gly	Gly	Gln	Val	Asp	Gln	Glu	Ala	Val	Lys	Ala	Tyr	Arg
		115				120					125				
Asn	Glu	Leu	Glu	Gln	Leu	Asp	Asp	His	Asp	Leu	Tyr	Glu	Arg	Leu	Gln
	130				135					140					
Val	Asn	Asn	Ile	Thr	Ile	Glu	Gln	Val	Asn	Arg	Arg	Arg	Ala	Ile	Arg
145				150					155					160	
Ala	Leu	Glu	Leu	Ala	Gln	Phe	Ala	Asp	Glu	Leu	Glu	Asn	Ala	Glu	Thr

				165					170					175			
Ala	Tyr	Glu	Pro	Leu	Ile	Ile	Gly	Leu	Asn	Asp	Asp	Arg	Gln	Val	Ile		
			180					185					190				
Tyr	Asp	Arg	Ile	Asn	Gln	Arg	Val	Asn	Arg	Met	Ile	Glu	Asn	Gly	Leu		
		195					200					205					
Leu	Glu	Glu	Ala	Lys	Trp	Leu	Tyr	Glu	His	Tyr	Pro	Thr	Val	Gln	Ala		
	210					215					220						
Ser	Arg	Gly	Ile	Gly	Tyr	Lys	Glu	Leu	Phe	Pro	Tyr	Phe	Val	Gly	Glu		
225				230						235				240			
Met	Thr	Leu	Ala	Glu	Ala	Ser	Asp	Gln	Leu	Lys	Gln	Asn	Thr	Arg	Arg		
			245					250					255				
Phe	Ala	Lys	Arg	Gln	Leu	Thr	Trp	Phe	Arg	Asn	Arg	Met	Ala	Val	Ser		
	260							265					270				
Phe	Thr	Ala	Ile	Thr	Ala	Pro	Asp	Tyr	Pro	Gln	Val	Val	His	Asp	Arg		
	275						280					285					
Val	Arg	Asp	Phe	Leu	Gly	Gln	Lys	Glu	Lys	Ser							
	290					295											

<210> SEQ ID NO 425

<211> LENGTH: 723

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 425

ttgcaaaata	atttgcta	at	ttttccgaa	ttcttttcca	gatc	tagttc	tcca	atctat	60
gaatatgtta	taataaggat	tatg	aaatta	ctacttttta	ttaccattgc	ctatttactt			120
ggttctattc	caactggact	atgg	attgga	cagtactttt	accacatcaa	cttacgagag			180
catggatcag	gaaatactgg	aacc	acaaat	acttttccgga	tttttaggtgt	caaggcagga			240
acagctacct	tagctattga	tatg	tttaaa	gggacacttt	caatattgtt	accaattatt			300
tttggtatga	cttcaatttc	atcc	attgct	atcggctttt	tcgcagtttt	agggcatact			360
tttcctat	ttt	tgccaactt	taaagg	tggt	aaggccgtag	caacaagtgc	tggtgtattg		420
ctaggctttg	ctccgttata	tctctttttt	ttagcatcta	tctttgtttt	agttctctat				480
ttatttagta	tgatatcttt	agctagtgtg	gtttcagcta	tcgttggtgt	gttatctgtt				540
ttaacatttc	ctgccattca	ttttctttta	ccaaattatg	actacttttt	aacttttatt				600
gtgatattac	ttgcgttcat	tattattata	agacacaaag	ataacattag	tcgtatcaaa				660
catcatactg	aaaatcta	accttgggggg	ctaaatttaa	gcaaacaagt	gcctaaaaaa				720
taa									723

<210> SEQ ID NO 426

<211> LENGTH: 240

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 426

Met	Gln	Asn	Asn	Leu	Leu	Ile	Phe	Ser	Glu	Phe	Phe	Ser	Arg	Ser	Ser
1			5					10					15		
Ser	Pro	Ile	Tyr	Glu	Tyr	Val	Ile	Ile	Arg	Ile	Met	Lys	Leu	Leu	Leu
		20					25				30				
Phe	Ile	Thr	Ile	Ala	Tyr	Leu	Leu	Gly	Ser	Ile	Pro	Thr	Gly	Leu	Trp
	35					40				45					
Ile	Gly	Gln	Tyr	Phe	Tyr	His	Ile	Asn	Leu	Arg	Glu	His	Gly	Ser	Gly
	50				55			60							
Asn	Thr	Gly	Thr	Thr	Asn	Thr	Phe	Arg	Ile	Leu	Gly	Val	Lys	Ala	Gly
65				70				75					80		
Thr	Ala	Thr	Leu	Ala	Ile	Asp	Met	Phe	Lys	Gly	Thr	Leu	Ser	Ile	Leu
			85				90					95			
Leu	Pro	Ile	Ile	Phe	Gly	Met	Thr	Ser	Ile	Ser	Ser	Ile	Ala	Ile	Gly
	100						105					110			
Phe	Phe	Ala	Val	Leu	Gly	His	Thr	Phe	Pro	Ile	Phe	Ala	Asn	Phe	Lys

		115					120					125					
Gly	Gly	Lys	Ala	Val	Ala	Thr	Ser	Ala	Gly	Val	Leu	Leu	Gly	Phe	Ala		
	130						135					140					
Pro	Leu	Tyr	Leu	Phe	Phe	Leu	Ala	Ser	Ile	Phe	Val	Leu	Val	Leu	Tyr		
145						150					155				160		
Leu	Phe	Ser	Met	Ile	Ser	Leu	Ala	Ser	Val	Val	Ser	Ala	Ile	Val	Gly		
				165					170					175			
Val	Leu	Ser	Val	Leu	Thr	Phe	Pro	Ala	Ile	His	Phe	Leu	Leu	Pro	Asn		
			180					185					190				
Tyr	Asp	Tyr	Phe	Leu	Thr	Phe	Ile	Val	Ile	Leu	Leu	Ala	Phe	Ile	Ile		
	195						200					205					
Ile	Ile	Arg	His	Lys	Asp	Asn	Ile	Ser	Arg	Ile	Lys	His	His	Thr	Glu		
	210					215					220						
Asn	Leu	Ile	Pro	Trp	Gly	Leu	Asn	Leu	Ser	Lys	Gln	Val	Pro	Lys	Lys		
225					230					235					240		

<210> SEQ ID NO 427

<211> LENGTH: 651

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 427

atgattaata	tcccattaat	gaaagatagt	ttaggatttg	tgttatcggg	attaccttat	60
acccttggtg	tttcggtgct	cagttttttt	acgggtctgt	ttttagggtt	aggcctagcc	120
cttctgggaa	ggtcacgtca	gccgttgatt	cattatcttg	ttagagcgta	catctctatt	180
atgcgagggtg	tgccgatgat	cgtggtgctc	tttgttcttt	atttcgggtt	gccttattat	240
ggtttagaat	tgccagcttt	actttgcgct	tatcttggtt	tttctatggg	tagcgctgcc	300
tatatttctg	aagtttttctg	ctcttctata	gaagctattg	acaagggaca	atgggaagca	360
gctaaggctt	tagggttgcc	atatgctctt	atgggtaaga	aaattattct	tcctcaagcc	420
tttcgaattg	cagtttcctcc	tttaggaaat	gtcattattg	atatgggttaa	aagttcgtcg	480
ctagctgcca	tgattaccgt	accagatatt	tttcaaaatg	ccaaaattat	tggcggtaga	540
gagtgggatt	acatgtccat	gtatatttta	gtagccttta	tctattggct	tattgctttt	600
ttgttagaac	gttaccaaga	attcttagaa	aataagctag	cacttggtta	a	651

<210> SEQ ID NO 428

<211> LENGTH: 216

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 428

Met	Ile	Asn	Ile	Pro	Leu	Met	Lys	Asp	Ser	Leu	Gly	Phe	Val	Leu	Ser
1				5					10					15	
Gly	Leu	Pro	Tyr	Thr	Leu	Gly	Ile	Ser	Leu	Leu	Ser	Phe	Phe	Thr	Gly
		20						25					30		
Leu	Phe	Leu	Gly	Leu	Gly	Leu	Ala	Leu	Leu	Gly	Arg	Ser	Arg	Gln	Pro
		35					40					45			
Leu	Ile	His	Tyr	Leu	Val	Arg	Ala	Tyr	Ile	Ser	Ile	Met	Arg	Gly	Val
	50					55				60					
Pro	Met	Ile	Val	Val	Leu	Phe	Val	Leu	Tyr	Phe	Gly	Leu	Pro	Tyr	Tyr
65					70				75				80		
Gly	Leu	Glu	Leu	Pro	Ala	Leu	Leu	Cys	Ala	Tyr	Leu	Gly	Phe	Ser	Met
			85					90					95		
Val	Ser	Ala	Ala	Tyr	Ile	Ser	Glu	Val	Phe	Arg	Ser	Ser	Ile	Glu	Ala
		100					105						110		
Ile	Asp	Lys	Gly	Gln	Trp	Glu	Ala	Lys	Ala	Leu	Gly	Leu	Pro	Tyr	
	115					120				125					
Ala	Leu	Met	Val	Lys	Lys	Ile	Ile	Leu	Pro	Gln	Ala	Phe	Arg	Ile	Ala
	130					135				140					
Val	Pro	Pro	Leu	Gly	Asn	Val	Ile	Ile	Asp	Met	Val	Lys	Ser	Ser	Ser

145		150		155		160									
Leu	Ala	Ala	Met	Ile	Thr	Val	Pro	Asp	Ile	Phe	Gln	Asn	Ala	Lys	Ile
		165							170					175	
Ile	Gly	Gly	Arg	Glu	Trp	Asp	Tyr	Met	Ser	Met	Tyr	Ile	Leu	Val	Ala
		180						185					190		
Phe	Ile	Tyr	Trp	Leu	Ile	Ala	Phe	Leu	Leu	Glu	Arg	Tyr	Gln	Glu	Phe
		195					200					205			
Leu	Glu	Asn	Lys	Leu	Ala	Leu	Val								
	210					215									

<210> SEQ ID NO 429
 <211> LENGTH: 1260
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 429

```

ttgtttatta gaaaaaatagg aggtgacatg tttaatcgta tccgcattcg ttttatcatg      60
attgctttcta ttgccatttt tattattttta agttcaattg ttggtattat taacacggca      120
cgctgttacc aaagtcaaca agaaattaac cgtatttttac atttaatttc ctcaaataaaa      180
ggtaaattac ctggcactac ggaaagctct aaacgacttg gaacgaaact gtctgaagat      240
agcctaagcc agtttcggta ttatagtgtc atttttaaatg ctaatggaca tctactttct      300
tctaatactg ctaatatattc agcttttagat agagaagaag cccaatattt tgctagactt      360
tttgctaagt ctggggaaga aaaaggcagt taccgtcacc aagatagtgt ttattcgtac      420
ttgattactc agctgccaaa tgaagaaaaa ctggttgtaa ttttagatac taccttttat      480
tttcgtagtg taggagattt attagctggt tcagtgatgt tggcctttgg aggatttatc      540
ttttttgttg ttttagtgag tcttttttcc ggtatggtca tcaaaccttt tgtccaaaat      600
tatgagaagc agcgtcgctt tattactaat gcaggccacg agttaaaaaac accactagcc      660
attatctcag ccaataatga attggtcgaa ttaatgactg gagaatcaga atggaccaag      720
agtacaagtg atcagggtgaa gcgattgaca ggcttgatta atcaaattgat tactttggct      780
cgtttgaggg aacagccaga tgtggtatta catatggtag acttttcagc tattgctcaa      840
gatgcagctg aagattttta gagtctgggt ttgaaaagatg gtaaacgttt tgatttgacg      900
attcaaccga atattatgat taaagcggag gaaaagtcac tgtttgaact tgtgacaatt      960
ttagttgata atgccaataa atattgtgat cctaaaggct tgggtcaagg atctttaacc     1020
actattggaa gaagacgaaa acgagcgaaa ttagaagttt ctaataccta tttggaagga     1080
aaatccattg attacagccg cttcttttgaa cgcttttatc gcgaagacga atcccataat     1140
agcaaagaaa aagggttatgg aattggttta tctatggcag aaagtatggt taagttattt     1200
aaaggaacga taactgtaaa ttataaaaac gatgctattg tttttacagt ggtgatttga     1260

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<210> SEQ ID NO 430
 <211> LENGTH: 419
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 430

Met	Phe	Ile	Arg	Lys	Ile	Gly	Gly	Asp	Met	Phe	Asn	Arg	Ile	Arg	Ile
1				5					10					15	
Arg	Phe	Ile	Met	Ile	Ala	Ser	Ile	Ala	Ile	Phe	Ile	Ile	Leu	Ser	Ser
			20					25					30		
Ile	Val	Gly	Ile	Ile	Asn	Thr	Ala	Arg	Cys	Tyr	Gln	Ser	Gln	Gln	Glu
		35					40					45			
Ile	Asn	Arg	Ile	Leu	His	Leu	Ile	Ser	Ser	Asn	Lys	Gly	Lys	Leu	Pro
	50					55				60					
Gly	Thr	Thr	Glu	Ser	Ser	Lys	Arg	Leu	Gly	Thr	Lys	Leu	Ser	Glu	Asp
65					70					75				80	
Ser	Leu	Ser	Gln	Phe	Arg	Tyr	Tyr	Ser	Val	Ile	Phe	Asn	Ala	Asn	Gly
			85					90						95	
His	Leu	Leu	Ser	Ser	Asn	Thr	Ala	Asn	Ile	Ser	Ala	Leu	Asp	Arg	Glu
			100					105					110		
Glu	Ala	Gln	Tyr	Phe	Ala	Arg	Leu	Phe	Ala	Lys	Ser	Gly	Glu	Glu	Lys

		115					120					125					
Gly	Ser	Tyr	Arg	His	Gln	Asp	Ser	Val	Tyr	Ser	Tyr	Leu	Ile	Thr	Gln		
	130					135					140						
Leu	Pro	Asn	Glu	Glu	Lys	Leu	Val	Val	Ile	Leu	Asp	Thr	Thr	Phe	Tyr		
145					150					155					160		
Phe	Arg	Ser	Val	Gly	Asp	Leu	Leu	Ala	Val	Ser	Val	Met	Leu	Ala	Phe		
				165					170					175			
Gly	Gly	Phe	Ile	Phe	Phe	Val	Val	Leu	Val	Ser	Leu	Phe	Ser	Gly	Met		
		180						185				190					
Val	Ile	Lys	Pro	Phe	Val	Gln	Asn	Tyr	Glu	Lys	Gln	Arg	Arg	Phe	Ile		
	195					200					205						
Thr	Asn	Ala	Gly	His	Glu	Leu	Lys	Thr	Pro	Leu	Ala	Ile	Ile	Ser	Ala		
210					215					220							
Asn	Asn	Glu	Leu	Val	Glu	Leu	Met	Thr	Gly	Glu	Ser	Glu	Trp	Thr	Lys		
225				230					235						240		
Ser	Thr	Ser	Asp	Gln	Val	Lys	Arg	Leu	Thr	Gly	Leu	Ile	Asn	Gln	Met		
			245					250						255			
Ile	Thr	Leu	Ala	Arg	Leu	Glu	Glu	Gln	Pro	Asp	Val	Val	Leu	His	Met		
	260					265							270				
Val	Asp	Phe	Ser	Ala	Ile	Ala	Gln	Asp	Ala	Ala	Glu	Asp	Phe	Lys	Ser		
	275					280					285						
Leu	Val	Leu	Lys	Asp	Gly	Lys	Arg	Phe	Asp	Leu	Thr	Ile	Gln	Pro	Asn		
290					295					300							
Ile	Met	Ile	Lys	Ala	Glu	Glu	Lys	Ser	Leu	Phe	Glu	Leu	Val	Thr	Ile		
305				310					315						320		
Leu	Val	Asp	Asn	Ala	Asn	Lys	Tyr	Cys	Asp	Pro	Lys	Gly	Leu	Val	Lys		
			325					330						335			
Val	Ser	Leu	Thr	Thr	Ile	Gly	Arg	Arg	Arg	Lys	Arg	Ala	Lys	Leu	Glu		
	340					345							350				
Val	Ser	Asn	Thr	Tyr	Leu	Glu	Gly	Lys	Ser	Ile	Asp	Tyr	Ser	Arg	Phe		
	355					360					365						
Phe	Glu	Arg	Phe	Tyr	Arg	Glu	Asp	Glu	Ser	His	Asn	Ser	Lys	Glu	Lys		
370					375						380						
Gly	Tyr	Gly	Ile	Gly	Leu	Ser	Met	Ala	Glu	Ser	Met	Val	Lys	Leu	Phe		
385				390					395					400			
Lys	Gly	Thr	Ile	Thr	Val	Asn	Tyr	Lys	Asn	Asp	Ala	Ile	Val	Phe	Thr		
			405					410						415			
Val	Val	Ile															

<210> SEQ ID NO 431

<211> LENGTH: 1020

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 431

atgagaaaaa	gatgctattc	aacttcagct	gcagtattgg	cagcagtgac	tttattttgtt	60
ctatcggtag	atcgtggtgt	tatagcagat	agtttttctg	ctaatcaaga	gattagatat	120
tcggaagtaa	caccttatca	cgttacttcc	gttttgacca	aaggagttac	tcctccagca	180
aacttcactc	aaggtgaaga	tgtttttcac	gctccttatg	ttgctaacca	aggatgggat	240
gatattacca	aaacattcaa	tgaaaaagac	gatcttcttt	gcggggctgc	cacagcaggg	300
aatatgcttc	actggtggtt	cgatcaaaac	aaagaccaa	ttaaacgtta	tttggaagag	360
catccagaaa	agcaaaaaat	aaacttcaat	ggcgaacaga	tgtttgacgt	aaaagaagct	420
atcgacacta	aaaaccacca	gctagatagt	aaattatttg	aatattttta	agaaaaagct	480
ttcccttata	tattactata	acaccttaga	gttttccctg	atcatgtaat	tgatatgttc	540
attaacggct	accgccttag	tctaactaac	cacggtccaa	cgccagtaaa	agaaggtagt	600
aaagatcccc	gaggtggtat	ttttgacgcc	gtatttcaaa	gaggtgatca	aagtaagcta	660
ttgacaagtc	gtcatgattt	taaagaaaaa	aatctcaaa	aatcagtgta	tctcattaag	720
aaagagttaa	ccgaaggcaa	ggctctaggc	ctatcacaca	cctacgctaa	cgtacgcata	780

aaccatgtta	taaacctgtg	gggagctgac	tttgattcta	acgggaacct	taaagctatt	840
tatgtaacag	actctgatag	taatgcatct	attggtatga	agaaatactt	tggtggtgtt	900
aattccgctg	gaaaagtagc	tatttctgct	aaagaaataa	aagaagataa	tattggtgct	960
caagtactag	ggttatttac	actttcaaca	gggcaagata	gttggaatca	gaccaattaa	1020

<210> SEQ ID NO 432
 <211> LENGTH: 339
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 432

Met	Arg	Lys	Arg	Cys	Tyr	Ser	Thr	Ser	Ala	Ala	Val	Leu	Ala	Ala	Val
1				5					10					15	
Thr	Leu	Phe	Val	Leu	Ser	Val	Asp	Arg	Gly	Val	Ile	Ala	Asp	Ser	Phe
			20					25					30		
Ser	Ala	Asn	Gln	Glu	Ile	Arg	Tyr	Ser	Glu	Val	Thr	Pro	Tyr	His	Val
		35					40					45			
Thr	Ser	Val	Trp	Thr	Lys	Gly	Val	Thr	Pro	Pro	Ala	Asn	Phe	Thr	Gln
	50					55					60				
Gly	Glu	Asp	Val	Phe	His	Ala	Pro	Tyr	Val	Ala	Asn	Gln	Gly	Trp	Tyr
65					70					75					80
Asp	Ile	Thr	Lys	Thr	Phe	Asn	Gly	Lys	Asp	Asp	Leu	Leu	Cys	Gly	Ala
				85					90					95	
Ala	Thr	Ala	Gly	Asn	Met	Leu	His	Trp	Trp	Phe	Asp	Gln	Asn	Lys	Asp
			100					105					110		
Gln	Ile	Lys	Arg	Tyr	Leu	Glu	Glu	His	Pro	Glu	Lys	Gln	Lys	Ile	Asn
		115					120					125			
Phe	Asn	Gly	Glu	Gln	Met	Phe	Asp	Val	Lys	Glu	Ala	Ile	Asp	Thr	Lys
	130					135					140				
Asn	His	Gln	Leu	Asp	Ser	Lys	Leu	Phe	Glu	Tyr	Phe	Lys	Glu	Lys	Ala
145					150					155					160
Phe	Pro	Tyr	Leu	Ser	Thr	Lys	His	Leu	Gly	Val	Phe	Pro	Asp	His	Val
				165					170					175	
Ile	Asp	Met	Phe	Ile	Asn	Gly	Tyr	Arg	Leu	Ser	Leu	Thr	Asn	His	Gly
			180					185					190		
Pro	Thr	Pro	Val	Lys	Glu	Gly	Ser	Lys	Asp	Pro	Arg	Gly	Gly	Ile	Phe
		195					200						205		
Asp	Ala	Val	Phe	Thr	Arg	Gly	Asp	Gln	Ser	Lys	Leu	Leu	Thr	Ser	Arg
	210					215					220				
His	Asp	Phe	Lys	Glu	Lys	Asn	Leu	Lys	Glu	Ile	Ser	Asp	Leu	Ile	Lys
225					230					235					240
Lys	Glu	Leu	Thr	Glu	Gly	Lys	Ala	Leu	Gly	Leu	Ser	His	Thr	Tyr	Ala
				245					250					255	
Asn	Val	Arg	Ile	Asn	His	Val	Ile	Asn	Leu	Trp	Gly	Ala	Asp	Phe	Asp
			260					265					270		
Ser	Asn	Gly	Asn	Leu	Lys	Ala	Ile	Tyr	Val	Thr	Asp	Ser	Asp	Ser	Asn
	275						280					285			
Ala	Ser	Ile	Gly	Met	Lys	Lys	Tyr	Phe	Val	Gly	Val	Asn	Ser	Ala	Gly
	290					295					300				
Lys	Val	Ala	Ile	Ser	Ala	Lys	Glu	Ile	Lys	Glu	Asp	Asn	Ile	Gly	Ala
305					310					315					320
Gln	Val	Leu	Gly	Leu	Phe	Thr	Leu	Ser	Thr	Gly	Gln	Asp	Ser	Trp	Asn
				325					330					335	
Gln	Thr	Asn													

<210> SEQ ID NO 433
 <211> LENGTH: 600
 <212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 433

```
ttgaagggtga aaaaaaggag aagaagggct aaatcatcag taaatcgact tgtcttaggg      60
ttagtattac ttaatctgat tgtagtatg tggacactaa aattgggaaa ccagcgatta      120
gctccgatatg cggatcacga aactctgaca tttgtcagga agattagtca tgctgctcaa      180
tcagtcgctc aaaagaaaca gttatatagt tcggtgatga tggctcaggc cattttagaa      240
tccaataatg gtaagtcaca actaagtcaa aaaccttatt ataatttttt cgggattaag      300
gggagctata aagaacggtc agtcattttt ccaactttag aagacgatgg acaagggaat      360
ctttatcaaa ttgatgctgc ttttcgttcc tatgggagcc tgacagcttg ttttttagat      420
tacgcaagag ttttgaatga tccactttat gacaaaaccc acaaaaagt ttggtctcat      480
tatcaagatg ctactgcaac cttaacaggc acttacgcca ctgatacaac ttaccatacc      540
aaattaaatg aattgattga atggtatcaa ctactaatt ttgatggtct aatgaaatag      600
```

<210> SEQ ID NO 434

<211> LENGTH: 199

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 434

```
Met Lys Val Lys Lys Arg Arg Arg Arg Ala Lys Ser Ser Val Asn Arg
 1             5             10            15
Leu Val Leu Gly Leu Val Leu Leu Asn Leu Ile Val Ser Met Trp Thr
   20            25            30
Leu Lys Leu Gly Asn Gln Arg Leu Ala Pro Tyr Ala Asp His Glu Thr
   35            40            45
Leu Thr Phe Val Arg Lys Ile Ser His Ala Ala Gln Ser Val Ala Gln
   50            55            60
Lys Lys Gln Leu Tyr Ser Ser Val Met Met Ala Gln Ala Ile Leu Glu
 65            70            75            80
Ser Asn Asn Gly Lys Ser Gln Leu Ser Gln Lys Pro Tyr Tyr Asn Phe
   85            90            95
Phe Gly Ile Lys Gly Ser Tyr Lys Glu Arg Ser Val Ile Phe Pro Thr
  100           105           110
Leu Glu Asp Asp Gly Gln Gly Asn Leu Tyr Gln Ile Asp Ala Ala Phe
  115           120           125
Arg Ser Tyr Gly Ser Leu Thr Ala Cys Phe Leu Asp Tyr Ala Arg Val
  130           135           140
Leu Asn Asp Pro Leu Tyr Asp Lys Thr His Lys Lys Phe Trp Ser His
 145           150           155           160
Tyr Gln Asp Ala Thr Ala Thr Leu Thr Gly Thr Tyr Ala Thr Asp Thr
           165           170           175
Thr Tyr His Thr Lys Leu Asn Glu Leu Ile Glu Trp Tyr Gln Leu Thr
           180           185           190
Asn Phe Asp Gly Leu Met Lys
           195
```

<210> SEQ ID NO 435

<211> LENGTH: 1947

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 435

```
atgaaaattc aagattttatt gagaaaagat attatgattc tcgattttaca ggctattttct      60
aaagaagttg ccattgacga gatgattact aaattagttg aaaaagatat tgtacatgat      120
tttgatgtct ttaaaaagag tatcatgaca cgtgaagaac aaacatcaac agggcttgggt      180
gatgggattg ccatgcctca ttctaaaaat attgtagtag ataaaccagc ggtcttgttt      240
gcgaaatcaa ataaaggtgt ggattacaag gctttagatg gtcaaccaac ggatctcttc      300
tttatgattg ctgcgcctca aggagcaaat gatactcact tggctgcact agcagaatta      360
tcacaatacc ttttgaaaga cggctttgct gataaacttc gtgctgcagc gacaccagaa      420
```

```

gcagtcattg ctgtttttga tgaagcgctca acagctaaag aagaagtgggt tgctccaaca 480
agtgggtcaag acttttatcgt tgctgtttaca gcttgtccga caggaattgc tcacacttat 540
atggcagaag aggcctttgaa aaaacaagct gcagaaatgg gagtagctat taaagttgaa 600
acaaacgggtg cttctgggtgt ggctaatacgt ttaaccgctg aagatattca gagagctaaa 660
ggaggttattg ttgcagctga taaagcgggt gaaatggacc gttttgatgg taaacaattc 720
attgctcgcc ctggtgcaga tggatatcaag aaaagtcagg aattgatttc tttgatttta 780
aacaatgaag gaaacactta tcatgctaaa aatggaaaat ctgaaacagc agtatcaact 840
gagaaaacaa gtttaggcgg tgctttctat aaacacttga tgggcgggtgt ctcaacaatg 900
ttgccatttg ttattgggtg cgggattatg attgctctag catttttatt ggataacatg 960
cttgggtgtgc caaatgatca gcttgggaagt cttggatcct atcatgaaat agcagctatt 1020
tttatgaaca ttggtggagc agccttttcc ttcattgttac cagtactagc aggttatatc 1080
gcttatttcta ttgctgaaaa accgggccta gtagctgggt ttgtggcagg tgccattgcc 1140
tcaaatgggtc ttgcttttgg taaggtacca tttgcagcag gaggagaagt gagcttgggc 1200
ttaacggggcg tgccatcagg tttccttggg gcgcttctgg gtggtttcct tgccggtgggt 1260
gttattcttg cccttcgtaa attggtggca ggcctaccac gttctctaga aggggttaaa 1320
tctatcctcc ttaccatt acttggcgct cttgtcactg gtttcttgat gctttttgtc 1380
aatattccaa tggcagctat taacacagcc cttaatgatt tcttacaagg tctttcagga 1440
agctctgctg tccttatggg acttcttgtt ggtggaatga tggctgttga catgggtgggt 1500
cctgttaata aggcagctta tgtttttggg acaggaactt tagcagctac tgtggcaaat 1560
ggtggttcgg tcgttatggc cgctgttatg gcaggtggta tgggtacctc tcttgctgtt 1620
ttttagacca ctctcttgtt taaagataaa ttaccaaaag aagaacgtga atcaggcttg 1680
acaaatattg ttatgggact ttcattcatc accgaaggag caattccgtt tgggtgcagct 1740
gacccagcac gtgcgattcc tagctttatc gcaggttctg ccttgacagg agctcttgtt 1800
ggtttggctg gtattaaatt aatggcgcca catggtggta tcttcgtaat cgctttaaca 1860
agcaatccaa tcttatatct tgtctttgtt gtgattggtg cccttgatc aggtatctta 1920
tttggcgctc ttcgcaaaaa agcctaa 1947

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<210> SEQ ID NO 436

<211> LENGTH: 648

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 436

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Met Lys Ile Gln Asp Leu Leu Arg Lys Asp Ile Met Ile Leu Asp Leu
1           5           10           15
Gln Ala Ile Ser Lys Glu Val Ala Ile Asp Glu Met Ile Thr Lys Leu
20           25           30
Val Glu Lys Asp Ile Val His Asp Phe Asp Val Phe Lys Lys Ser Ile
35           40           45
Met Thr Arg Glu Glu Gln Thr Ser Thr Gly Leu Gly Asp Gly Ile Ala
50           55           60
Met Pro His Ser Lys Asn Ile Val Val Asp Lys Pro Ala Val Leu Phe
65           70           75           80
Ala Lys Ser Asn Lys Gly Val Asp Tyr Lys Ala Leu Asp Gly Gln Pro
85           90           95
Thr Asp Leu Phe Phe Met Ile Ala Ala Pro Gln Gly Ala Asn Asp Thr
100          105          110
His Leu Ala Ala Leu Ala Glu Leu Ser Gln Tyr Leu Leu Lys Asp Gly
115          120          125
Phe Ala Asp Lys Leu Arg Ala Ala Ala Thr Pro Glu Ala Val Ile Ala
130          135          140
Val Phe Asp Glu Ala Ser Thr Ala Lys Glu Glu Val Val Ala Pro Thr
145          150          155          160
Ser Gly Gln Asp Phe Ile Val Ala Val Thr Ala Cys Pro Thr Gly Ile
165          170          175
Ala His Thr Tyr Met Ala Glu Glu Ala Leu Lys Lys Gln Ala Ala Glu
180          185          190
Met Gly Val Ala Ile Lys Val Glu Thr Asn Gly Ala Ser Gly Val Ala

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		195					200				205				
Asn	Arg	Leu	Thr	Ala	Glu	Asp	Ile	Gln	Arg	Ala	Lys	Gly	Val	Ile	Val
	210					215					220				
Ala	Ala	Asp	Lys	Ala	Val	Glu	Met	Asp	Arg	Phe	Asp	Gly	Lys	Gln	Phe
225					230					235					240
Ile	Ala	Arg	Pro	Val	Ala	Asp	Gly	Ile	Lys	Lys	Ser	Gln	Glu	Leu	Ile
				245					250					255	
Ser	Leu	Ile	Leu	Asn	Asn	Glu	Gly	Asn	Thr	Tyr	His	Ala	Lys	Asn	Gly
			260					265					270		
Lys	Ser	Glu	Thr	Ala	Val	Ser	Thr	Glu	Lys	Thr	Ser	Leu	Gly	Gly	Ala
		275					280					285			
Phe	Tyr	Lys	His	Leu	Met	Gly	Gly	Val	Ser	Gln	Met	Leu	Pro	Phe	Val
	290					295					300				
Ile	Gly	Gly	Gly	Ile	Met	Ile	Ala	Leu	Ala	Phe	Leu	Leu	Asp	Asn	Met
305					310					315					320
Leu	Gly	Val	Pro	Asn	Asp	Gln	Leu	Gly	Ser	Leu	Gly	Ser	Tyr	His	Glu
				325					330					335	
Ile	Ala	Ala	Ile	Phe	Met	Asn	Ile	Gly	Gly	Ala	Ala	Phe	Ser	Phe	Met
			340					345					350		
Leu	Pro	Val	Leu	Ala	Gly	Tyr	Ile	Ala	Tyr	Ser	Ile	Ala	Glu	Lys	Pro
		355					360					365			
Gly	Leu	Val	Ala	Gly	Phe	Val	Ala	Gly	Ala	Ile	Ala	Ser	Asn	Gly	Leu
	370					375					380				
Ala	Phe	Gly	Lys	Val	Pro	Phe	Ala	Ala	Gly	Gly	Glu	Val	Ser	Leu	Gly
385					390					395					400
Leu	Thr	Gly	Val	Pro	Ser	Gly	Phe	Leu	Gly	Ala	Leu	Val	Gly	Gly	Phe
				405					410					415	
Leu	Ala	Gly	Gly	Val	Ile	Leu	Ala	Leu	Arg	Lys	Leu	Leu	Ala	Gly	Leu
			420					425					430		
Pro	Arg	Ser	Leu	Glu	Gly	Val	Lys	Ser	Ile	Leu	Leu	Tyr	Pro	Leu	Leu
		435					440					445			
Gly	Val	Leu	Val	Thr	Gly	Phe	Leu	Met	Leu	Phe	Val	Asn	Ile	Pro	Met
	450					455					460				
Ala	Ala	Ile	Asn	Thr	Ala	Leu	Asn	Asp	Phe	Leu	Gln	Gly	Leu	Ser	Gly
465					470					475					480
Ser	Ser	Ala	Val	Leu	Met	Gly	Leu	Leu	Val	Gly	Gly	Met	Met	Ala	Val
				485					490					495	
Asp	Met	Gly	Gly	Pro	Val	Asn	Lys	Ala	Ala	Tyr	Val	Phe	Gly	Thr	Gly
			500					505					510		
Thr	Leu	Ala	Ala	Thr	Val	Ala	Asn	Gly	Gly	Ser	Val	Val	Met	Ala	Ala
		515					520					525			
Val	Met	Ala	Gly	Gly	Met	Val	Pro	Pro	Leu	Ala	Val	Phe	Val	Ala	Thr
	530					535					540				
Leu	Leu	Phe	Lys	Asp	Lys	Phe	Thr	Lys	Glu	Glu	Arg	Glu	Ser	Gly	Leu


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<210> SEQ ID NO 437
<211> LENGTH: 1059
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 437
atgacaacaa cagataaaga gacatttagt tcttttatga ataaggtctt ggctggtaca      60
gcgattgcta tcgttgtggc actcattcca aatgctatct tagcgacttt cttaaaaccg      120
cttttgccaa atatggcagc tgctgaattt ttacacattg tgcaagtctt ccaattcttc      180
acgccgatta tggctggttt cttgattggg caacaattta agtttaatcc tatgcaacag      240
ttggctgttg gtggagctgc ttatatcggc tctggagcct gggcttatac agaagtcatt      300
caaaaagggtg tggcgacagg aacattccaa cttagaggta ttggggactt aatcaatatg      360
atgattacag ctagccttgc ggtttttagc gtgaaatatt ttgggaataa atttggctct      420
ttaaccatta tcttggtacc tatcactata ggaactggcg taggttatat tggttggaaa      480
tttttgcctt atgtgtctta cgtgacaacc ctgatcggac aagggaataa ttcttttaca      540
accttacaac ctattttaat gtctatttta attgcagttg ctttctcgct tatcattggt      600
agtccgattt caactgttgc aatcggttta gctattgggc ttaatggaat ggctgcggga      660
gcagcttcta tgggaattgc atcgacagca gcagtcctag tgtgggcgac gcttaaagtt      720
aataaatctg gtgtaccaat tgctatcgca cttgggggcta tgaaaatgat gatgccaaac      780
ttcttgaaac atcctatcat ggctattccg atggtgttca ctgcagcaat tagctcatta      840
acagtaccat tgtttaatct tgttggaaac ccagcttcat ctggttttgg cttagttggt      900
gcagtaggtc cgattgcttc tttagcaggt ggtagctcaa tacttattat tacccttgc      960
tggatcattg ttccgtttgc gggtgctttt gcggcgcata aggtttctaa agatattcta     1020
aaactgtata aagaagacat tttcgtcttt gaaggctaa      1059

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<210> SEQ ID NO 438
<211> LENGTH: 352
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 438
Met Thr Thr Thr Asp Lys Glu Thr Phe Ser Ser Phe Met Asn Lys Val
1      5      10      15
Leu Ala Gly Thr Ala Ile Ala Ile Val Val Ala Leu Ile Pro Asn Ala
20     25     30
Ile Leu Ala Thr Phe Leu Lys Pro Leu Leu Pro Asn Met Ala Ala Ala
35     40     45
Glu Phe Leu His Ile Val Gln Val Phe Gln Phe Phe Thr Pro Ile Met
50     55     60
Ala Gly Phe Leu Ile Gly Gln Gln Phe Lys Phe Asn Pro Met Gln Gln
65     70     75     80
Leu Ala Val Gly Gly Ala Ala Tyr Ile Gly Ser Gly Ala Trp Ala Tyr
85     90     95
Thr Glu Val Ile Gln Lys Gly Val Ala Thr Gly Thr Phe Gln Leu Arg
100    105    110
Gly Ile Gly Asp Leu Ile Asn Met Met Ile Thr Ala Ser Leu Ala Val
115    120    125
Leu Ala Val Lys Tyr Phe Gly Asn Lys Phe Gly Ser Leu Thr Ile Ile
130    135    140
Leu Leu Pro Ile Thr Ile Gly Thr Gly Val Gly Tyr Ile Gly Trp Lys
145    150    155    160
Phe Leu Pro Tyr Val Ser Tyr Val Thr Thr Leu Ile Gly Gln Gly Ile
165    170    175
Asn Ser Phe Thr Thr Leu Gln Pro Ile Leu Met Ser Ile Leu Ile Ala
180    185    190
Val Ala Phe Ser Leu Ile Ile Val Ser Pro Ile Ser Thr Val Ala Ile
195    200    205
Gly Leu Ala Ile Gly Leu Asn Gly Met Ala Ala Gly Ala Ala Ser Met

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210	215	220
Gly Ile Ala Ser Thr	Ala Ala Val Leu Val	Trp Ala Thr Leu Lys Val
225	230	235
Asn Lys Ser Gly Val	Pro Ile Ala Ile Ala	Leu Gly Ala Met Lys Met
245	250	255
Met Met Pro Asn Phe	Leu Lys His Pro	Ile Met Ala Ile Pro Met Val
260	265	270
Phe Thr Ala Ala Ile	Ser Ser Leu Thr Val	Pro Leu Phe Asn Leu Val
275	280	285
Gly Thr Pro Ala Ser	Ser Gly Phe Gly Leu Val	Gly Ala Val Gly Pro
290	295	300
Ile Ala Ser Leu Ala	Gly Gly Ser Ser Ile	Leu Ile Ile Ile Leu Ala
305	310	315
Trp Ile Ile Val Pro	Phe Ala Val Ala Phe	Ala Ala His Lys Val Ser
325	330	335
Lys Asp Ile Leu Lys	Leu Tyr Lys Glu Asp	Ile Phe Val Phe Glu Gly
340	345	350

<210> SEQ ID NO 439
 <211> LENGTH: 876
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 439

atgccagcaa gtaaaaaagt caccattatt tttatattaa atcttagttt ttccctcatt	60
gaatttattt ttgggacatt attcttttctg ggtgctattt tagcagatgc tgtccacgat	120
tttggagatg ccattgctat tggatctca gctatcttag aaagaaaggc tgtaaaaaaa	180
gagagtccaa atttttctact aggctataag cgatttagcc ttttaggagc gctaacgaca	240
aatctaatac ttattagcgg gtcattatta gtaatgattg aaacgatacc aaaattatgg	300
catcctacta ttgttaatta tgacggtatg ttcgttttag ctatttttgc aattataatc	360
aatggatttg ctagcttcat cattcactct aaccagacaa aaaatgaaga aatattaagc	420
cttcactttt tagaagatat ccttgggtgg ttagccatta tcatactgtc actgatctta	480
aaatggaaac cttggtacat tcttgatcct ttattatcaa ttgccattgc ttcttttata	540
ttatctaaag ctcttccaaa gttagtagca actgctaaca tttttttaga tgggtgttcct	600
gattctatag actattgcac tttgcaccat gaactcagcc aacttcctca tatagtgtct	660
gttaatcagc ttaatgtttg gtcgatggat ggtattgatc atagagcaac tatacattgc	720
tgcttgagag aatctaccac tgaaaaacat tgcaaaaaat ctattagact gatttgtcaa	780
aggtacaata taaactcagt cactgtggaa atcgatactt ctttaaacga acaccaacat	840
cactgttctt ctctttctag tattgaagtc aactaa	876

<210> SEQ ID NO 440
 <211> LENGTH: 291
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 440

Met Pro Ala Ser Lys Lys Val Thr Ile Ile Phe Ile Leu Asn Leu Ser	1	5	10	15
Phe Ser Leu Ile Glu Phe Ile Phe Gly Thr Leu Phe Phe Ser Gly Ala	20	25	30	
Ile Leu Ala Asp Ala Val His Asp Phe Gly Asp Ala Ile Ala Ile Gly	35	40	45	
Ile Ser Ala Ile Leu Glu Arg Lys Ala Val Lys Lys Glu Ser Pro Asn	50	55	60	
Phe Ser Leu Gly Tyr Lys Arg Phe Ser Leu Leu Gly Ala Leu Thr Thr	65	70	75	80
Asn Leu Ile Leu Ile Ser Gly Ser Leu Leu Val Met Ile Glu Thr Ile	85	90	95	
Pro Lys Leu Trp His Pro Thr Ile Val Asn Tyr Asp Gly Met Phe Val				

			100					105				110					
Leu	Ala	Ile	Phe	Ala	Ile	Ile	Ile	Asn	Gly	Phe	Ala	Ser	Phe	Ile	Ile		
		115					120					125					
His	Ser	Asn	Gln	Thr	Lys	Asn	Glu	Glu	Ile	Leu	Ser	Leu	His	Phe	Leu		
		130					135					140					
Glu	Asp	Ile	Leu	Gly	Trp	Leu	Ala	Ile	Ile	Ile	Leu	Ser	Leu	Ile	Leu		
		145					150				155				160		
Lys	Trp	Lys	Pro	Trp	Tyr	Ile	Leu	Asp	Pro	Leu	Leu	Ser	Ile	Ala	Ile		
			165						170					175			
Ala	Ser	Phe	Ile	Leu	Ser	Lys	Ala	Leu	Pro	Lys	Leu	Val	Ala	Thr	Ala		
			180						185				190				
Asn	Ile	Phe	Leu	Asp	Gly	Val	Pro	Asp	Ser	Ile	Asp	Tyr	Cys	Thr	Leu		
		195					200					205					
His	His	Glu	Leu	Ser	Gln	Leu	Pro	His	Ile	Val	Ser	Val	Asn	Gln	Leu		
		210					215					220					
Asn	Val	Trp	Ser	Met	Asp	Gly	Ile	Asp	His	Arg	Ala	Thr	Ile	His	Cys		
		225				230				235					240		
Cys	Leu	Arg	Glu	Ser	Thr	Thr	Glu	Lys	His	Cys	Lys	Lys	Ser	Ile	Arg		
				245					250					255			
Leu	Ile	Cys	Gln	Arg	Tyr	Asn	Ile	Asn	Ser	Val	Thr	Val	Glu	Ile	Asp		
			260					265					270				
Thr	Ser	Leu	Asn	Glu	His	Gln	His	His	Cys	Ser	Ser	Leu	Ser	Ser	Ile		
		275					280						285				
Glu	Val	Asn															
		290															

<210> SEQ ID NO 441

<211> LENGTH: 1260

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 441

gtgaaagatg	tcatttatga	tgtggaagaa	gtgccaaagg	caggtatggt	agttggtttg	60
tcctttcagc	acttatttgc	tatgttttgt	gcgactgttc	tggttcccat	tctagttgga	120
attgacccat	cagttgcttt	gttatctagt	ggtttaggaa	cccttgccca	cttatcagtg	180
accaaattta	aaattccagc	ctacatgggc	tcaagttttg	cttatatagc	agctatgcag	240
ttactgatga	agacaaatgg	tattggtgct	gtagctcaag	gggctatgac	aggaggtctc	300
gtttacctga	ttgtagcttt	gattgttaaa	gctattggca	atgattggat	tgataacatc	360
ttaccaccga	ttgtggtttg	tccgattggt	atggtcattg	gtctaagcct	agcttctaca	420
gctgttaatg	atgtcatgct	aaaaaatggg	aactataatc	tgacttatct	tgttattggg	480
ttagtcacct	tattatcagt	tatttttttc	aatatattatg	gtaagggaa	tgttgctatt	540
gtaccgcttt	tattagggct	attagttggt	tatgtttag	cccttttagt	gggtgttctc	600
accggtcaag	aaattgttga	ttttaccaat	gtggctcagg	ccaaatggtt	tagtatccca	660
tcagtggaaa	ttcctttctt	aacctacggg	gttaaattct	acccaagtgc	cattttaact	720
atggcaccga	ttgcctttgt	tacaatgaca	gaacattttg	gacacattat	ggctctaaat	780
agtttgacaa	aaagagatta	tttcaaggat	ccaggacttg	aaaagacttt	aactgggtgat	840
ggttttgcgc	aaatcattgc	cggcttctta	ggggcacctc	cggtcacttc	ttatggtgaa	900
aacatcggtg	taatggcttt	gaataaaaata	ttctcggtct	atgttattgc	aggtgccgca	960
gtgattgccg	ctctcctcag	ttttatcggt	aaggatcag	ccttaattca	atctattcca	1020
acaccagtta	ttggaggtat	atcagttgcc	ttgtttggtg	tgatagcttc	tagcggtttg	1080
aaaatcttga	ttgaatccaa	agttgatatg	gataataaga	aaaacttatt	gattgctagt	1140
gttatttttg	tctctgggat	tggaggattg	atgcttcaag	taaatggtct	tcaaatttca	1200
ggtgtcgctt	tctcaacact	ccttggcatc	atcttatatc	aggtacttcc	tgaaaaatag	1260

<210> SEQ ID NO 442

<211> LENGTH: 419

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 442

Met	Lys	Asp	Val	Ile	Tyr	Asp	Val	Glu	Glu	Val	Pro	Lys	Ala	Gly	Met
1				5					10					15	
Leu	Val	Gly	Leu	Ser	Phe	Gln	His	Leu	Phe	Ala	Met	Phe	Gly	Ala	Thr
			20					25					30		
Val	Leu	Val	Pro	Ile	Leu	Val	Gly	Ile	Asp	Pro	Ser	Val	Ala	Leu	Leu
			35				40					45			
Ser	Ser	Gly	Leu	Gly	Thr	Leu	Ala	His	Leu	Ser	Val	Thr	Lys	Phe	Lys
	50					55					60				
Ile	Pro	Ala	Tyr	Met	Gly	Ser	Ser	Phe	Ala	Tyr	Ile	Ala	Ala	Met	Gln
65					70					75					80
Leu	Leu	Met	Lys	Thr	Asn	Gly	Ile	Gly	Ala	Val	Ala	Gln	Gly	Ala	Met
				85					90					95	
Thr	Gly	Gly	Leu	Val	Tyr	Leu	Ile	Val	Ala	Leu	Ile	Val	Lys	Ala	Ile
			100					105					110		
Gly	Asn	Asp	Trp	Ile	Asp	Asn	Ile	Leu	Pro	Pro	Ile	Val	Val	Gly	Pro
			115				120					125			
Ile	Val	Met	Val	Ile	Gly	Leu	Ser	Leu	Ala	Ser	Thr	Ala	Val	Asn	Asp
	130					135					140				
Val	Met	Leu	Lys	Asn	Gly	Asn	Tyr	Asn	Leu	Thr	Tyr	Leu	Val	Ile	Gly
145					150					155					160
Leu	Val	Thr	Leu	Leu	Ser	Val	Ile	Phe	Phe	Asn	Ile	Tyr	Gly	Lys	Gly
				165					170					175	
Ile	Val	Ala	Ile	Val	Pro	Leu	Leu	Leu	Gly	Leu	Leu	Val	Gly	Tyr	Val
			180					185					190		
Val	Ala	Leu	Leu	Val	Gly	Val	Leu	Thr	Gly	Gln	Glu	Ile	Val	Asp	Phe
	195						200					205			
Thr	Asn	Val	Ala	Gln	Ala	Lys	Trp	Phe	Ser	Ile	Pro	Ser	Val	Glu	Ile
	210					215					220				
Pro	Phe	Leu	Thr	Tyr	Gly	Val	Lys	Phe	Tyr	Pro	Ser	Ala	Ile	Leu	Thr
225					230					235					240
Met	Ala	Pro	Ile	Ala	Phe	Val	Thr	Met	Thr	Glu	His	Phe	Gly	His	Ile
				245					250					255	
Met	Val	Leu	Asn	Ser	Leu	Thr	Lys	Arg	Asp	Tyr	Phe	Lys	Asp	Pro	Gly
			260					265					270		
Leu	Glu	Lys	Thr	Leu	Thr	Gly	Asp	Gly	Phe	Ala	Gln	Ile	Ile	Ala	Gly
		275				280						285			
Phe	Leu	Gly	Ala	Pro	Pro	Val	Thr	Ser	Tyr	Gly	Glu	Asn	Ile	Gly	Val
	290					295					300				
Met	Ala	Leu	Asn	Lys	Ile	Phe	Ser	Val	Tyr	Val	Ile	Ala	Gly	Ala	Ala
305					310					315					320
Val	Ile	Ala	Ala	Leu	Leu	Ser	Phe	Ile	Gly	Lys	Val	Ser	Ala	Leu	Ile
				325					330					335	
Gln	Ser	Ile	Pro	Thr	Pro	Val	Ile	Gly	Gly	Ile	Ser	Val	Ala	Leu	Phe
			340					345					350		
Gly	Val	Ile	Ala	Ser	Ser	Gly	Leu	Lys	Ile	Leu	Ile	Glu	Ser	Lys	Val
	355					360						365			
Asp	Met	Asp	Asn	Lys	Lys	Asn	Leu	Leu	Ile	Ala	Ser	Val	Ile	Leu	Val
	370					375					380				
Ser	Gly	Ile	Gly	Gly	Leu	Met	Leu	Gln	Val	Asn	Gly	Leu	Gln	Ile	Ser
385					390					395					400
Gly	Val	Ala	Phe	Ser	Thr	Leu	Leu	Gly	Ile	Ile	Leu	Tyr	Gln	Val	Leu
				405					410					415	
Pro	Glu	Lys													

<210> SEQ ID NO 443

<211> LENGTH: 459

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<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 443
atgaaaaaac gattgtttgt gcttagcttg atcctccttg tagctttgga tcaacttagt    60
aaattttgga ttgtttctca tatagcgctt ggagaagtga aaccctttat cccaggtatc    120
gtcagcttga cttacttgca aaacaatggg gctgcctttt ccatattgca ggaccagcaa    180
tggttctttg ttgtcataac ggttttagtt atcggttatg ctatttatta ccttgctact    240
catccccatt taaatatctg gaaacaatta gctctcttgc ttattatttc tggtggaatc    300
gggaatttta ttgatcgctt gcgtttagct tacgtgattg atatgattca tttagacttt    360
gtggattttg ccatttttaa tgtggcagat tcatacctta ccgttggtgt catattatta    420
ttgatatggt tatggaaaga agaggattat ggaaattaa                                459

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<210> SEQ ID NO 444
<211> LENGTH: 152
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 444
Met Lys Lys Arg Leu Phe Val Leu Ser Leu Ile Leu Leu Val Ala Leu
 1             5             10            15
Asp Gln Leu Ser Lys Phe Trp Ile Val Ser His Ile Ala Leu Gly Glu
      20            25            30
Val Lys Pro Phe Ile Pro Gly Ile Val Ser Leu Thr Tyr Leu Gln Asn
      35            40            45
Asn Gly Ala Ala Phe Ser Ile Leu Gln Asp Gln Gln Trp Phe Phe Val
      50            55            60
Val Ile Thr Val Leu Val Ile Gly Tyr Ala Ile Tyr Tyr Leu Ala Thr
      65            70            75            80
His Pro His Leu Asn Ile Trp Lys Gln Leu Ala Leu Leu Leu Ile Ile
      85            90            95
Ser Gly Gly Ile Gly Asn Phe Ile Asp Arg Leu Arg Leu Ala Tyr Val
      100           105           110
Ile Asp Met Ile His Leu Asp Phe Val Asp Phe Ala Ile Phe Asn Val
      115           120           125
Ala Asp Ser Tyr Leu Thr Val Gly Val Ile Leu Leu Leu Ile Cys Leu
      130           135           140
Trp Lys Glu Glu Asp Tyr Gly Asn
145                        150

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<210> SEQ ID NO 445
<211> LENGTH: 1287
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 445
atgattaatc cttcaaaaaca aaaccaaacg attttttttat ggaatatgtt aggaagttta    60
tcaacagctg taatatcagt tatattactt atggtgggta ctaggttact aacttcggct    120
gattcagata tttacgcctt tgcctattct tttgctaata tgatggtagt tgttggactt    180
tttcagggtc gtaattatca agcaacagat attaatgaaa aatattcctt tagtcagtac    240
ttagtggcaa gactgatgac ttgtttatta atgttagcca taacagtaat ttatttaacg    300
ttaactaaga cagatagcta caagagtaca attgtctttc tagtctgttt ctatagatcg    360
acagatgctt tttcggattt atatcaggga atgttccaac aacatgaacg gctggatatt    420
gcaggtaaat cgctagccta cagaaatact cttattttta tgggtgtacac agcaataata    480
ttatattcca aaaatcttac tttagcatta gtagctgtct gtatagtttc attagttttt    540
ataatgtatt atgacattgg tcattcgaaa aaatttcaaa agttgatgtt tagtgaatta    600
ttaagtaata tttcatttca aaacagttta aagttattaa aagaaaagttt tccacttttt    660
ctaaacgggt ttttgattat ctatatattt actcaaccaa aatacgctat tgaactaatg    720
acgactttag gtgaagttgc tttgggctct caaacaattt ttaatatattt atttatgccca    780
gcctttgtta tgaatttgct aattttattt tttagacctc atattacaca gatggctatt    840

```

gctttaatca	gaggtcaaat	aaaagagttt	aataagatac	aagttcaatt	gtttgcttat	900
ttaggagttt	tttcactgat	agcgttagtt	ggaagtgggt	tgtttggtat	tcccttttta	960
tcaatactat	atggtactaa	ccttacggat	tattgggtag	attttatgtt	gattatgcta	1020
ggaggctcga	ttggtagttt	tgcgacagtt	atcgataata	tcttaaccgc	tatgagaaaa	1080
cagcaacttc	ttcttattcc	atatacagga	ggatttttga	tttcgttatt	aattaccaat	1140
ctttttgtta	tgaaatatca	tatttttagga	gctgctttga	gctttttaat	aacaatgttg	1200
gtttggttgg	gattatccat	tatgatttat	ctatttatta	tgaatagatt	taagaaggga	1260
agagttaatg	caacaatcta	tgactaa				1287

<210> SEQ ID NO 446

<211> LENGTH: 428

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 446

Met	Ile	Asn	Pro	Ser	Lys	Gln	Asn	Gln	Thr	Ile	Phe	Leu	Trp	Asn	Met
1				5					10					15	
Leu	Gly	Ser	Leu	Ser	Thr	Ala	Val	Ile	Ser	Val	Ile	Leu	Leu	Met	Val
			20					25					30		
Val	Thr	Arg	Leu	Leu	Thr	Ser	Ala	Asp	Ser	Asp	Ile	Tyr	Ala	Phe	Ala
		35					40					45			
Tyr	Ser	Phe	Ala	Asn	Met	Met	Val	Val	Val	Gly	Leu	Phe	Gln	Val	Arg
	50					55					60				
Asn	Tyr	Gln	Ala	Thr	Asp	Ile	Asn	Glu	Lys	Tyr	Ser	Phe	Ser	Gln	Tyr
65					70					75				80	
Leu	Val	Ala	Arg	Leu	Met	Thr	Cys	Leu	Leu	Met	Leu	Ala	Ile	Thr	Val
			85						90					95	
Ile	Tyr	Leu	Thr	Leu	Thr	Lys	Thr	Asp	Ser	Tyr	Lys	Ser	Thr	Ile	Val
		100						105					110		
Phe	Leu	Val	Cys	Phe	Tyr	Arg	Ser	Thr	Asp	Ala	Phe	Ser	Asp	Leu	Tyr
		115					120					125			
Gln	Gly	Met	Phe	Gln	Gln	His	Glu	Arg	Leu	Asp	Ile	Ala	Gly	Lys	Ser
	130					135					140				
Leu	Ala	Tyr	Arg	Asn	Thr	Leu	Ile	Phe	Met	Val	Tyr	Thr	Ala	Ile	Ile
145					150					155					160
Leu	Tyr	Ser	Lys	Asn	Leu	Thr	Leu	Ala	Leu	Val	Ala	Val	Cys	Ile	Val
			165						170					175	
Ser	Leu	Val	Phe	Ile	Met	Tyr	Tyr	Asp	Ile	Gly	His	Ser	Lys	Lys	Phe
		180						185					190		
Gln	Lys	Leu	Met	Phe	Ser	Glu	Leu	Leu	Ser	Asn	Ile	Ser	Phe	Gln	Asn
	195						200					205			
Ser	Leu	Lys	Leu	Leu	Lys	Glu	Ser	Phe	Pro	Leu	Phe	Leu	Asn	Gly	Phe
	210					215					220				
Leu	Ile	Ile	Tyr	Ile	Tyr	Thr	Gln	Pro	Lys	Tyr	Ala	Ile	Glu	Leu	Met
225					230					235					240
Thr	Thr	Leu	Gly	Glu	Val	Ala	Leu	Gly	Ser	Gln	Thr	Ile	Phe	Asn	Ile
			245						250					255	
Leu	Phe	Met	Pro	Ala	Phe	Val	Met	Asn	Leu	Leu	Ile	Leu	Phe	Phe	Arg
		260						265					270		
Pro	His	Ile	Thr	Gln	Met	Ala	Ile	Ala	Leu	Ile	Arg	Gly	Gln	Ile	Lys
	275						280					285			
Glu	Phe	Asn	Lys	Ile	Gln	Val	Gln	Leu	Phe	Ala	Tyr	Leu	Gly	Val	Phe
	290					295					300				
Ser	Leu	Ile	Ala	Leu	Val	Gly	Ser	Gly	Leu	Phe	Gly	Ile	Pro	Phe	Leu
305					310					315					320
Ser	Ile	Leu	Tyr	Gly	Thr	Asn	Leu	Thr	Asp	Tyr	Trp	Val	Asp	Phe	Met
			325						330					335	
Leu	Ile	Met	Leu	Gly	Gly	Ser	Ile	Gly	Ser	Phe	Ala	Thr	Val	Ile	Asp

			340					345					350			
Asn	Ile	Leu	Thr	Ala	Met	Arg	Lys	Gln	Gln	Leu	Leu	Leu	Ile	Pro	Tyr	
		355					360					365				
Thr	Gly	Gly	Phe	Leu	Ile	Ser	Leu	Leu	Ile	Thr	Asn	Leu	Phe	Val	Met	
	370					375					380					
Lys	Tyr	His	Ile	Leu	Gly	Ala	Ala	Leu	Ser	Phe	Leu	Ile	Thr	Met	Leu	
385					390					395					400	
Val	Trp	Leu	Gly	Leu	Ser	Ile	Met	Ile	Tyr	Leu	Phe	Ile	Met	Asn	Arg	
			405						410					415		
Phe	Lys	Lys	Gly	Arg	Val	Asn	Ala	Thr	Ile	Tyr	Asp					
			420					425								

<210> SEQ ID NO 447
 <211> LENGTH: 696
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 447

gtgaaaaagt	taatcattat	tcctgcttac	aatgaaagca	gtaatattgt	caatactata	60
cgtactattg	aatcagatgc	cccggatttt	gactatatca	ttattgatga	ttgctcaacg	120
gataatacgt	tagcaatatg	tcaaaaacag	gggttcaatg	ttatttcttt	gcccatatac	180
ctgggaattg	gcggtgcggt	gcaaactggc	tatcgttatg	cacaaagatg	tggatatgac	240
gttgcagttc	aagtagatgg	agatggtcag	cacaatccat	gctatttgga	aaaaatgggt	300
gaggtattag	ttcaatcttc	agtaaataatg	gtaattggat	cacgatttat	cacaaaagaa	360
gggtttcagt	catcatttgc	tcgacgtatc	ggcataaagt	attttacttg	gcttattgcg	420
ctactaacag	gaaaaaaaaat	aacagatgca	acgtcaggtc	taaggttaat	tgaccgttca	480
ttgattgaac	gttttgctaa	tcattatcca	gatgattatc	ctgaacctga	aacagttggt	540
gatgtattgg	ttagtcattt	taaagtgaaa	gaaattcctg	ttgtaatgaa	tgagcgacaa	600
ggcgggtgtg	catctatctc	gttgacgaaa	tcggtctatt	atatgattaa	agtgacttta	660
gctatttttag	ttgtagaatt	gaaaggaaat	cgttaa			696

<210> SEQ ID NO 448
 <211> LENGTH: 231
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 448

Met	Lys	Lys	Leu	Ile	Ile	Ile	Pro	Ala	Tyr	Asn	Glu	Ser	Ser	Asn	Ile
1			5						10					15	
Val	Asn	Thr	Ile	Arg	Thr	Ile	Glu	Ser	Asp	Ala	Pro	Asp	Phe	Asp	Tyr
		20					25					30			
Ile	Ile	Ile	Asp	Asp	Cys	Ser	Thr	Asp	Asn	Thr	Leu	Ala	Ile	Cys	Gln
	35				40					45					
Lys	Gln	Gly	Phe	Asn	Val	Ile	Ser	Leu	Pro	Ile	Asn	Leu	Gly	Ile	Gly
	50				55				60						
Gly	Ala	Val	Gln	Thr	Gly	Tyr	Arg	Tyr	Ala	Gln	Arg	Cys	Gly	Tyr	Asp
65			70						75					80	
Val	Ala	Val	Gln	Val	Asp	Gly	Asp	Gly	Gln	His	Asn	Pro	Cys	Tyr	Leu
		85						90					95		
Glu	Lys	Met	Val	Glu	Val	Leu	Val	Gln	Ser	Ser	Val	Asn	Met	Val	Ile
		100						105					110		
Gly	Ser	Arg	Phe	Ile	Thr	Lys	Glu	Gly	Phe	Gln	Ser	Ser	Phe	Ala	Arg
	115					120						125			
Arg	Ile	Gly	Ile	Lys	Tyr	Phe	Thr	Trp	Leu	Ile	Ala	Leu	Leu	Thr	Gly
	130					135					140				
Lys	Lys	Ile	Thr	Asp	Ala	Thr	Ser	Gly	Leu	Arg	Leu	Ile	Asp	Arg	Ser
145				150					155					160	
Leu	Ile	Glu	Arg	Phe	Ala	Asn	His	Tyr	Pro	Asp	Asp	Tyr	Pro	Glu	Pro
			165					170						175	

Glu	Thr	Val	Val	Asp	Val	Leu	Val	Ser	His	Phe	Lys	Val	Lys	Glu	Ile
			180					185					190		
Pro	Val	Val	Met	Asn	Glu	Arg	Gln	Gly	Gly	Val	Ser	Ser	Ile	Ser	Leu
		195					200					205			
Thr	Lys	Ser	Val	Tyr	Tyr	Met	Ile	Lys	Val	Thr	Leu	Ala	Ile	Leu	Val
	210					215					220				
Val	Arg	Leu	Lys	Gly	Asn	Arg									
225					230										

<210> SEQ ID NO 449

<211> LENGTH: 2475

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 449

atgattaaag	acacattttt	aaaaaccaat	tggttaaata	ttagtcacca	tattatcctt	60
cttgttttgc	gtttttat	cagtttttac	agtttggcga	aagaactagt	aagctccacg	120
gcacaaccgg	taaactatta	tgctcattta	ctaaatgttt	cttttgtggg	atatattata	180
tcaactgattg	gattatctta	ttatttgagt	cgccaagtta	gtcgacagtt	gtttttgaaa	240
actagtttta	ttgtgatatc	ttatctaatt	gtcagctatt	gggtacaaat	aacacagcac	300
ctgaatgata	aacggtttga	tatctgggtca	ttaactaaaa	atcaatttta	tcaatttcaa	360
gctctacctt	ctttactcat	tatttttagtg	atggccactt	taataaaaaat	attggcagca	420
tattttgcaa	tagaaaaaga	tagatttgagg	ctattaggct	atcaaggtaa	tactttttct	480
gtagctctga	ttttagcagt	tgtgccaatt	aatgacatac	atctgttaaa	actaataagt	540
tctcgatttt	ctgaattagt	aacagcaggt	aatagccaaa	ttgcactgtt	aaaaataagt	600
ggactgttga	tagttttact	tgctcatattt	gcaacaatca	tatacgtggg	tttaaatgct	660
ctaaaacacc	ttaagtcaaa	taaaccttca	ttttcagtag	cagctactac	tagtttgttt	720
ttagcattag	tttttaacta	tacgttccag	tatggagtaa	aagggtgatga	agcattgcta	780
ggatattatg	ttttccctgg	agctactctt	tttcagatag	tagctattac	actagttgct	840
cttttagcat	acgtgataac	gaatagatat	tggccaacta	ccttcttttt	gcttattctg	900
ggaacaatta	tttctgttgt	taatgattta	aaagaatcaa	tgagaagcga	gccgttatta	960
gtaactgatt	ttgtttgggt	acaagaatta	ggtttagtga	caagctttgt	taaaaaatcg	1020
gtgattgtag	aaatggttgt	aggacttgct	atttgtattg	tggtagcttg	gtatctacat	1080
ggccgagttt	tagcagggaa	attattttatg	agccctgtca	aacgggcaag	tgctgtatta	1140
ggtttattta	ttgtatcttg	tagtatgtta	ataccatttt	cttatgaaaa	agaaggtaaa	1200
atattatctg	gtcttccgat	tatttcgggt	ttaaataatg	ataatgacat	aaactggtta	1260
ggtttttcaa	caaagtctag	gtacaaatct	ttagcatatg	tttggacaag	acaggtgacc	1320
aagaaaaata	tggaaaaacc	gacaaattat	agccaagaaa	caatagcgag	tatcgctcag	1380
aagtaccaa	aattagcaga	agatattaat	aaagacagaa	aaaataatat	tgctgaccac	1440
acggttattt	atcttttaag	tgaaagcttg	tcagatcctg	atagagtatc	aaatgttact	1500
gttagccacg	atgttttacc	taatatcaag	gcaatcaaaa	atagcacaac	tcggtgactc	1560
atgcagtcag	actcctacgg	gggtggaacg	gctaacatgg	agtttcaaac	gttaacaagc	1620
ttaccttttt	ataatttttc	ttcttcagta	tctgttcttt	attcagaagt	ctttcctaaa	1680
atggccaaac	ctcatacgat	tagtgagttt	taccaaggaa	aaaatcgtat	tgcgatgcat	1740
cctgctagtg	ctaacaattt	taatagaaaa	acagtttata	gtaatttagg	tttttccaaa	1800
ttcttagctc	tatcgggttc	taaggataag	tttaagaaca	ttgaaaatgt	cggtttattg	1860
actagcgata	aaactgtcta	taataatatt	ttatctttta	ttaatcctag	tgaaagccaa	1920
tttttctcag	ttattacaat	gcaaaatcat	attccttggt	catccgatta	tcctgaagaa	1980
attgttgctg	aaggaaaaaa	tttcacggaa	gaagaaaaatc	acaacctaac	aagttagtct	2040
cggttattat	cgtttactga	taaggaaaca	agagcatttt	tagaaaaatt	aacacaaatt	2100
aacaagccta	tcacagtggg	gttttacgga	gatcattttac	ccggtttata	tcctgatagt	2160
gcttttaaca	agcatattga	aaataaatatc	cttactgatt	attttatttg	gagtaatggg	2220
actaacgaga	aaaaaaatca	tccgcttatc	aactcaagtg	attttactgc	agctttatct	2280
gagcagatctg	attcaaaagt	atcaccttac	tatgctttgt	taacagaggt	actgaataaa	2340
gctatgtctg	ataaatcacc	agatagtcct	gaagttaaag	ctatttcagaa	tgatttataaa	2400
aatatccaat	acgatgtgac	tataggaaaa	ggttaccctt	tgaaacacaa	aacttttttt	2460
aagatatcac	gttaa					2475

<210> SEQ ID NO 450

<211> LENGTH: 824

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 450

Met	Ile	Lys	Asp	Thr	Phe	Leu	Lys	Thr	Asn	Trp	Leu	Asn	Ile	Ser	His
1				5					10					15	
His	Ile	Ile	Leu	Leu	Val	Phe	Gly	Phe	Tyr	Phe	Ser	Phe	Tyr	Ser	Leu
			20					25					30		
Ala	Lys	Glu	Leu	Val	Ser	Ser	Thr	Ala	Gln	Pro	Val	Asn	Tyr	Tyr	Ala
		35					40					45			
His	Leu	Leu	Asn	Val	Ser	Phe	Val	Gly	Tyr	Ile	Ile	Ser	Leu	Ile	Gly
	50					55					60				
Leu	Ser	Tyr	Tyr	Leu	Ser	Arg	Gln	Val	Ser	Arg	Gln	Leu	Phe	Leu	Lys
65					70					75					80
Thr	Ser	Phe	Ile	Val	Ile	Ser	Tyr	Leu	Ile	Val	Ser	Tyr	Trp	Val	Gln
				85					90					95	
Ile	Thr	Gln	His	Leu	Asn	Asp	Lys	Arg	Phe	Asp	Ile	Trp	Ser	Leu	Thr
			100					105					110		
Lys	Asn	Gln	Phe	Tyr	Gln	Phe	Gln	Ala	Leu	Pro	Ser	Leu	Leu	Ile	Ile
		115					120					125			
Leu	Val	Met	Ala	Thr	Leu	Ile	Lys	Ile	Leu	Ala	Ala	Tyr	Phe	Ala	Ile
	130					135					140				
Glu	Lys	Asp	Arg	Phe	Gly	Leu	Leu	Gly	Tyr	Gln	Gly	Asn	Thr	Phe	Ser
145					150					155					160
Val	Ala	Leu	Ile	Leu	Ala	Val	Val	Pro	Ile	Asn	Asp	Ile	His	Leu	Leu
				165					170					175	
Lys	Leu	Ile	Ser	Ser	Arg	Phe	Ser	Glu	Leu	Val	Thr	Ala	Gly	Asn	Ser
			180					185					190		
Gln	Ile	Ala	Leu	Leu	Lys	Ile	Ser	Gly	Leu	Leu	Ile	Val	Leu	Leu	Val
	195						200					205			
Ile	Phe	Ala	Thr	Ile	Ile	Tyr	Val	Val	Leu	Asn	Ala	Leu	Lys	His	Leu
	210					215					220				
Lys	Ser	Asn	Lys	Pro	Ser	Phe	Ser	Val	Ala	Ala	Thr	Thr	Ser	Leu	Phe
225					230					235					240
Leu	Ala	Leu	Val	Phe	Asn	Tyr	Thr	Phe	Gln	Tyr	Gly	Val	Lys	Gly	Asp
				245					250					255	
Glu	Ala	Leu	Leu	Gly	Tyr	Tyr	Val	Phe	Pro	Gly	Ala	Thr	Leu	Phe	Gln
			260				265						270		
Ile	Val	Ala	Ile	Thr	Leu	Val	Ala	Leu	Leu	Ala	Tyr	Val	Ile	Thr	Asn
	275						280						285		
Arg	Tyr	Trp	Pro	Thr	Thr	Phe	Phe	Leu	Leu	Ile	Leu	Gly	Thr	Ile	Ile
	290					295					300				
Ser	Val	Val	Asn	Asp	Leu	Lys	Glu	Ser	Met	Arg	Ser	Glu	Pro	Leu	Leu
305					310					315					320
Val	Thr	Asp	Phe	Val	Trp	Leu	Gln	Glu	Leu	Gly	Leu	Val	Thr	Ser	Phe
				325					330					335	
Val	Lys	Lys	Ser	Val	Ile	Val	Glu	Met	Val	Val	Gly	Leu	Ala	Ile	Cys
			340					345					350		
Ile	Val	Val	Ala	Trp	Tyr	Leu	His	Gly	Arg	Val	Leu	Ala	Gly	Lys	Leu
	355						360					365			
Phe	Met	Ser	Pro	Val	Lys	Arg	Ala	Ser	Ala	Val	Leu	Gly	Leu	Phe	Ile
	370					375					380				
Val	Ser	Cys	Ser	Met	Leu	Ile	Pro	Phe	Ser	Tyr	Glu	Lys	Glu	Gly	Lys
385					390					395					400
Ile	Leu	Ser	Gly	Leu	Pro	Ile	Ile	Ser	Ala	Leu	Asn	Asn	Asp	Asn	Asp
				405					410					415	


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<400> SEQUENCE: 451
atgtataaag tttcaattat ttgcaccaat tataacaaag ctcccttggat atctgatgca      60
cttgacagtt ttttaagcca agtgacagat tttgaggttg aaattattgt tattgatgat      120
gcttctacag atgactcacg agagatttta aagagttatc aaaaaaagtc ttcaggaaaa      180
attaaattac tctttaacga aactaatatt ggaataacaa agacttggat aaaagcatgc      240
ctttatgcaa aaggcaaata tattgctaga tgtgatgggtg atgattactg gacggatagt      300
tttaaactcc aaaaacaagt tgatgtctta gaagcttcca aacggtcacg atgggtgtaat      360
actgattttg actttgtaaa tagtcaaggc gacttattat atgctaatagc tttttcatct      420
gggtcatacac ctttgacaga tacttacgaa aaagttttag ccttaaaagg gatgacgatg      480
gcatcgacat ggtagttga tgctgattta atgagacaag taaaccaaaa aatcaatgta      540
gatacaccag acgatacttt tgatattcaa ctagagttat ttcaactgac tcaactgacc      600
tatattaaag actcaacgac gatttatcgc atgacaaccg attctgattc aagacctact      660
gatacaccaa aaatgattta tcgtattcaa aaactacttg atactcagtt aaattactta      720
aaaaagtata atcaggtaga tacaaaagaa gtgtctgaac tattattaca acaagatgct      780
aagcaagaaa tacgaattca tgagttgagt tgctttattc aagaattaca acaactatc      840
gtagataaaa caaagcagca agaaacacgt gaagtggagt tgcaaaatgt catagaagaa      900
caaaaaaatc aactatctga attaagacaa caataccatg ccattattaa ttcacgtcaa      960
tggaataaca cgtctaagct cattgctttt attaggagaa aaaaatga      1008

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<210> SEQ ID NO 452
<211> LENGTH: 335
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 452

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Met Tyr Lys Val Ser Ile Ile Cys Thr Asn Tyr Asn Lys Ala Pro Trp
1          5          10          15
Ile Ser Asp Ala Leu Asp Ser Phe Leu Ser Gln Val Thr Asp Phe Glu
20          25          30
Val Glu Ile Ile Val Ile Asp Asp Ala Ser Thr Asp Asp Ser Arg Glu
35          40          45
Ile Leu Lys Ser Tyr Gln Lys Lys Ser Ser Gly Lys Ile Lys Leu Leu
50          55          60
Phe Asn Glu Thr Asn Ile Gly Ile Thr Lys Thr Trp Ile Lys Ala Cys
65          70          75          80
Leu Tyr Ala Lys Gly Lys Tyr Ile Ala Arg Cys Asp Gly Asp Asp Tyr
85          90          95
Trp Thr Asp Ser Phe Lys Leu Gln Lys Gln Val Asp Val Leu Glu Ala
100         105         110
Ser Lys Arg Ser Arg Trp Cys Asn Thr Asp Phe Asp Phe Val Asn Ser
115         120         125
Gln Gly Asp Leu Leu Tyr Ala Asn Ala Phe Ser Ser Gly His Thr Pro
130         135         140
Leu Thr Asp Thr Tyr Glu Lys Val Leu Ala Leu Lys Gly Met Thr Met
145         150         155         160
Ala Ser Thr Trp Leu Val Asp Ala Asp Leu Met Arg Gln Val Asn Gln
165         170         175
Lys Ile Asn Val Asp Thr Pro Asp Asp Thr Phe Asp Ile Gln Leu Glu
180         185         190
Leu Phe Gln Leu Thr Gln Leu Thr Tyr Ile Lys Asp Ser Thr Thr Ile
195         200         205
Tyr Arg Met Thr Thr Asp Ser Asp Ser Arg Pro Thr Asp Thr Pro Lys
210         215         220
Met Ile Tyr Arg Ile Gln Lys Leu Leu Asp Thr Gln Leu Asn Tyr Leu
225         230         235         240
Lys Lys Tyr Asn Gln Val Asp Thr Lys Glu Val Ser Glu Leu Leu Leu
245         250         255
Gln Gln Asp Ala Lys Gln Glu Ile Arg Ile His Glu Leu Ser Cys Phe

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Gly	Thr	Met	Met	Ile	Thr	His	Ala	Leu	Ala	Glu	Glu	Trp	Thr	Thr	Cys	
				165					170						175	
Asp	Gly	Leu	Leu	Met	His	Asp	Trp	Tyr	Leu	Ala	Leu	Leu	Ala	Ser	Ala	
				180				185						190		
Ile	Gly	Lys	Leu	Val	Tyr	Leu	Asp	Ile	Pro	Thr	Glu	Leu	Tyr	Arg	Gln	
		195					200						205			
His	Asp	Ala	Asn	Val	Leu	Gly	Ala	Arg	Thr	Trp	Ser	Lys	Arg	Met	Lys	
	210					215					220					
Asn	Trp	Leu	Thr	Pro	His	His	Leu	Val	Asn	Lys	Tyr	Trp	Trp	Leu	Ile	
225					230					235					240	
Thr	Ser	Ser	Gln	Lys	Gln	Ala	Gln	Leu	Leu	Leu	Asp	Leu	Pro	Leu	Lys	
				245				250						255		
Pro	Asn	Asp	His	Glu	Leu	Val	Thr	Ala	Tyr	Val	Ser	Leu	Leu	Asp	Met	
			260					265						270		
Pro	Phe	Thr	Lys	Arg	Leu	Ala	Thr	Leu	Lys	Arg	Tyr	Gly	Phe	Arg	Lys	
		275					280					285				
Asn	Arg	Ile	Phe	His	Thr	Phe	Ile	Phe	Arg	Ser	Leu	Val	Val	Thr	Leu	
	290					295					300					
Phe	Gly	Tyr	Arg	Arg	Lys											
305					310											

<210> SEQ ID NO 455

<211> LENGTH: 1077

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 455

atgttttttag	cgcttaatga	aatgaaacaa	tccaaattgc	ggtatggttt	gattgctggt	60
ttgctatggt	tggttgccta	tttgatgttc	tttttgtcag	gattggcctt	tggtttgatg	120
caggagaacc	gctcggcggt	tgatcttttg	aaagctgaca	gtgttttact	agccaaggat	180
gctgacgcta	ccttgacctt	atcacagggt	tccagagctc	aagaaaatca	aataacagca	240
gacaaggtag	ctcctcttgc	tcaactcaat	accgtggcgt	ggtcagttaa	aaatcctaag	300
gatgccgaca	aagttaaggt	tagccttttc	gggattgatt	ctaatagctt	tattcgtcct	360
aacattgtaa	aaggtcgatt	atttaagact	aacaaagagg	ttgttttgga	tcaaagcctt	420
gcaaaagagg	aagcttttgc	gattggcaag	gacttttaca	catcgagttc	tagtcaagca	480
ttaactatcg	ttggttatac	tcaaaatgct	agatttagtg	ttgcaccagt	ggtttatatg	540
aatttggaag	cttttgaaac	attaaaatat	ggagaaccac	taccaaaaga	taagcaagtt	600
gttaatgctt	ttatcactaa	aggaagttta	acagattatc	ctaaaaaaga	cttccaaaaa	660
ttagatatta	aaacctttat	tactaaatta	cctgggtata	gcgctcaact	tttaactttt	720
ggctttatga	ttagttttct	tgtcattatt	tcagctatta	ttattggtat	ttttatgtat	780
attttgacta	ttcaaaaggc	acctattttt	gggattatga	aagcgcaagg	aattttctaac	840
aaaacgatta	cgaccgctgt	gcttatgcag	acattctttt	tgagtttttt	aggtagtggt	900
ttagggttgc	taggtacttg	gctgacatca	ttattattac	caacagtagt	accttttcaa	960
agcaattggg	ttttgtattt	ggctatatcc	gtagtatga	tctgttttgc	tctattaggg	1020
accttatttt	ctgtttttta	cattatacga	attgatcctt	tgaaagcaat	tggatag	1077

<210> SEQ ID NO 456

<211> LENGTH: 358

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 456

Met	Phe	Leu	Ala	Leu	Asn	Glu	Met	Lys	Gln	Ser	Lys	Leu	Arg	Tyr	Gly	
1				5					10					15		
Leu	Ile	Ala	Gly	Leu	Leu	Cys	Leu	Val	Ala	Tyr	Leu	Met	Phe	Phe	Leu	
			20					25					30			
Ser	Gly	Leu	Ala	Phe	Gly	Leu	Met	Gln	Glu	Asn	Arg	Ser	Ala	Val	Asp	
		35					40					45				
Leu	Trp	Lys	Ala	Asp	Ser	Val	Leu	Leu	Ala	Lys	Asp	Ala	Asp	Ala	Thr	

50	55	60
Leu Thr Leu Ser Gln Val Ser Arg Ala Gln Glu Asn Gln Ile Thr Ala		
65	70	75
Asp Lys Val Ala Pro Leu Ala Gln Leu Asn Thr Val Ala Trp Ser Val		80
	85	90
Lys Asn Pro Lys Asp Ala Asp Lys Val Lys Val Ser Leu Phe Gly Ile		95
	100	105
Asp Ser Asn Ser Phe Ile Arg Pro Asn Ile Val Lys Gly Arg Leu Phe		110
	115	120
Lys Thr Asn Lys Glu Val Val Leu Asp Gln Ser Leu Ala Lys Glu Glu		125
	130	135
Ala Phe Ala Ile Gly Lys Asp Phe Tyr Thr Ser Ser Ser Gln Ala		140
145	150	155
Leu Thr Ile Val Gly Tyr Thr Gln Asn Ala Arg Phe Ser Val Ala Pro		160
	165	170
Val Val Tyr Met Asn Leu Glu Ala Phe Glu Thr Leu Lys Tyr Gly Glu		175
	180	185
Pro Leu Pro Lys Asp Lys Gln Val Val Asn Ala Phe Ile Thr Lys Gly		190
	195	200
Ser Leu Thr Asp Tyr Pro Lys Lys Asp Phe Gln Lys Leu Asp Ile Lys		205
	210	215
Thr Phe Ile Thr Lys Leu Pro Gly Tyr Ser Ala Gln Leu Leu Thr Phe		220
225	230	235
Gly Phe Met Ile Ser Phe Leu Val Ile Ile Ser Ala Ile Ile Ile Gly		240
	245	250
Ile Phe Met Tyr Ile Leu Thr Ile Gln Lys Ala Pro Ile Phe Gly Ile		255
	260	265
Met Lys Ala Gln Gly Ile Ser Asn Lys Thr Ile Thr Thr Ala Val Leu		270
	275	280
Met Gln Thr Phe Phe Leu Ser Phe Leu Gly Ser Gly Leu Gly Leu Leu		285
	290	295
Gly Thr Trp Leu Thr Ser Leu Leu Leu Pro Thr Val Val Pro Phe Gln		300
305	310	315
Ser Asn Trp Phe Leu Tyr Leu Ala Ile Phe Val Ser Met Ile Cys Phe		320
	325	330
Ala Leu Leu Gly Thr Leu Phe Ser Val Phe Asn Ile Ile Arg Ile Asp		335
	340	345
Pro Leu Lys Ala Ile Gly		350
355		

<210> SEQ ID NO 457

<211> LENGTH: 483

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 457

atgccttact tactaagtcg acacgacagt atcgaaatcg ctatcaaacg gataatgctt	60
atcgtaactt taagcccagc aggttggcac cgattgcacc acttaaaagg aagttatgat	120
cacgcggttg atagagggca tttgctaggt tatgctttag ttggtggact gaaaggtttt	180
gatgcttcta ctggtaatcc tgataatatt gccactcaac taagttgggc taatcaagca	240
aataaaccct acttgacagg tcagaattac tatgaagggt tagtacgtcg tgctttagat	300
aaggggcatc gcgtccgcta ccgtgtcacc ctactttatg atggtgataa tctactagcc	360
agcggtagcc atttggaggc taaatcctct gatgacagct tgacttttaa cgtgtttgtt	420
ccaaatgtcc aagcaggatt gaccgctgac tatcggacgg gacaaatagc tatcaatctc	480
taa	483

<210> SEQ ID NO 458

<211> LENGTH: 160

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 458

```
Met Pro Tyr Leu Leu Ser Arg His Asp Ser Ile Glu Ile Ala Ile Lys
 1           5           10           15
Arg Ile Met Leu Ile Val Thr Leu Ser Pro Ala Gly Trp His Arg Leu
 20           25           30
His His Leu Lys Gly Ser Tyr Asp His Ala Val Asp Arg Gly His Leu
 35           40           45
Leu Gly Tyr Ala Leu Val Gly Gly Leu Lys Gly Phe Asp Ala Ser Thr
 50           55           60
Gly Asn Pro Asp Asn Ile Ala Thr Gln Leu Ser Trp Ala Asn Gln Ala
 65           70           75           80
Asn Lys Pro Tyr Leu Thr Gly Gln Asn Tyr Tyr Glu Gly Leu Val Arg
 85           90           95
Arg Ala Leu Asp Lys Gly His Arg Val Arg Tyr Arg Val Thr Leu Leu
100          105          110
Tyr Asp Gly Asp Asn Leu Leu Ala Ser Gly Ser His Leu Glu Ala Lys
115          120          125
Ser Ser Asp Asp Ser Leu Thr Phe Asn Val Phe Val Pro Asn Val Gln
130          135          140
Ala Gly Leu Thr Ala Asp Tyr Arg Thr Gly Gln Ile Ala Ile Asn Leu
145          150          155          160
```

<210> SEQ ID NO 459

<211> LENGTH: 495

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 459

```
atgtcaatca cttttggtga actcgttggg aattttattc tagtaacagg ttctgtaatc      60
gtcttggttac tcttgatcaa aaaattcgct tggggtgcga ttgaatcgat ttacagaca      120
cgctcacaac aaatctctcg agatattgat caggctgagc aatcacgtct aagtgtcaa      180
cagtttagagg caaaaagtca agctaaccta gatgctagtc gtttacaagc aagtaaaatc      240
attagtgatg ccaaagaaat tgggtcaatta caagggtgata aattggtggc agaagctact      300
gatgaagcaa aacgcttgaa agaaaaagcg ttgacagata ttgaacaaag caaatcagac      360
gctattttcag cagtcaaaac agaaatgtct gatttaacgg ttcttttagc ggaaaaaatt      420
atgggagcca atcttgataa gacggcgcaa agccagctta ttgacagtta tcttgatgac      480
ttaggagaag cttaa                                     495
```

<210> SEQ ID NO 460

<211> LENGTH: 164

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 460

```
Met Ser Ile Thr Phe Gly Glu Leu Val Gly Asn Phe Ile Leu Val Thr
 1           5           10           15
Gly Ser Val Ile Val Leu Leu Leu Leu Ile Lys Lys Phe Ala Trp Gly
 20           25           30
Ala Ile Glu Ser Ile Leu Gln Thr Arg Ser Gln Gln Ile Ser Arg Asp
 35           40           45
Ile Asp Gln Ala Glu Gln Ser Arg Leu Ser Ala Gln Gln Leu Glu Ala
 50           55           60
Lys Ser Gln Ala Asn Leu Asp Ala Ser Arg Leu Gln Ala Ser Lys Ile
 65           70           75           80
Ile Ser Asp Ala Lys Glu Ile Gly Gln Leu Gln Gly Asp Lys Leu Val
 85           90           95
Ala Glu Ala Thr Asp Glu Ala Lys Arg Leu Lys Glu Lys Ala Leu Thr
```

	100		105		110										
Asp	Ile	Glu	Gln	Ser	Lys	Ser	Asp	Ala	Ile	Ser	Ala	Val	Lys	Thr	Glu
	115		120		125										
Met	Ser	Asp	Leu	Thr	Val	Leu	Leu	Ala	Glu	Lys	Ile	Met	Gly	Ala	Asn
	130		135		140										
Leu	Asp	Lys	Thr	Ala	Gln	Ser	Gln	Leu	Ile	Asp	Ser	Tyr	Leu	Asp	Asp
	145		150		155									160	
Leu	Gly	Glu	Ala												

<210> SEQ ID NO 461
 <211> LENGTH: 717
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 461

atggaagaag	ctaaaaatacc	tatgctgaag	cttggtccaa	taaccttttaa	tttgacccta	60
cttgctgttt	gtattgtcac	aattgcgatt	gtctttgcct	ttgttttttg	ggcaagtcgc	120
caaatgaaat	tgaaaccaga	agggaagcaa	actgctttag	aatattttaat	cagttttgtg	180
gatggtattg	gagaagagca	cttagatcat	aatctacaaa	aatcttattc	gctgttactc	240
tttaccattt	ttctctttgt	ggctgtcgct	aataatttag	ggttattttac	taagttagag	300
acagttaatg	gctataacct	atggacctcg	ccaacagcca	atctggcttt	tgaccttgct	360
ctatctcttt	ttattacctt	aatggtacac	attgaagggg	ttagacggcg	tggcttggtt	420
gcccatttga	aacgtttggc	tacaccgtgg	ccaatgactc	cgatgaattt	attagaagag	480
ttcacaaatt	tcttatcact	tgccattagg	ttattcggtg	atatctttgc	cggggaagtt	540
gttacagggt	tgattgttca	actggccaat	tatcgagttt	attggtggcc	gattgctttc	600
ctagtcaata	tggcgtggac	agccttttca	gtctttattt	cctgcataca	ggctttcgtt	660
ttcacaaaac	tgacagcgac	ctatctagga	aagaaaagtc	atgaatcaga	agaataa	717

<210> SEQ ID NO 462
 <211> LENGTH: 238
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 462

Met	Glu	Glu	Ala	Lys	Ile	Pro	Met	Leu	Lys	Leu	Gly	Pro	Ile	Thr	Phe
1				5					10					15	
Asn	Leu	Thr	Leu	Leu	Ala	Val	Cys	Ile	Val	Thr	Ile	Ala	Ile	Val	Phe
			20					25					30		
Ala	Phe	Val	Phe	Trp	Ala	Ser	Arg	Gln	Met	Lys	Leu	Lys	Pro	Glu	Gly
		35				40					45				
Lys	Gln	Thr	Ala	Leu	Glu	Tyr	Leu	Ile	Ser	Phe	Val	Asp	Gly	Ile	Gly
	50				55					60					
Glu	Glu	His	Leu	Asp	His	Asn	Leu	Gln	Lys	Ser	Tyr	Ser	Leu	Leu	Leu
65				70					75					80	
Phe	Thr	Ile	Phe	Leu	Phe	Val	Ala	Val	Ala	Asn	Asn	Leu	Gly	Leu	Phe
			85					90					95		
Thr	Lys	Leu	Glu	Thr	Val	Asn	Gly	Tyr	Asn	Leu	Trp	Thr	Ser	Pro	Thr
		100					105					110			
Ala	Asn	Leu	Ala	Phe	Asp	Leu	Ala	Leu	Ser	Leu	Phe	Ile	Thr	Leu	Met
	115					120					125				
Val	His	Ile	Glu	Gly	Val	Arg	Arg	Gly	Leu	Val	Ala	His	Leu	Lys	
	130				135				140						
Arg	Leu	Ala	Thr	Pro	Trp	Pro	Met	Thr	Pro	Met	Asn	Leu	Leu	Glu	Glu
145			150					155						160	
Phe	Thr	Asn	Phe	Leu	Ser	Leu	Ala	Ile	Arg	Leu	Phe	Gly	Asn	Ile	Phe
			165					170					175		
Ala	Gly	Glu	Val	Val	Thr	Gly	Leu	Ile	Val	Gln	Leu	Ala	Asn	Tyr	Arg
		180					185					190			
Val	Tyr	Trp	Trp	Pro	Ile	Ala	Phe	Leu	Val	Asn	Met	Ala	Trp	Thr	Ala

	195						200					205							
Phe	Ser	Val	Phe	Ile	Ser	Cys	Ile	Gln	Ala	Phe	Val	Phe	Thr	Lys	Leu				
	210						215					220							
Thr	Ala	Thr	Tyr	Leu	Gly	Lys	Lys	Val	Asn	Glu	Ser	Glu	Glu						
225						230					235								

<210> SEQ ID NO 463
 <211> LENGTH: 1128
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 463

atggttttat	ttcatttaat	caaaaaagaa	agtttacaga	tttttagaaa	ccgaacagcc	60
ttattgatga	tggtgatttt	tccaattttg	atgatcggtta	ttttaagttt	tgccttttaa	120
tcaagtttta	atactgcgac	aacagtcctt	aaattgacca	ttcgttacca	attagagggt	180
gaaaaaacgg	attaccagaa	aaattttctt	gcttttttaa	aagtttttaa	ccaaaaactt	240
catttagaga	ctaaacctag	taattctctt	gaaaaagatc	gacaaagggt	cagtgaagga	300
gccttaacgg	ctgttttaga	agtgaagaag	aatcagacca	ttaagggttat	tactaataat	360
attaatcagc	aaaatgcaga	tttgatcaat	atgctagtaa	aaaattatgt	tgataatgct	420
aaaacttatg	actcgatagc	agctctttat	cctcaacaat	taaatcatat	cagaaagcga	480
agtgtggact	atgttaaggt	cagttcaata	cagacaagta	aaggaatgac	atcagctgat	540
tattatgcta	tttccatggt	taccatgatt	actttttata	gtatgatgtc	tgcgatgaac	600
cttgttttgt	cagatcgta	acaacggatt	acaaatcgta	ttcacttaac	aggagtttct	660
ccaagttttt	tggtctttgg	gaaattaata	ggtgctatgt	tagcaacaac	tggtcaattg	720
agtcttttat	acattttttac	aagggttggt	ttacgagtta	attggggcac	taatgagtgg	780
atgcttattg	gtataacagc	ctccttagtc	tatctctctg	tagctatagg	tatcgggcta	840
ggtataagca	ttaaaaaatga	ggctttttta	acggttgcat	ccaatactat	tattcctata	900
ttcgccctttt	taggaggcag	ttacgttcca	ttgacaacat	tacacagctc	tattattaat	960
caattgtcga	atataatctcc	tattaaatgg	gttaatgata	gtttgttcta	tcttattttt	1020
ggtggtcaat	ataatccgat	tcctgtaact	ttgatcggtta	atattagtat	cggaacaatt	1080
tttataatat	tggcattgat	aggtatgaga	aagcagggtga	cgacatga		1128

<210> SEQ ID NO 464
 <211> LENGTH: 375
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 464

Met	Val	Leu	Phe	His	Leu	Ile	Lys	Lys	Glu	Ser	Leu	Gln	Ile	Phe	Arg
1				5					10					15	
Asn	Arg	Thr	Ala	Leu	Leu	Met	Met	Val	Ile	Phe	Pro	Ile	Leu	Met	Ile
			20					25					30		
Val	Ile	Leu	Ser	Phe	Ala	Phe	Lys	Ser	Ser	Phe	Asn	Thr	Ala	Thr	Thr
		35					40					45			
Val	Pro	Lys	Leu	Thr	Ile	Arg	Tyr	Gln	Leu	Glu	Gly	Glu	Lys	Thr	Asp
	50					55				60					
Tyr	Gln	Lys	Asn	Phe	Leu	Ala	Phe	Leu	Lys	Val	Leu	Asn	Gln	Lys	Leu
65				70					75					80	
His	Leu	Glu	Thr	Lys	Pro	Ser	Asn	Ser	Leu	Glu	Lys	Asp	Arg	Gln	Arg
			85					90					95		
Val	Ser	Glu	Gly	Ala	Leu	Thr	Ala	Val	Leu	Glu	Val	Lys	Lys	Asn	Gln
		100						105					110		
Thr	Ile	Lys	Val	Ile	Thr	Asn	Asn	Ile	Asn	Gln	Gln	Asn	Ala	Asp	Leu
		115				120						125			
Ile	Asn	Met	Leu	Val	Lys	Asn	Tyr	Val	Asp	Asn	Ala	Lys	Thr	Tyr	Asp
	130					135				140					
Ser	Ile	Ala	Ala	Leu	Tyr	Pro	Gln	Gln	Leu	Asn	His	Ile	Arg	Lys	Arg
145				150						155				160	
Ser	Val	Asp	Tyr	Val	Lys	Val	Ser	Ser	Ile	Gln	Thr	Ser	Lys	Gly	Met

				165				170					175				
Thr	Ser	Ala	Asp	Tyr	Tyr	Ala	Ile	Ser	Met	Phe	Thr	Met	Ile	Thr	Phe		
			180					185					190				
Tyr	Ser	Met	Met	Ser	Ala	Met	Asn	Leu	Val	Leu	Ser	Asp	Arg	Gln	Gln		
		195					200					205					
Arg	Ile	Thr	Asn	Arg	Ile	His	Leu	Thr	Gly	Val	Ser	Pro	Ser	Phe	Leu		
	210				215						220						
Val	Phe	Gly	Lys	Leu	Ile	Gly	Ala	Met	Leu	Ala	Thr	Thr	Val	Gln	Leu		
225					230					235					240		
Ser	Leu	Leu	Tyr	Ile	Phe	Thr	Arg	Phe	Val	Leu	Arg	Val	Asn	Trp	Gly		
			245					250					255				
Thr	Asn	Glu	Trp	Met	Leu	Ile	Gly	Ile	Thr	Ala	Ser	Leu	Val	Tyr	Leu		
		260						265					270				
Ser	Val	Ala	Ile	Gly	Ile	Gly	Leu	Gly	Ile	Ser	Ile	Lys	Asn	Glu	Ala		
		275					280					285					
Phe	Leu	Thr	Val	Ala	Ser	Asn	Thr	Ile	Ile	Pro	Ile	Phe	Ala	Phe	Leu		
	290					295					300						
Gly	Gly	Ser	Tyr	Val	Pro	Leu	Thr	Thr	Leu	His	Ser	Ser	Ile	Ile	Asn		
305					310					315					320		
Gln	Leu	Ser	Asn	Ile	Ser	Pro	Ile	Lys	Trp	Val	Asn	Asp	Ser	Leu	Phe		
			325					330					335				
Tyr	Leu	Ile	Phe	Gly	Gly	Gln	Tyr	Asn	Pro	Ile	Pro	Val	Thr	Leu	Ile		
		340					345					350					
Val	Asn	Ile	Ser	Ile	Gly	Thr	Ile	Phe	Ile	Ile	Leu	Ala	Leu	Ile	Gly		
	355					360					365						
Met	Arg	Lys	Gln	Val	Thr	Thr											
	370					375											

<210> SEQ ID NO 465

<211> LENGTH: 672

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 465

atgcctttgt	ccatccaatg	ccttaatctt	tgttttttgt	tggttaacttt	ttgtccttca	60
attcctatgc	aagctatttt	tggaaaggaa	gatagtgggt	atgcatttaa	tttaattgggt	120
tttctaagag	caactctgat	ttatgacatt	ttggctttgg	taagtattta	tgttttgtca	180
cctcaaataa	ccttgtctct	tgaaagtatt	gatagtaaga	cgttctttat	gggacttgta	240
ttttgcgtct	tgatagtact	gattgaactc	gttttcttac	atggttttacg	ttgttggcaa	300
aaaaagcaat	ggcttcctgc	aactttctcg	tttgtaggaa	cgacaaatga	ttgggtctaag	360
attggctatc	ctttattact	agctttatct	gaagagacga	tttatcgttt	tttgtggttt	420
aatatattag	cttttcaatg	gcatttacca	acaattattg	ttttaattgt	aactagtttt	480
tgctatgctt	taaatcactt	attgatgggg	aaatccattt	tttatgctaa	gttggttaaca	540
ggcatcattt	atggtagtat	ttacatgctg	actagtcaat	tgtggttggg	tgtgataatg	600
catgtaggag	gtaacttgct	agttgagtgt	cttagccatc	ttcaaacaaa	aaagaagaag	660
gaggtgacat	ga					672

<210> SEQ ID NO 466

<211> LENGTH: 223

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 466

Met	Pro	Leu	Ser	Ile	Gln	Cys	Leu	Asn	Leu	Cys	Phe	Leu	Leu	Val	Thr
1			5					10					15		
Phe	Cys	Pro	Ser	Ile	Pro	Met	Gln	Ala	Ile	Phe	Gly	Lys	Glu	Asp	Ser
		20					25				30				
Gly	Tyr	Ala	Phe	Asn	Leu	Ile	Gly	Phe	Leu	Arg	Ala	Thr	Leu	Ile	Tyr
	35					40					45				

Asp	Ile	Leu	Ala	Leu	Val	Ser	Ile	Tyr	Val	Leu	Ser	Pro	Gln	Ile	Thr
50						55				60					
Leu	Ser	Leu	Glu	Ser	Ile	Asp	Ser	Lys	Thr	Phe	Phe	Met	Gly	Leu	Val
65					70					75				80	
Phe	Cys	Val	Leu	Ile	Val	Leu	Ile	Glu	Leu	Val	Phe	Leu	His	Gly	Leu
				85					90					95	
Arg	Cys	Trp	Gln	Lys	Lys	Gln	Trp	Leu	Pro	Ala	Thr	Phe	Ser	Phe	Val
			100					105					110		
Gly	Thr	Thr	Asn	Asp	Trp	Ser	Lys	Ile	Gly	Tyr	Pro	Leu	Leu	Leu	Ala
		115				120						125			
Leu	Phe	Glu	Glu	Thr	Ile	Tyr	Arg	Phe	Leu	Trp	Phe	Asn	Ile	Leu	Ala
	130					135					140				
Phe	Gln	Trp	His	Leu	Pro	Thr	Ile	Ile	Val	Leu	Ile	Val	Thr	Ser	Phe
145					150					155					160
Cys	Tyr	Ala	Leu	Asn	His	Leu	Leu	Met	Gly	Lys	Ser	Ile	Phe	Tyr	Ala
				165					170					175	
Lys	Leu	Val	Thr	Gly	Ile	Ile	Tyr	Gly	Ser	Ile	Tyr	Met	Leu	Thr	Ser
			180					185					190		
Gln	Leu	Trp	Leu	Val	Val	Ile	Met	His	Val	Gly	Gly	Asn	Leu	Leu	Val
	195					200						205			
Glu	Cys	Leu	Ser	His	Leu	Gln	Thr	Lys	Lys	Lys	Lys	Glu	Val	Thr	
	210					215						220			

<210> SEQ ID NO 467

<211> LENGTH: 759

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 467

atgaaattat	ctaaacaaaa	ggcaagtttg	cttaccgctg	ttttactggt	actttctctt	60
tctataacga	caataactgt	tgacgcagct	agggtagcaa	cttatccgaa	tgtatcccat	120
gcaaacacac	attataaaaa	tactgtttct	agtaagctct	taccttttac	tgctaattat	180
cagttacaac	ttggtgagtt	ggataacctt	aaccgcgcta	ccttttcaca	tatccaactg	240
caagatagac	acgaaactaa	agatgtacgc	actaaaataa	attatgaccc	tgtgggatgg	300
cacaactatc	aatttccata	cggagatggc	tcaaaatctt	catgggtaat	gaatcgtggg	360
catctagtcg	gatatcaatt	ttgtggatta	aacgatgaac	caagaaattt	agtggcaatg	420
acagcctggc	taaacacagg	tgcttattca	ggagcaaata	acagcaatcc	tgaagggatg	480
ttatactatg	aaaaccgttt	agattcttgg	cttgcaactc	accctgactt	ttggctagat	540
tataaaagtca	ctcctatata	tagtggcaat	gaagtagtgc	ctcgacaaat	tgaattacag	600
tatgttggaa	ttgattcatc	tggtgagttg	cttactataa	ggctaaatag	taataaagaa	660
agtattgatg	aaaatggtgt	tactacagta	atcttagaaa	actctgctcc	aaatatcaac	720
cttgactatt	taaatggaac	tgccactcct	aaaaactaa			759

<210> SEQ ID NO 468

<211> LENGTH: 252

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 468

Met	Lys	Leu	Ser	Lys	Gln	Lys	Ala	Ser	Leu	Leu	Thr	Ala	Val	Leu	Leu
1				5					10					15	
Leu	Leu	Ser	Leu	Ser	Ile	Thr	Thr	Ile	Thr	Val	Asp	Ala	Ala	Arg	Val
			20					25					30		
Arg	Thr	Tyr	Pro	Asn	Val	Ser	His	Ala	Asn	Thr	His	Tyr	Lys	Asn	Thr
		35				40					45				
Val	Ser	Ser	Lys	Leu	Leu	Pro	Phe	Thr	Ala	Asn	Tyr	Gln	Leu	Gln	Leu
	50					55				60					
Gly	Glu	Leu	Asp	Asn	Leu	Asn	Arg	Ala	Thr	Phe	Ser	His	Ile	Gln	Leu
65				70						75				80	

Gln	Asp	Arg	His	Glu	Thr	Lys	Asp	Val	Arg	Thr	Lys	Ile	Asn	Tyr	Asp	
				85					90				95			
Pro	Val	Gly	Trp	His	Asn	Tyr	Gln	Phe	Pro	Tyr	Gly	Asp	Gly	Ser	Lys	
			100					105					110			
Ser	Ser	Trp	Val	Met	Asn	Arg	Gly	His	Leu	Val	Gly	Tyr	Gln	Phe	Cys	
		115					120					125				
Gly	Leu	Asn	Asp	Glu	Pro	Arg	Asn	Leu	Val	Ala	Met	Thr	Ala	Trp	Leu	
	130					135					140					
Asn	Thr	Gly	Ala	Tyr	Ser	Gly	Ala	Asn	Asp	Ser	Asn	Pro	Glu	Gly	Met	
145					150					155					160	
Leu	Tyr	Tyr	Glu	Asn	Arg	Leu	Asp	Ser	Trp	Leu	Ala	Leu	His	Pro	Asp	
			165						170					175		
Phe	Trp	Leu	Asp	Tyr	Lys	Val	Thr	Pro	Ile	Tyr	Ser	Gly	Asn	Glu	Val	
		180						185					190			
Val	Pro	Arg	Gln	Ile	Glu	Leu	Gln	Tyr	Val	Gly	Ile	Asp	Ser	Ser	Gly	
	195						200					205				
Glu	Leu	Leu	Thr	Ile	Arg	Leu	Asn	Ser	Asn	Lys	Glu	Ser	Ile	Asp	Glu	
	210					215				220						
Asn	Gly	Val	Thr	Thr	Val	Ile	Leu	Glu	Asn	Ser	Ala	Pro	Asn	Ile	Asn	
225					230					235					240	
Leu	Asp	Tyr	Leu	Asn	Gly	Thr	Ala	Thr	Pro	Lys	Asn					
				245					250							

<210> SEQ ID NO 469

<211> LENGTH: 267

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 469

atgaataaac	gcattaagaa	aaaacgtaaa	ctagaaacag	cagttgtgat	gcttggtgca	60
gaaaatgcca	tgcaggttga	agcaattaaa	aatcaaaaaca	aacaaatcat	ggagctaaaa	120
tcaatcgttc	aacgaaacgc	tctggcaaca	aacgaagagt	tagcgactgt	taaagctgct	180
actttagata	accaatcagt	tatcaaggca	attggtgaca	cggttgacta	tattaagaaa	240
aactacaaac	ggaagtgggg	gaaataa				267

<210> SEQ ID NO 470

<211> LENGTH: 88

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 470

Met	Asn	Lys	Arg	Ile	Lys	Lys	Lys	Arg	Lys	Leu	Glu	Thr	Ala	Val	Val	
1				5				10					15			
Met	Leu	Val	Ala	Glu	Asn	Ala	Met	Gln	Val	Glu	Ala	Ile	Lys	Asn	Gln	
		20					25					30				
Asn	Lys	Gln	Ile	Met	Glu	Leu	Lys	Ser	Ile	Val	Gln	Arg	Asn	Ala	Leu	
	35					40				45						
Ala	Thr	Asn	Glu	Glu	Leu	Ala	Thr	Val	Lys	Ala	Ala	Thr	Leu	Asp	Asn	
	50				55					60						
Gln	Ser	Val	Ile	Lys	Ala	Ile	Gly	Asp	Thr	Val	Asp	Tyr	Ile	Lys	Lys	
65				70					75					80		
Asn	Tyr	Lys	Arg	Lys	Trp	Gly	Lys									
				85												

<210> SEQ ID NO 471

<211> LENGTH: 849

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 471

```

atgagaagaa aaataaaaacc tattgtttgtg ctagtcttct ttatttttact ggcaatggta      60
ttgattatcg gaaaaagaca agctaatacat gcgaaacaaa aagaagttga agacgctaag      120
agtcataattc ctattgcaac cagtaatcct ggtaaagcaa aaactagcac ttctgaaacc      180
gaagacttta ttttaaattcc tattgtttgat gtttccggct ggcaactccc tgaagaaatt      240
gattatgaca cattgtcacg tcacatctct ggcgcaattg tacgtgtcta tggaggatcg      300
caaattacag ctcataacaa cgctgctttt acaactggaa ttgacaaatc ttttaaaacg      360
catatcaaag aatttcaaaa acgaaatgtt cctgtagctg tttacagtta cgcacttggt      420
cgtagtacta aagagatgaa agaagaggcc cgagctttct acaaaaaacgc tgctccctat      480
aatccaactt actactggat tgatgtcgaa gaagccacta tgaaagatat gaataaaggc      540
gtaacagcct tccgagaaga gcttaaaaaa cttggtgctg aaaatgttgg tctctatatt      600
ggaacttatt ttatggcaga acaagatatt tcaacaaaag gtttcgattc tgtatggatt      660
ccgacttatg gtagtgattc tggctattat gaggctgctc ctaatacaac cttagattac      720
gatttacacc aatacacctc acaaggttat ctcagtgggt ttaacaatgc tttagattta      780
aatcaaattg ccgtaacaaa agacactaaa aaaacgtttg agaagttatt tggcaactcc      840
aacaattaa

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<210> SEQ ID NO 472

<211> LENGTH: 282

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 472

```

Met Arg Arg Lys Ile Lys Pro Ile Val Val Leu Val Phe Phe Ile Leu
1           5           10           15
Leu Ala Met Val Leu Ile Ile Gly Lys Arg Gln Ala Asn His Ala Lys
20           25           30
Gln Lys Glu Val Glu Asp Ala Lys Ser His Ile Pro Ile Ala Thr Ser
35           40           45
Asn Pro Gly Lys Ala Lys Thr Ser Thr Ser Glu Thr Glu Asp Phe Ile
50           55           60
Leu Asn Pro Ile Val Asp Val Ser Gly Trp Gln Leu Pro Glu Glu Ile
65           70           75           80
Asp Tyr Asp Thr Leu Ser Arg His Ile Ser Gly Ala Ile Val Arg Val
85           90           95
Tyr Gly Gly Ser Gln Ile Thr Ala His Asn Asn Ala Ala Phe Thr Thr
100          105          110
Gly Ile Asp Lys Ser Phe Lys Thr His Ile Lys Glu Phe Gln Lys Arg
115          120          125
Asn Val Pro Val Ala Val Tyr Ser Tyr Ala Leu Gly Arg Ser Thr Lys
130          135          140
Glu Met Lys Glu Glu Ala Arg Ala Phe Tyr Lys Asn Ala Ala Pro Tyr
145          150          155          160
Asn Pro Thr Tyr Tyr Trp Ile Asp Val Glu Glu Ala Thr Met Lys Asp
165          170          175
Met Asn Lys Gly Val Thr Ala Phe Arg Glu Glu Leu Lys Lys Leu Gly
180          185          190
Ala Glu Asn Val Gly Leu Tyr Ile Gly Thr Tyr Phe Met Ala Glu Gln
195          200          205
Asp Ile Ser Thr Lys Gly Phe Asp Ser Val Trp Ile Pro Thr Tyr Gly
210          215          220
Ser Asp Ser Gly Tyr Tyr Glu Ala Ala Pro Asn Thr Thr Leu Asp Tyr
225          230          235          240
Asp Leu His Gln Tyr Thr Ser Gln Gly Tyr Leu Ser Gly Phe Asn Asn
245          250          255
Ala Leu Asp Leu Asn Gln Ile Ala Val Thr Lys Asp Thr Lys Lys Thr
260          265          270
Phe Glu Lys Leu Phe Gly Asn Ser Asn Asn
275          280

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<210> SEQ ID NO 473
<211> LENGTH: 480
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 473
  atgggctaaaa aaacaaaact caaaaaaaccc ttagtagaac aaatcctcga taaggctaatt    60
  attgctcatc aaggactcaa gcttaatgct ttagaaggcg actttccaga tgatcttcaa    120
  ccatcagata tttaacaagac acttgctctg actggtgac aaacagggtcc tctaattggc    180
  attattccat taacagaaca cttatcagaa aaacaattgg caaaagtatc aggtaacaaa    240
  aaagtgtcca tggttcctca aaaagacttg caaaagacaa caggctatat tcacgggtgcc    300
  aataatcctg ttgggattcg tcaaaaacat tcatatccta tttttattga ccaaactgca    360
  ctggaaaaag gtcaaataat cgtttcagct ggtgaagttg ggcgttctat aaagatttct    420
  agccaggctc tagctgattt cgttggcgca agctttgctg atttaaagaa gagaaaatga    480

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<210> SEQ ID NO 474
<211> LENGTH: 159
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 474
  Met Ala Lys Lys Thr Lys Leu Lys Lys Thr Leu Val Glu Gln Ile Leu
   1             5             10             15
  Asp Lys Ala Asn Ile Ala His Gln Gly Leu Lys Leu Asn Ala Leu Glu
             20             25             30
  Gly Asp Phe Pro Asp Asp Leu Gln Pro Ser Asp Ile Tyr Lys Thr Leu
             35             40             45
  Ala Leu Thr Gly Asp Gln Thr Gly Pro Leu Ile Gly Ile Ile Pro Leu
             50             55             60
  Thr Glu His Leu Ser Glu Lys Gln Leu Ala Lys Val Ser Gly Asn Lys
             65             70             75             80
  Lys Val Ser Met Val Pro Gln Lys Asp Leu Gln Lys Thr Thr Gly Tyr
             85             90             95
  Ile His Gly Ala Asn Asn Pro Val Gly Ile Arg Gln Lys His Ser Tyr
             100            105            110
  Pro Ile Phe Ile Asp Gln Thr Ala Leu Glu Lys Gly Gln Ile Ile Val
             115            120            125
  Ser Ala Gly Glu Val Gly Arg Ser Ile Lys Ile Ser Ser Gln Ala Leu
             130            135            140
  Ala Asp Phe Val Gly Ala Ser Phe Ala Asp Leu Lys Lys Arg Lys
             145            150            155

```

```

<210> SEQ ID NO 475
<211> LENGTH: 408
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 475
  atggacttag ttggaatctc actgatgatt attgcactcg catttggtgc tttggtgatt    60
  ttcttgatta ttgtattaaa gaaagtctca gaaacaattg atgaagccaa aaaaacgatt    120
  tctgtattga caagtgatgt taatgtgaca cttcatcaaa ctaatgatat tttagcaaaa    180
  gctaatatcc ttgttgaaga tgtaaatggg aaagtagcaa ccatcgatcc actgtttggt    240
  gctattgctg atttgtcaga aagtccttca gatttaaata gtcaagcaag gcattttggg    300
  caaaaagcaa ctaatgctac aggtaatgtt tcaaaagctg gaaaattagc attagtgtgt    360
  aaagtagcct caaaagtatt tggaaaaaaa ggagaaaagc atgaataa    408

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<210> SEQ ID NO 476
<211> LENGTH: 135
<212> TYPE: PRT

```

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 476

```
Met Asp Leu Val Gly Ile Ser Leu Met Ile Ile Ala Leu Ala Phe Val
1           5           10           15
Ala Leu Val Ile Phe Leu Ile Ile Val Leu Lys Lys Val Ser Glu Thr
20           25           30
Ile Asp Glu Ala Lys Lys Thr Ile Ser Val Leu Thr Ser Asp Val Asn
35           40           45
Val Thr Leu His Gln Thr Asn Asp Ile Leu Ala Lys Ala Asn Ile Leu
50           55           60
Val Glu Asp Val Asn Gly Lys Val Ala Thr Ile Asp Pro Leu Phe Val
65           70           75           80
Ala Ile Ala Asp Leu Ser Glu Ser Leu Ser Asp Leu Asn Ser Gln Ala
85           90           95
Arg His Phe Gly Gln Lys Ala Thr Asn Ala Thr Gly Asn Val Ser Lys
100          105          110
Ala Gly Lys Leu Ala Leu Val Gly Lys Val Ala Ser Lys Val Phe Gly
115          120          125
Lys Lys Gly Glu Lys His Glu
130          135
```

<210> SEQ ID NO 477

<211> LENGTH: 780

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 477

```
atgatcaatc ccattgcctt aaaatgtggt ccactagcca tccactggta tgctctatgt      60
atcttgtcag gacttgtttt ggcggtttac ttagcatcaa aagaagcacc caaaaaagga      120
atatcatctg atgctatttt cgattttatt ctgattgctt ttccacttgc tattgttgggt      180
gcaagaattt actatgttat ttttgaatgg tcttattatg tcaagcattt agatgaaatc      240
atagccattt ggaatggcgg tattgctatt tatggcggtc tcattacagg agctcttgta      300
cttttggtt actgttataa caaggtgctc aatcccattc attttttaga tattgccgca      360
ccaagtgtca tggtcgctca agctatcggg cgctggggaa attttatcaa ccaagaagcc      420
tatggtaaaag ctgtgagcca gttaaattac ttaccaagct ttattcaaaa gcaaatgttt      480
atagaggggaa gttaccgcat tccgaccttt ctctatgaat cactttggaa tcttttgggc      540
tttgtcatta ttatgatgtg gcgtcgtaag ccaaaaagtc tattagatgg agaaatcttt      600
gcattttact taatttggtg tggtagtggg agactagtca ttgaagggtat gcgaacagat      660
agtcttatgt ttttaggtat tcgcatctcc caatatgtgt ctgccttatt aattattatt      720
ggcttaatct ttgttataaa aagacgtcgt caaaaaggaa tttcttatta tcaagaataa      780
```

<210> SEQ ID NO 478

<211> LENGTH: 259

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 478

```
Met Ile Asn Pro Ile Ala Leu Lys Cys Gly Pro Leu Ala Ile His Trp
1           5           10           15
Tyr Ala Leu Cys Ile Leu Ser Gly Leu Val Leu Ala Val Tyr Leu Ala
20           25           30
Ser Lys Glu Ala Pro Lys Lys Gly Ile Ser Ser Asp Ala Ile Phe Asp
35           40           45
Phe Ile Leu Ile Ala Phe Pro Leu Ala Ile Val Gly Ala Arg Ile Tyr
50           55           60
Tyr Val Ile Phe Glu Trp Ser Tyr Tyr Val Lys His Leu Asp Glu Ile
65           70           75           80
Ile Ala Ile Trp Asn Gly Gly Ile Ala Ile Tyr Gly Gly Leu Ile Thr
85           90           95
```

Gly	Ala	Leu	Val	Leu	Leu	Ala	Tyr	Cys	Tyr	Asn	Lys	Val	Leu	Asn	Pro
			100					105					110		
Ile	His	Phe	Leu	Asp	Ile	Ala	Ala	Pro	Ser	Val	Met	Val	Ala	Gln	Ala
		115					120					125			
Ile	Gly	Arg	Trp	Gly	Asn	Phe	Ile	Asn	Gln	Glu	Ala	Tyr	Gly	Lys	Ala
	130					135					140				
Val	Ser	Gln	Leu	Asn	Tyr	Leu	Pro	Ser	Phe	Ile	Gln	Lys	Gln	Met	Phe
145					150					155				160	
Ile	Glu	Gly	Ser	Tyr	Arg	Ile	Pro	Thr	Phe	Leu	Tyr	Glu	Ser	Leu	Trp
			165						170					175	
Asn	Leu	Leu	Gly	Phe	Val	Ile	Ile	Met	Met	Trp	Arg	Arg	Lys	Pro	Lys
		180						185					190		
Ser	Leu	Leu	Asp	Gly	Glu	Ile	Phe	Ala	Phe	Tyr	Leu	Ile	Trp	Tyr	Gly
	195					200					205				
Ser	Gly	Arg	Leu	Val	Ile	Glu	Gly	Met	Arg	Thr	Asp	Ser	Leu	Met	Phe
	210					215					220				
Leu	Gly	Ile	Arg	Ile	Ser	Gln	Tyr	Val	Ser	Ala	Leu	Leu	Ile	Ile	Ile
225					230					235				240	
Gly	Leu	Ile	Phe	Val	Ile	Lys	Arg	Arg	Arg	Gln	Lys	Gly	Ile	Ser	Tyr
			245					250					255		
Tyr	Gln	Glu													

<210> SEQ ID NO 479
 <211> LENGTH: 1863
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 479

atgacgtatc	aagaaactgc	caaggctatt	ttagcggcgg	ttggtggcaa	aacaaatatt	60
caacgtgtga	cacactgtgt	aacacgtcta	cgcttagtac	tgaaaaatga	tgagaaagtt	120
aaagatcagc	aagtcaaaagc	catttcaaat	gtgattggcg	tgatgcgcaa	aaacggccag	180
taccaaatta	tcttgggcaa	tgatgtcaat	aattattacc	aagccttttt	aagcctaggg	240
cattttgaca	atcaagatga	agatcattct	tcaaaagcga	aaggaagtat	ccttgagcgc	300
ttgattgaaa	ccattgctgg	cgtgattaca	ccgctgattc	cagcccttct	tggtggtgga	360
atgctcaaag	tggtgggaat	cttgcttctc	atgcttggct	tagcgagtgc	ggactctcaa	420
accgttgcct	ttattaactt	cttggcgat	gcggcttatt	attttatgcc	tgtcatgatt	480
gcctattcag	cagcggcgcg	ctttaagggtg	acacctgttt	tagcagcgac	gatcgaggg	540
attttattgc	atcctgcctt	tgttgcaatg	gtagcagaag	gtaaaccatt	gactttattt	600
ggagcaccag	tcactcctgc	tagctatggc	tcactctgta	ttcccatttt	gatgatgggt	660
tacttgatgc	aatacattga	aaaatgggtc	aatcgcttgg	tgccaagcgt	gatgaaaagc	720
ttcttacagc	caaccttaat	cattttgatt	tctggctttt	tggctttagt	ggttgtaggt	780
cctcttggtg	tgattattgg	tcaagggtta	tctaatacca	tgctcgctat	ttatcatgtg	840
gctccgtggc	tagcacttgc	tattttggga	gcgattatgc	cgcttggtgt	catgacgggg	900
atgcactggg	cttttgacc	aatctttttg	gccgcttcgg	tcgcaacacc	agatgtcttg	960
attttaccag	caatgttggc	ttctaatttg	gctcaaggag	ccgcatcttt	ggctgttgcc	1020
tttaaaacaa	agcagaaaca	aacacgtcaa	gttgcccttg	ccgcggggat	ttcagctttg	1080
ctggcaggta	tcacggaacc	ggcactttat	ggggtcacac	tgaaatttaa	aaagccactc	1140
tatgcagcca	tgatttcagg	tggtctgggt	ggagccttta	ttggttttgt	caatattgct	1200
tcttatacct	ttgtcgtacc	ttctattatt	ggtttaccac	agtacatcaa	cccatcaggc	1260
ggagctaatt	ttacaaatgc	tttgattgcc	ggaaactgca	cgatttgtgt	agccttcagt	1320
ttgacttggt	tcatgggaat	tgatgaagag	tcccaaaagc	aagtgaagtgt	tgacgagat	1380
atgtcacaag	ttaagagcgg	cttgtcaacc	aaacaaacgt	tgtatgctcc	aatgacaggt	1440
gagatgcttt	ttctatcaga	agttcctgat	gaaacctttt	cttccaagtt	attaggagaa	1500
ggatttgcca	tattaccaag	cgaagggtgag	gtctatgccc	cctttgatgg	tgaagtcac	1560
actttctttc	caaccaagca	tgctgttgcc	ttaaaaaaca	cacgtggtgt	ggaagtcttg	1620
attcatgtcg	gtattgatac	ggttgagtta	aaagggcaag	gtttcgagca	gttagtgtct	1680
gttggcgatg	tcgtgaaacg	aggccaggca	cttctaataa	tggatattga	tttcattact	1740
tcaaaaggct	attcactcat	cagtcctgtg	gtcgtgacca	attcggctga	gcagttggag	1800

attattattc aagatgacaa aaaaatggtg actaaagagg acgctttggt agtcatttta 1860
taa 1863

```
<210> SEQ ID NO 480
<211> LENGTH: 620
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 480
```

Met	Thr	Tyr	Gln	Glu	Thr	Ala	Lys	Ala	Ile	Leu	Ala	Ala	Val	Gly	Gly
1				5					10					15	
Lys	Thr	Asn	Ile	Gln	Arg	Val	Thr	His	Cys	Val	Thr	Arg	Leu	Arg	Leu
			20					25					30		
Val	Leu	Lys	Asn	Asp	Glu	Lys	Val	Lys	Asp	Gln	Gln	Val	Lys	Ala	Ile
		35					40					45			
Ser	Asn	Val	Ile	Gly	Val	Met	Arg	Lys	Asn	Gly	Gln	Tyr	Gln	Ile	Ile
	50					55				60					
Leu	Gly	Asn	Asp	Val	Asn	Asn	Tyr	Tyr	Gln	Ala	Phe	Leu	Ser	Leu	Gly
65				70					75						80
His	Phe	Asp	Asn	Gln	Asp	Glu	Asp	His	Ser	Ser	Lys	Ala	Lys	Gly	Ser
			85					90						95	
Ile	Leu	Glu	Arg	Leu	Ile	Glu	Thr	Ile	Ala	Gly	Val	Ile	Thr	Pro	Leu
			100					105					110		
Ile	Pro	Ala	Leu	Leu	Gly	Gly	Gly	Met	Leu	Lys	Val	Val	Gly	Ile	Leu
		115					120					125			
Leu	Pro	Met	Leu	Gly	Leu	Ala	Ser	Ala	Asp	Ser	Gln	Thr	Val	Ala	Phe
	130					135					140				
Ile	Asn	Phe	Phe	Gly	Asp	Ala	Ala	Tyr	Tyr	Phe	Met	Pro	Val	Met	Ile
145				150						155					160
Ala	Tyr	Ser	Ala	Ala	Ala	Arg	Phe	Lys	Val	Thr	Pro	Val	Leu	Ala	Ala
			165					170						175	
Thr	Ile	Ala	Gly	Ile	Leu	Leu	His	Pro	Ala	Phe	Val	Ala	Met	Val	Ala
			180					185					190		
Glu	Gly	Lys	Pro	Leu	Thr	Leu	Phe	Gly	Ala	Pro	Val	Thr	Pro	Ala	Ser
		195					200					205			
Tyr	Gly	Ser	Ser	Val	Ile	Pro	Ile	Leu	Met	Met	Val	Tyr	Leu	Met	Gln
	210					215					220				
Tyr	Ile	Glu	Lys	Trp	Val	Asn	Arg	Leu	Val	Pro	Ser	Val	Met	Lys	Ser
225				230						235					240
Phe	Leu	Gln	Pro	Thr	Leu	Ile	Ile	Leu	Ile	Ser	Gly	Phe	Leu	Ala	Leu
			245					250					255		
Val	Val	Val	Gly	Pro	Leu	Gly	Val	Ile	Ile	Gly	Gln	Gly	Leu	Ser	Asn
			260					265					270		
Thr	Met	Leu	Ala	Ile	Tyr	His	Val	Ala	Pro	Trp	Leu	Ala	Leu	Ala	Ile
		275					280					285			
Leu	Gly	Ala	Ile	Met	Pro	Leu	Val	Val	Met	Thr	Gly	Met	His	Trp	Ala
	290					295					300				
Phe	Ala	Pro	Ile	Phe	Leu	Ala	Ala	Ser	Val	Ala	Thr	Pro	Asp	Val	Leu
305				310						315					320
Ile	Leu	Pro	Ala	Met	Leu	Ala	Ser	Asn	Leu	Ala	Gln	Gly	Ala	Ala	Ser
			325					330					335		
Leu	Ala	Val	Ala	Phe	Lys	Thr	Lys	Gln	Lys	Gln	Thr	Arg	Gln	Val	Ala
			340					345					350		
Leu	Ala	Ala													

385					390					395				400	
Ser	Tyr	Thr	Phe	Val	Val	Pro	Ser	Ile	Ile	Gly	Leu	Pro	Gln	Tyr	Ile
				405					410					415	
Asn	Pro	Ser	Gly	Gly	Ala	Asn	Phe	Thr	Asn	Ala	Leu	Ile	Ala	Gly	Thr
			420					425					430		
Ala	Thr	Ile	Val	Leu	Ala	Phe	Ser	Leu	Thr	Trp	Phe	Met	Gly	Ile	Asp
		435					440					445			
Glu	Glu	Ser	Pro	Lys	Gln	Val	Ser	Val	Ala	Ala	Asp	Met	Ser	Gln	Val
	450					455					460				
Lys	Ser	Gly	Leu	Ser	Thr	Lys	Gln	Thr	Leu	Tyr	Ala	Pro	Met	Thr	Gly
465					470					475					480
Glu	Met	Leu	Phe	Leu	Ser	Glu	Val	Pro	Asp	Glu	Thr	Phe	Ser	Ser	Lys
			485					490						495	
Leu	Leu	Gly	Glu	Gly	Phe	Ala	Ile	Leu	Pro	Ser	Glu	Gly	Glu	Val	Tyr
		500						505					510		
Ala	Pro	Phe	Asp	Gly	Glu	Val	Ile	Thr	Phe	Phe	Pro	Thr	Lys	His	Ala
		515					520					525			
Val	Ala	Leu	Lys	Asn	Thr	Arg	Gly	Val	Glu	Val	Leu	Ile	His	Val	Gly
	530					535					540				
Ile	Asp	Thr	Val	Glu	Leu	Lys	Gly	Gln	Gly	Phe	Glu	Gln	Leu	Val	Ser
545					550					555					560
Val	Gly	Asp	Val	Val	Lys	Arg	Gly	Gln	Ala	Leu	Leu	Lys	Met	Asp	Ile
			565					570						575	
Asp	Phe	Ile	Thr	Ser	Lys	Gly	Tyr	Ser	Leu	Ile	Ser	Pro	Val	Val	Val
		580						585					590		
Thr	Asn	Ser	Ala	Glu	Gln	Leu	Glu	Ile	Ile	Ile	Gln	Asp	Asp	Lys	Lys
	595					600					605				
Met	Val	Thr	Lys	Glu	Asp	Ala	Leu	Leu	Val	Ile	Leu				
	610					615					620				

<210> SEQ ID NO 481

<211> LENGTH: 1368

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 481

atgtcacatc	atcaacaaac	cgtttcaaaa	caaacaatta	tggcgattat	cgccatagca	60
ctcattgggtt	tttcaggaat	tttgtctgaa	accagtatga	atgtcacctt	cccgacactg	120
atgtcagtct	atcagttacc	cttaaatagc	ttgcaatgga	tgacgaccat	ttattttacta	180
gcagtggcga	ttatgatgac	cacttcggct	acactgaaaa	aaaatgtgcg	ggaaagaccc	240
ctctttttta	tggccacagg	tctttttaca	tttggcacca	tcttggccgt	tctgacctag	300
tcctttgcga	tcatgttgct	agcccgcat	tttcaaggca	ttggtactgg	tctggtaatg	360
cctcagatgt	ttaatattat	tttagagcgt	gtcccaatgc	ataaggtagg	tctatttatg	420
ggatttgctg	gtcttattat	tagcttagca	cctgcttttg	ggcctactta	tgggggcttt	480
atgattagcc	atttttagtg	gcaatggatt	tttatctgta	tactccctgt	accactgatt	540
gcagggtattc	tagcttatta	ttacctgaa	gattctccag	taagcgaaaa	agtacccttt	600
gactgggttg	catttattgc	actatcgatt	agcttaactt	ctgccttatt	agctattact	660
agtctagaaa	acggcagtg	taatttgtat	tacttagggc	tttttattct	cagctttatc	720
ctcttcctct	acaagaatct	cacagctaag	caaccctttc	ttgatattcg	cattctcaaa	780
attccctctc	taaccttttg	cctgattccc	ttttttgtct	tccagctgat	taatttaggc	840
ataaattttc	taacgcaaaa	ctttattgtc	atggaaaaga	ttgctaatag	ttctcaagct	900
ggtatggtgt	tactacctgg	taccttactc	ggagctctac	tagcacctgc	ttttggtaaa	960
ctttatgatc	aaaaaaggagc	aagactttcg	ctttatttag	gaaatgcctt	atttagttta	1020
tcattgatta	ttatgacact	tcaaacaaga	cattttatgc	ttttaccatt	cactctttta	1080
tatattttat	tcacgttttg	gcgtaacatg	ggctttaata	atagcttagc	cacggctatt	1140
cgagaattgc	ctgccgagaa	aaatgccgat	gccacggcca	tttttcagat	gatgcagcaa	1200
tttgctggcg	ctctaggaac	tgctatggca	tcactgatag	caaatagtca	agcagaattc	1260
acaagcgggtg	tccagtctgt	ctaccttctc	tttactat	ttgctctact	tgattttatc	1320

tttttctttg ctatgtttta ccatttaggg aaaaaaggat tagcctaa

1368

<210> SEQ ID NO 482

<211> LENGTH: 455

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 482

Met	Ser	His	His	Gln	Gln	Thr	Val	Ser	Lys	Gln	Thr	Ile	Met	Ala	Ile
1			5					10					15		
Ile	Ala	Ile	Ala	Leu	Ile	Gly	Phe	Ser	Gly	Ile	Leu	Ser	Glu	Thr	Ser
		20						25				30			
Met	Asn	Val	Thr	Phe	Pro	Thr	Leu	Met	Ser	Val	Tyr	Gln	Leu	Pro	Leu
	35					40					45				
Asn	Ser	Leu	Gln	Trp	Met	Thr	Thr	Ile	Tyr	Leu	Leu	Ala	Val	Ala	Ile
	50				55					60					
Met	Met	Thr	Thr	Ser	Ala	Thr	Leu	Lys	Lys	Asn	Val	Arg	Glu	Arg	Pro
65				70					75					80	
Leu	Phe	Phe	Met	Ala	Thr	Gly	Leu	Phe	Thr	Phe	Gly	Thr	Ile	Leu	Ala
			85			90						95			
Val	Leu	Thr	Gln	Ser	Phe	Ala	Ile	Met	Leu	Leu	Ala	Arg	Ile	Phe	Gln
		100					105					110			
Gly	Ile	Gly	Thr	Gly	Leu	Val	Met	Pro	Gln	Met	Phe	Asn	Ile	Ile	Leu
	115					120					125				
Glu	Arg	Val	Pro	Met	His	Lys	Val	Gly	Leu	Phe	Met	Gly	Phe	Ala	Gly
	130				135				140						
Leu	Ile	Ile	Ser	Leu	Ala	Pro	Ala	Phe	Gly	Pro	Thr	Tyr	Gly	Gly	Phe
145				150					155					160	
Met	Ile	Ser	His	Phe	Ser	Trp	Gln	Trp	Ile	Phe	Ile	Cys	Ile	Leu	Pro
			165			170						175			
Val	Pro	Leu	Ile	Ala	Gly	Ile	Leu	Ala	Tyr	Tyr	Tyr	Leu	Glu	Asp	Ser
		180				185						190			
Pro	Val	Ser	Glu	Lys	Val	Pro	Phe	Asp	Trp	Leu	Ala	Phe	Ile	Ala	Leu
	195				200						205				
Ser	Ile	Ser	Leu	Thr	Ser	Ala	Leu	Leu	Ala	Ile	Thr	Ser	Leu	Glu	Asn
	210				215						220				
Gly	Ser	Val	Asn	Leu	Tyr	Tyr	Leu	Gly	Leu	Phe	Ile	Leu	Ser	Phe	Ile
225				230					235					240	
Leu	Phe	Leu	Tyr	Lys	Asn	Leu	Thr	Ala	Lys	Gln	Pro	Phe	Leu	Asp	Ile
			245			250							255		
Arg	Ile	Leu	Lys	Ile	Pro	Ser	Leu	Thr	Phe	Gly	Leu	Ile	Pro	Phe	Phe
	260					265						270			
Val	Phe	Gln	Leu	Ile	Asn	Leu	Gly	Ile	Asn	Phe	Leu	Thr	Pro	Asn	Phe
	275					280						285			
Ile	Val	Met	Glu	Lys	Ile	Ala	Asn	Ser	Ser	Gln	Ala	Gly	Met	Val	Leu
	290				295						300				
Leu	Pro	Gly	Thr	Leu	Leu	Gly	Ala	Leu	Leu	Ala	Pro	Ala	Phe	Gly	Lys
305				310					315					320	
Leu	Tyr	Asp	Gln	Lys	Gly	Ala	Arg	Leu	Ser	Leu	Tyr	Leu	Gly	Asn	Ala
			325			330						335			
Leu	Phe	Ser	Leu	Ser	Leu	Ile	Ile	Met	Thr	Leu	Gln	Thr	Arg	His	Phe
	340					345						350			
Met	Leu	Leu	Pro	Phe	Thr	Leu	Leu	Tyr	Ile	Leu	Phe	Thr	Phe	Gly	Arg
	355				360							365			
Asn	Met	Gly	Phe	Asn	Asn	Ser	Leu	Ala	Thr	Ala	Ile	Arg	Glu	Leu	Pro
	370				375						380				
Ala	Glu	Lys	Asn	Ala	Asp	Ala	Thr	Ala	Ile	Phe	Gln	Met	Met	Gln	Gln
385				390					395					400	

Phe	Ala	Gly	Ala	Leu	Gly	Thr	Ala	Met	Ala	Ser	Leu	Ile	Ala	Asn	Ser
				405					410					415	
Gln	Ala	Glu	Phe	Thr	Ser	Gly	Val	Gln	Ser	Val	Tyr	Leu	Leu	Phe	Thr
			420					425					430		
Ile	Phe	Ala	Leu	Leu	Asp	Phe	Ile	Phe	Phe	Phe	Ala	Met	Phe	Tyr	His
		435					440					445			
Leu	Gly	Lys	Lys	Gly	Leu	Ala									
		450				455									

<210> SEQ ID NO 483
 <211> LENGTH: 1095
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 483

ttgactcaac	taaaaactca	atatccctcg	ctcatcatag	acgctagctt	catcaccttg	60
gcggcaaatg	caacgggtcaa	gccccaggat	aagacctaca	ataccgtcaa	tcttctcaac	120
agatttttcc	ttatctggct	tgatgttgcc	tccaggggct	tgtcgcatca	ccacgttttg	180
tcccatccat	ttaaggactg	gatgaccaac	atgttagatt	ttccctacca	tcatgagttt	240
atagagttcc	ttggacggtg	gactcatatc	cttatagccc	tgcccaaaag	gcaccatggt	300
caagtcgaca	ccgcaattcc	aaggtatctt	ctggtaacca	tcagagagaa	gacagggatt	360
gtaaaattaa	ccactgtgca	aaatacagcg	ttcactaccc	agtcgaatca	actcaaaaaa	420
caatacgggc	agttcttggt	aacagaatct	aataactggt	gtgcatgccc	aggctgtgat	480
agaccactca	ttctaaccag	tggaactta	gcagcagaaa	attacgaggt	ttcagccatt	540
gaaaaagata	aggacgctga	agcactgaat	ctgatagccc	tctgcccaga	tggtttttta	600
acctatcaag	cagataggcg	caaaaaaatt	gtaacaactc	taaaaaatgt	taaaaagatt	660
ctagtctctg	cacataacag	ccaacaagcg	atctctgata	tgaagttaga	cagtgggaatt	720
gtttcagttt	tgactagtct	caataaacta	aatgtgatg	aatataatat	ctcctatgac	780
tcgaagcaat	tgactgataa	gatatcacct	gagaacaatc	gtacgcttta	tcaattgggt	840
aaaaaccaag	ttattgataa	ctacttaacc	attcaaaaaa	tcacgtaaaa	tttggacaaa	900
caaggaaaaa	ttgattacga	gaaaatccaa	tatcaaacgc	gatcgatgta	taaaaagtta	960
aaagcagcca	agcataataa	tctggctatt	ttcaataacta	tttcggaaaa	actccatctg	1020
gctacactac	aggacatcta	cttctgtcag	atgattgtct	cttactttat	ccaaaaatgc	1080
gaggtacttg	aataa					1095

<210> SEQ ID NO 484
 <211> LENGTH: 364
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 484

Met	Thr	Gln	Leu	Lys	Thr	Gln	Tyr	Pro	Ser	Leu	Ile	Ile	Asp	Ala	Ser
1				5					10					15	
Phe	Ile	Thr	Leu	Ala	Ala	Asn	Ala	Thr	Val	Lys	Pro	Gln	Asp	Lys	Thr
			20					25					30		
Tyr	Asn	Thr	Val	Asn	Leu	Leu	Asn	Arg	Phe	Phe	Leu	Ile	Trp	Leu	Asp
		35					40					45			
Val	Ala	Ser	Arg	Gly	Leu	Ser	His	His	His	Val	Leu	Ser	His	Pro	Phe
		50				55					60				
Lys	Asp	Trp	Met	Thr	Asn	Met	Leu	Asp	Phe	Pro	Tyr	His	His	Glu	Phe
65					70				75					80	
Ile	Glu	Phe	Leu	Gly	Arg	Trp	Thr	His	Ile	Leu	Ile	Ala	Leu	Pro	Lys
			85					90					95		
Arg	His	His	Gly	Gln	Val	Asp	Thr	Ala	Ile	Pro	Arg	Tyr	Leu	Leu	Val
			100					105					110		
Thr	Ile	Arg	Glu	Lys	Thr	Gly	Ile	Val	Lys	Leu	Thr	Thr	Val	Gln	Asn
		115				120						125			
Thr	Ala	Phe	Thr	Thr	Gln	Ser	Asn	Gln	Leu	Lys	Lys	Gln	Tyr	Gly	Gln
		130				135						140			

Phe	Leu	Leu	Thr	Glu	Ser	Asn	Asn	Cys	Cys	Ala	Cys	Pro	Gly	Cys	Asp
145					150					155					160
Arg	Pro	Leu	Ile	Leu	Thr	Ser	Gly	Asn	Leu	Ala	Ala	Glu	Asn	Tyr	Glu
				165					170						175
Val	Ser	Ala	Ile	Glu	Lys	Asp	Lys	Asp	Ala	Glu	Ala	Leu	Asn	Leu	Ile
			180					185					190		
Ala	Leu	Cys	Pro	Asp	Gly	Phe	Leu	Thr	Tyr	Gln	Ala	Asp	Arg	Arg	Lys
	195					200					205				
Lys	Ile	Val	Thr	Thr	Leu	Lys	Asn	Val	Lys	Lys	Ile	Leu	Val	Ser	Ala
	210					215					220				
His	Asn	Ser	Gln	Gln	Ala	Ile	Ser	Asp	Met	Lys	Leu	Asp	Ser	Gly	Ile
225					230					235					240
Val	Ser	Val	Leu	Thr	Ser	Leu	Asn	Lys	Leu	Lys	Cys	Asp	Glu	Tyr	Asn
			245						250					255	
Ile	Ser	Tyr	Asp	Ser	Lys	Gln	Leu	Thr	Asp	Lys	Ile	Ser	Pro	Glu	Asn
			260					265					270		
Asn	Arg	Thr	Leu	Tyr	Gln	Leu	Val	Lys	Asn	Gln	Val	Ile	Asp	Asn	Tyr
	275						280					285			
Leu	Thr	Ile	Gln	Lys	Ile	Ile	Val	Asn	Leu	Asp	Lys	Gln	Gly	Lys	Ile
	290					295					300				
Asp	Tyr	Glu	Lys	Ile	Gln	Tyr	Gln	Thr	Arg	Ser	Met	Tyr	Lys	Lys	Leu
305					310					315					320
Lys	Ala	Ala	Lys	His	Asn	Asn	Leu	Ala	Ile	Phe	Asn	Thr	Ile	Ser	Glu
				325					330					335	
Lys	Leu	His	Leu	Ala	Thr	Leu	Gln	Asp	Ile	Tyr	Phe	Cys	Gln	Met	Ile
			340					345					350		
Val	Ser	Tyr	Phe	Ile	Gln	Lys	Cys	Glu	Val	Leu	Glu				
	355						360								

<210> SEQ ID NO 485

<211> LENGTH: 1353

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 485

atgactagag	atatcattgg	aaacttatcc	acatttgaat	tagcgatcct	tatcttactt	60
gtttttgttg	ctttttactt	tatccatctt	gcggtgcgtg	attaccgaaa	tgcacgtatt	120
attcggatga	tgagccataa	aatccgagac	ttgattaatg	gtcgctatac	tgatataatc	180
gacgaaaaag	cagacattga	gttaatggag	ctttcagacc	agttaaataa	cctgtcagat	240
gtttttcgct	tgacgcatga	aaatcttgcc	caagaaaaaa	atcgcttggc	aagtattttg	300
gcttatatgt	cagatgggtg	acttgctaca	gaccggtctg	gtaaaatcat	catgattaac	360
gagacagctc	gcaagcaatt	aaatttaagt	aaagaagagg	cactaaagaa	aaacattaca	420
gatttgttag	aagggtgatac	ttcatatacc	taccgtgatt	tggtatccaa	aacaccagtg	480
gtaactgtta	atagccgaaa	tgatatgggt	gagtttgtct	cattacgctt	gcgctttgcg	540
ttgaatagga	gagagagtgg	ttttatttcg	ggcttggttg	tggtgctcca	tgacaccaca	600
gaacaggaaa	aagaagaacg	tgaacgccgt	ctttttgtct	ctaagtgaag	tcatgaatta	660
aggacccctt	taacttcggt	taaaatcctac	ttggaggctc	ttgatgaagg	tgactttaaa	720
gaagatatgg	ctccaagttt	cataaaaagtt	tctcttgatg	aaactaatcg	gatgatgcgt	780
atgatttcag	atctttttaa	cctgtctcgg	attgataatc	aagtaacca	attagcagta	840
gagatgacta	attttactgc	ttttataact	tctattttaa	acagatttga	tttggttaaa	900
aatcagcata	caggtagcag	aaaagtctat	gaaattgtaa	gagattaccc	tattacctct	960
gtctggattg	aaattgataa	tgataaaaatg	acacagggtta	tcgagaatat	tttgaacaat	1020
gccattaagt	attctccaga	tggtggaaaa	attacagtcc	gtatgaaaac	aacagatacc	1080
caattaatta	tttccatttc	agaccaagga	ctaggtatcc	ctaaaaacaga	tttgctctct	1140
atttttgatc	ggttctatcg	tgtagacaag	gcaagaagtc	gtgccaagg	agggaccggt	1200
ctaggccttg	ccattgctaa	agaaatcatc	aagcagcacc	atggctttat	ctgggctaag	1260
agtgactatg	gtaaaggatc	gacctttact	attgtcttgc	cttatgaaaa	agatgcagcc	1320
atctatgaag	aatgggagga	agatgtagac	taa			1353

<210> SEQ ID NO 486
 <211> LENGTH: 450
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 486

Met	Thr	Arg	Asp	Ile	Ile	Gly	Asn	Leu	Ser	Thr	Phe	Glu	Leu	Ala	Ile	1	5	10	15
Leu	Ile	Leu	Leu	Val	Phe	Val	Ala	Phe	Tyr	Phe	Ile	His	Leu	Ala	Val	20	25	30	
Arg	Asp	Tyr	Arg	Asn	Ala	Arg	Ile	Ile	Arg	Met	Met	Ser	His	Lys	Ile	35	40	45	
Arg	Asp	Leu	Ile	Asn	Gly	Arg	Tyr	Thr	Asp	Ile	Ile	Asp	Glu	Lys	Ala	50	55	60	
Asp	Ile	Glu	Leu	Met	Glu	Leu	Ser	Asp	Gln	Leu	Asn	Asp	Leu	Ser	Asp	65	70	75	80
Val	Phe	Arg	Leu	Thr	His	Glu	Asn	Leu	Ala	Gln	Glu	Lys	Asn	Arg	Leu	85	90	95	
Ala	Ser	Ile	Leu	Ala	Tyr	Met	Ser	Asp	Gly	Val	Leu	Ala	Thr	Asp	Arg	100	105	110	
Ser	Gly	Lys	Ile	Ile	Met	Ile	Asn	Glu	Thr	Ala	Arg	Lys	Gln	Leu	Asn	115	120	125	
Leu	Ser	Lys	Glu	Glu	Ala	Leu	Lys	Lys	Asn	Ile	Thr	Asp	Leu	Leu	Glu	130	135	140	
Gly	Asp	Thr	Ser	Tyr	Thr	Tyr	Arg	Asp	Leu	Val	Ser	Lys	Thr	Pro	Val	145	150	155	160
Val	Thr	Val	Asn	Ser	Arg	Asn	Asp	Met	Gly	Glu	Phe	Val	Ser	Leu	Arg	165	170	175	
Leu	Arg	Phe	Ala	Leu	Asn	Arg	Arg	Glu	Ser	Gly	Phe	Ile	Ser	Gly	Leu	180	185	190	
Val	Val	Val	Leu	His	Asp	Thr	Thr	Glu	Gln	Glu	Lys	Glu	Glu	Arg	Glu	195	200	205	
Arg	Arg	Leu	Phe	Val	Ser	Asn	Val	Ser	His	Glu	Leu	Arg	Thr	Pro	Leu	210	215	220	
Thr	Ser	Val	Lys	Ser	Tyr	Leu	Glu	Ala	Leu	Asp	Glu	Gly	Ala	Leu	Lys	225	230	235	240
Glu	Asp	Ile	Ala	Pro	Ser	Phe	Ile	Lys	Val	Ser	Leu	Asp	Glu	Thr	Asn	245	250	255	
Arg	Met	Met	Arg	Met	Ile	Ser	Asp	Leu	Leu	Asn	Leu	Ser	Arg	Ile	Asp	260	265	270	
Asn	Gln	Val	Thr	Gln	Leu	Ala	Val	Glu	Met	Thr	Asn	Phe	Thr	Ala	Phe	275	280	285	
Ile	Thr	Ser	Ile	Leu	Asn	Arg	Phe	Asp	Leu	Val	Lys	Asn	Gln	His	Thr	290	295	300	
Gly	Thr	Gly	Lys	Val	Tyr	Glu	Ile	Val	Arg	Asp	Tyr	Pro	Ile	Thr	Ser	305	310	315	320
Val	Trp	Ile	Glu	Ile	Asp	Asn	Asp	Lys	Met	Thr	Gln	Val	Ile	Glu	Asn	325	330	335	
Ile	Leu	Asn	Asn	Ala	Ile	Lys	Tyr	Ser	Pro	Asp	Gly	Gly	Lys	Ile	Thr	340	345	350	
Val	Arg	Met	Lys	Thr	Thr	Asp	Thr	Gln	Leu	Ile	Ile	Ser	Ile	Ser	Asp	355	360	365	
Gln	Gly	Leu	Gly	Ile	Pro	Lys	Thr	Asp	Leu	Pro	Leu	Ile	Phe	Asp	Arg	370	375	380	
Phe	Tyr	Arg	Val	Asp	Lys	Ala	Arg	Ser	Arg	Ala	Gln	Gly	Gly	Thr	Gly	385	390	395	400
Leu	Gly	Leu	Ala	Ile	Ala	Lys	Glu	Ile	Ile	Lys	Gln	His	His	Gly	Phe				

				405					410					415			
Ile	Trp	Ala	Lys	Ser	Asp	Tyr	Gly	Lys	Gly	Ser	Thr	Phe	Thr	Ile	Val		
			420						425					430			
Leu	Pro	Tyr	Glu	Lys	Asp	Ala	Ala	Ile	Tyr	Glu	Glu	Trp	Glu	Glu	Asp		
			435				440						445				
Val	Asp																
	450																

<210> SEQ ID NO 487
 <211> LENGTH: 1335
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 487

atgcgtatag	gtctattcac	agatacctat	tttcacacaag	tttcaggagt	cgctactagt	60
attcgtacgt	taaaagaaga	gctagaaaaa	gaaggtcacg	aagtttatat	tttcaccact	120
actgatagag	atgtcaaacy	ctttgaagac	ccgaccatta	ttcgactgcc	aagtgttcct	180
tttgtgtcat	ttacggatag	acgtgtgggt	tatcgtggcc	tcatttcgtc	atacaaaatt	240
gcaaaacact	ataatcttga	tattattcat	acgcaaactg	agtttagctt	aggcttatta	300
gggaaaatga	taggcaaagc	tttgcgaaatt	cctgttgtcc	atacttacca	tacccaatat	360
gaggactacg	tgagttatat	tgccaacgga	aaaatcattc	gaccaagtat	ggcacaacct	420
cttccttaggg	gctatttgaa	ggatttggat	ggggttatct	gccaagtag	gattgtcctc	480
aatcttctag	aaggttacga	agttactatc	cctaagcggg	ttatcccaac	aggcattcct	540
ttggaaaaaat	atattcgtga	tgacatcaca	gcagaagaag	taaccaactt	aaaagcagaa	600
ttgggcatg	ctggtgatga	aacctatgta	ttgagtttgt	cacggatttc	ttatgaaaaa	660
aatattcaag	ctatcatcaa	tcagatgcca	gctatttttg	ctgaaaatgc	caagataaaag	720
cttattattg	taggaaatgg	cccctatttg	caagatttga	aacacttggc	gatgcagtta	780
gaggttgaca	aacacgtgac	ctttacaggc	atggtgcctc	atgataaggt	tgctctgtac	840
tataaggctt	gtgatttctt	tatctcagca	tcaactagtg	agactcaggg	cttgacctat	900
attgaaagtt	tggctagtgg	cactcctatt	attgctcatg	gcaatcctta	tttagatgat	960
gtggtgactg	ataaaaatgtt	tggcactctt	tattacgctg	aaacagattt	aactgatgct	1020
attattgatg	ccatactaaa	aacaccagtt	atggataaac	ggttatttagc	aaaaaaacgt	1080
tatgaaatct	cagcacagca	ctttggaaaa	tctatttaca	cgttctattt	agatacgtaa	1140
attgctagaa	atagcaaaga	agctcaaaaag	ctgagtcctt	atcttaataca	ttctggtaaa	1200
agtagttctc	taaaattagt	gcaagggtgct	attcacttgc	ctaaacgtgc	tgctaaggtc	1260
acagctatca	cctcagtaaa	agtagtcaag	gctcctatca	agctggtcca	tgctatcaaa	1320
gatttttctgg	attaa					1335

<210> SEQ ID NO 488
 <211> LENGTH: 444
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 488

Met	Arg	Ile	Gly	Leu	Phe	Thr	Asp	Thr	Tyr	Phe	Pro	Gln	Val	Ser	Gly	
1				5					10					15		
Val	Ala	Thr	Ser	Ile	Arg	Thr	Leu	Lys	Glu	Glu	Leu	Glu	Lys	Glu	Gly	
			20					25					30			
His	Glu	Val	Tyr	Ile	Phe	Thr	Thr	Thr	Asp	Arg	Asp	Val	Lys	Arg	Phe	
			35				40					45				
Glu	Asp	Pro	Thr	Ile	Ile	Arg	Leu	Pro	Ser	Val	Pro	Phe	Val	Ser	Phe	
	50					55					60					
Thr	Asp	Arg	Arg	Val	Val	Tyr	Arg	Gly	Leu	Ile	Ser	Ser	Tyr	Lys	Ile	
65				70					75					80		
Ala	Lys	His	Tyr	Asn	Leu	Asp	Ile	Ile	His	Thr	Gln	Thr	Glu	Phe	Ser	
			85					90					95			
Leu	Gly	Leu	Leu	Gly	Lys	Met	Ile	Gly	Lys	Ala	Leu	Arg	Ile	Pro	Val	
			100					105					110			
Val	His	Thr	Tyr	His	Thr	Gln	Tyr	Glu	Asp	Tyr	Val	Ser	Tyr	Ile	Ala	

		115					120					125					
Asn	Gly	Lys	Ile	Ile	Arg	Pro	Ser	Met	Val	Lys	Pro	Leu	Leu	Arg	Gly		
	130					135					140						
Tyr	Leu	Lys	Asp	Leu	Asp	Gly	Val	Ile	Cys	Pro	Ser	Arg	Ile	Val	Leu		
145					150					155					160		
Asn	Leu	Leu	Glu	Gly	Tyr	Glu	Val	Thr	Ile	Pro	Lys	Arg	Val	Ile	Pro		
			165					170						175			
Thr	Gly	Ile	Pro	Leu	Glu	Lys	Tyr	Ile	Arg	Asp	Asp	Ile	Thr	Ala	Glu		
		180						185					190				
Glu	Val	Thr	Asn	Leu	Lys	Ala	Glu	Leu	Gly	Ile	Ala	Gly	Asp	Glu	Thr		
	195						200				205						
Met	Leu	Ser	Leu	Ser	Arg	Ile	Ser	Tyr	Glu	Lys	Asn	Ile	Gln	Ala			
210					215					220							
Ile	Ile	Asn	Gln	Met	Pro	Ala	Ile	Leu	Ala	Glu	Asn	Ala	Lys	Ile	Lys		
225			230						235					240			
Leu	Ile	Ile	Val	Gly	Asn	Gly	Pro	Tyr	Leu	Gln	Asp	Leu	Lys	His	Leu		
		245						250						255			
Ala	Met	Gln	Leu	Glu	Val	Asp	Lys	His	Val	Thr	Phe	Thr	Gly	Met	Val		
	260							265					270				
Pro	His	Asp	Lys	Val	Ala	Leu	Tyr	Tyr	Lys	Ala	Cys	Asp	Phe	Phe	Ile		
	275						280					285					
Ser	Ala	Ser	Thr	Ser	Glu	Thr	Gln	Gly	Leu	Thr	Tyr	Ile	Glu	Ser	Leu		
290					295					300							
Ala	Ser	Gly	Thr	Pro	Ile	Ile	Ala	His	Gly	Asn	Pro	Tyr	Leu	Asp	Asp		
305				310					315					320			
Val	Val	Thr	Asp	Lys	Met	Phe	Gly	Thr	Leu	Tyr	Tyr	Ala	Glu	Thr	Asp		
		325						330						335			
Leu	Thr	Asp	Ala	Ile	Ile	Asp	Ala	Ile	Leu	Lys	Thr	Pro	Val	Met	Asp		
	340							345					350				
Lys	Arg	Leu	Ala	Lys	Lys	Arg	Tyr	Glu	Ile	Ser	Ala	Gln	His	Phe			
	355					360					365						
Gly	Lys	Ser	Ile	Tyr	Thr	Phe	Tyr	Leu	Asp	Thr	Leu	Ile	Ala	Arg	Asn		
370					375						380						
Ser	Lys	Glu	Ala	Gln	Lys	Leu	Ser	Leu	Tyr	Leu	Asn	His	Ser	Gly	Lys		
385				390					395					400			
Ser	Ser	Ser	Leu	Lys	Leu	Val	Gln	Gly	Ala	Ile	His	Leu	Pro	Lys	Arg		
		405						410					415				
Ala	Ala	Lys	Val	Thr	Ala	Ile	Thr	Ser	Val	Lys	Val	Val	Lys	Ala	Pro		
	420						425					430					
Ile	Lys	Leu	Val	His	Ala	Ile	Lys	Asp	Phe	Leu	Asp						
	435						440										

<210> SEQ ID NO 489

<211> LENGTH: 999

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 489

atgaaagtct	tattgtat	agaagcagaa	aattatctaa	gaaaatcagg	aattggtcga	60
gcgattaagc	atcaggctaa	agccttgta	cttggtggc	aacattttac	gactaatcca	120
agagaaactt	atgatttgg	tcatctcaat	acctatggt	taaaaagttg	gctgctgatg	180
ataaaagcac	aaaaagctgg	taagaagggt	atcatgcatg	ggcattctac	agaagaagat	240
tttagaaatt	cttttat	ttcaaata	ttatctcct	ggtttaaaaa	atacctttgt	300
cacttttaca	ataaggcaga	tgctatcatt	accctaccc	tatattctaa	gtctttgatt	360
gagagttatg	gagtgaagtc	acctat	gcagtgtcaa	atgggattga	ttggagcag	420
tacggagcag	atcctaaaaa	ggaagcagct	tttcgctcgct	actttgacat	taaagagggt	480
gaaaaagtg	ttatgggagc	aggattat	tttctgagga	aaggaattga	tgactttgtc	540
aaagttgccc	aagctatgcc	agatgttcgt	tttatctggt	ttggcgagac	caacaaatgg	600

gtcattcctg	ctcaagttcg	ccaaatgggc	aatggtaacc	acccgaaaaa	tcttattttc	660
ccaggataca	ttaaagggga	tgtttatgaa	ggcgccatga	ctgggtgcaga	tgcttttttc	720
tttccaagtc	gtgaagaaac	agaaggcatt	gttgtcttag	aagccttggc	cagtcgccag	780
caccttgttt	tacgtgatat	accagtttac	tacggatggg	ttgatcaaag	tagtgcggaa	840
ttagcaaccg	atataccagg	ttttatagaa	gctctgaaaa	aagtcttttc	tggtgccagc	900
aacaaagttg	aagctgggta	caagggtgcc	cagagtcgtc	gcctagaaac	ggttgccat	960
gccttagtag	atgtctataa	aaaagtaatg	gagttataa			999

<210> SEQ ID NO 490
 <211> LENGTH: 332
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 490

Met	Lys	Val	Leu	Leu	Tyr	Leu	Glu	Ala	Glu	Asn	Tyr	Leu	Arg	Lys	Ser	
1			5						10					15		
Gly	Ile	Gly	Arg	Ala	Ile	Lys	His	Gln	Ala	Lys	Ala	Leu	Ser	Leu	Val	
			20					25					30			
Gly	Gln	His	Phe	Thr	Thr	Asn	Pro	Arg	Glu	Thr	Tyr	Asp	Leu	Val	His	
		35				40						45				
Leu	Asn	Thr	Tyr	Gly	Leu	Lys	Ser	Trp	Leu	Leu	Met	Ile	Lys	Ala	Gln	
	50					55					60					
Lys	Ala	Gly	Lys	Lys	Val	Ile	Met	His	Gly	His	Ser	Thr	Glu	Glu	Asp	
65					70					75					80	
Phe	Arg	Asn	Ser	Phe	Ile	Phe	Ser	Asn	Leu	Leu	Ser	Pro	Trp	Phe	Lys	
			85						90					95		
Lys	Tyr	Leu	Cys	His	Phe	Tyr	Asn	Lys	Ala	Asp	Ala	Ile	Ile	Thr	Pro	
		100						105					110			
Thr	Leu	Tyr	Ser	Lys	Ser	Leu	Ile	Glu	Ser	Tyr	Gly	Val	Lys	Ser	Pro	
	115						120					125				
Ile	Phe	Ala	Val	Ser	Asn	Gly	Ile	Asp	Leu	Glu	Gln	Tyr	Gly	Ala	Asp	
	130					135					140					
Pro	Lys	Lys	Glu	Ala	Ala	Phe	Arg	Arg	Tyr	Phe	Asp	Ile	Lys	Glu	Gly	
145					150					155					160	
Glu	Lys	Val	Val	Met	Gly	Ala	Gly	Leu	Phe	Phe	Leu	Arg	Lys	Gly	Ile	
			165						170					175		
Asp	Asp	Phe	Val	Lys	Val	Ala	Gln	Ala	Met	Pro	Asp	Val	Arg	Phe	Ile	
		180						185					190			
Trp	Phe	Gly	Glu	Thr	Asn	Lys	Trp	Val	Ile	Pro	Ala	Gln	Val	Arg	Gln	
	195					200						205				
Met	Val	Asn	Gly	Asn	His	Pro	Lys	Asn	Leu	Ile	Phe	Pro	Gly	Tyr	Ile	
	210				215						220					
Lys	Gly	Asp	Val	Tyr	Glu	Gly	Ala	Met	Thr	Gly	Ala	Asp	Ala	Phe	Phe	
225					230					235					240	
Phe	Pro	Ser	Arg	Glu	Glu	Thr	Glu	Gly	Ile	Val	Val	Leu	Glu	Ala	Leu	
			245						250					255		
Ala	Ser	Arg	Gln	His	Leu	Val	Leu	Arg	Asp	Ile	Pro	Val	Tyr	Tyr	Gly	
		260						265					270			
Trp	Val	Asp	Gln	Ser	Ser	Ala	Glu	Leu	Ala	Thr	Asp	Ile	Pro	Gly	Phe	
	275						280					285				
Ile	Glu	Ala	Leu	Lys	Lys	Val	Phe	Ser	Gly	Ala	Ser	Asn	Lys	Val	Glu	
	290					295					300					
Ala	Gly	Tyr	Lys	Val	Ala	Gln	Ser	Arg	Arg	Leu	Glu	Thr	Val	Gly	His	
305					310					315					320	
Ala	Leu	Val	Asp	Val	Tyr	Lys	Lys	Val	Met	Glu	Leu					
			325						330							

<210> SEQ ID NO 491

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<211> LENGTH: 987
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 491
  ttgaaatatc tcagcttttg tgttacaatt gccctaaaat tccatttgaa agaaaagtct      60
  atgacactac tatctatcat tgtcccctgc tttaatgaag aagcaaacat tctcccttat      120
  tttgaagaaa tgcatacaact agaaacgtcc atgaccaacc aacttgcttt tgaatacatt      180
  tttattgatg atggttctaa ggataacacc ttgggtatatt tgcgtgagct agctgctcgc      240
  tttccaaatg tgcattatct gtcttttttca cgccattttg gcaaggaagc tgggctctta      300
  gctggactaa aagaagccaa aggcaattac attactgtga tggatgtgga tctgcaagat      360
  ccacccgaac ttttgccaat tatgtacgct aagctaaaag aagggttatga catcggtggc      420
  accaggcgcc aaaatagaca aggagaacca ctaattcggt caatgtgttc gaatctattt      480
  tatggactga tcaaacactt atcagatact gaaatgggtca atggagtctg ggattatcgg      540
  ttaatgacca gacaagtcgt tgatagcatt cttgagttgg gagagggttaa tcgttttttca      600
  aaagggatct tttcgtgggt tgggtatcgt atcacctatc ttagttttga aaaccaaaaa      660
  cgcaaatatg gaaaaagtcg ttggcattttt tgggagttgc tccgatattc tttagatggc      720
  tttatcaact tttcagaaat gccgttaacc attgctacct ggacaggggac tttcagcttt      780
  ttgattttcta ttttcgccat cttattttatc attatcagaa agatactctt tgggtatcct      840
  gtctctgggt gggccagcac tgtctctatt attttatttca tgggaggcat tcagctcttt      900
  tgcattgggt ttattggaaa atatattttca aaaatattcc ttgaaactaa aaaaaggcct      960
  ctctatatta tcaaagaaaa acattaa

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<210> SEQ ID NO 492
<211> LENGTH: 328
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 492
  Met Lys Tyr Leu Ser Phe Cys Val Thr Ile Ala Leu Lys Phe His Leu
  1          5          10          15
  Lys Glu Lys Ser Met Thr Leu Leu Ser Ile Ile Val Pro Cys Phe Asn
  20          25          30
  Glu Glu Ala Asn Ile Leu Pro Tyr Phe Glu Glu Met His Gln Leu Glu
  35          40          45
  Thr Ser Met Thr Asn Gln Leu Ala Phe Glu Tyr Ile Phe Ile Asp Asp
  50          55          60
  Gly Ser Lys Asp Asn Thr Leu Gly Ile Leu Arg Glu Leu Ala Ala Arg
  65          70          75          80
  Phe Pro Asn Val His Tyr Leu Ser Phe Ser Arg His Phe Gly Lys Glu
  85          90          95
  Ala Gly Leu Leu Ala Gly Leu Lys Glu Ala Lys Gly Asn Tyr Ile Thr
  100         105         110
  Val Met Asp Val Asp Leu Gln Asp Pro Pro Glu Leu Leu Pro Ile Met
  115         120         125
  Tyr Ala Lys Leu Lys Glu Gly Tyr Asp Ile Val Gly Thr Arg Arg Gln
  130         135         140
  Asn Arg Gln Gly Glu Pro Leu Ile Arg Ser Met Cys Ser Asn Leu Phe
  145         150         155         160
  Tyr Gly Leu Ile Lys His Leu Ser Asp Thr Glu Met Val Asn Gly Val
  165         170         175
  Arg Asp Tyr Arg Leu Met Thr Arg Gln Val Val Asp Ser Ile Leu Glu
  180         185         190
  Leu Gly Glu Val Asn Arg Phe Ser Lys Gly Ile Phe Ser Trp Val Gly
  195         200         205
  Tyr Arg Ile Thr Tyr Leu Ser Phe Glu Asn Gln Lys Arg Lys Tyr Gly
  210         215         220
  Lys Ser Arg Trp His Phe Trp Glu Leu Leu Arg Tyr Ser Leu Asp Gly
  225         230         235         240

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Phe	Ile	Asn	Phe	Ser	Glu	Met	Pro	Leu	Thr	Ile	Ala	Thr	Trp	Thr	Gly
				245					250					255	
Thr	Phe	Ser	Phe	Leu	Ile	Ser	Ile	Phe	Ala	Ile	Leu	Phe	Ile	Ile	Ile
			260					265					270		
Arg	Lys	Ile	Leu	Phe	Gly	Asp	Pro	Val	Ser	Gly	Trp	Ala	Ser	Thr	Val
		275				280					285				
Ser	Ile	Ile	Leu	Phe	Met	Gly	Gly	Ile	Gln	Leu	Phe	Cys	Met	Gly	Ile
	290					295				300					
Ile	Gly	Lys	Tyr	Ile	Ser	Lys	Ile	Phe	Leu	Glu	Thr	Lys	Lys	Arg	Pro
305					310					315					320
Leu	Tyr	Ile	Ile	Lys	Glu	Lys	His								
				325											

<210> SEQ ID NO 493

<211> LENGTH: 1194

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 493

gtgaactggc	gacaaaatct	aaaagtggct	tggcttggta	acttctttac	tggggcaagc	60
ttttcacttg	ttatgccttt	tatggctcta	tatgtggaaa	atttaggtac	tccgacagaa	120
ttagtagaat	actatgctgg	tctggcagtt	gctgtgacgg	cacttgcttc	agctttattt	180
gctcctgttt	gggggaagtt	ggctgatcgt	tatggccgaa	aacctatgat	gctgcgagcc	240
agttttgtta	tgacattttac	aatgggtggt	ttagctatta	ttcctaattgt	gttttggtta	300
ctcattttga	gattattaac	aggtgtctct	gcgggctatg	tgccaaatgc	cactgccttg	360
attgccagcc	aagccccaaa	agaggagtca	ggttatgctt	taggcacatt	agcaacagga	420
gtgacagcag	gcgctttaat	tggtccttta	ctagggggaa	ttttggcaga	gctattagga	480
attcgacaag	ttttcttatt	agttggtgtg	atattatttt	tatgttcctt	aatgacagct	540
gtttatgtta	aagaagagtt	taagccgggt	aggcgctttg	agatgatacc	tacaaaagtc	600
attttaaaac	aggtaaaaaag	tccccagatt	atgcttggtt	tatttgtgac	tagtatgatt	660
attcaaattt	cagctcaatc	agtggccccc	attttatcat	tgtatattcg	tcactttggt	720
caaactcaca	acttaatggt	tacttcaggc	ctggtagttt	cggccatggg	gttttctagc	780
ttattttagca	gttcttactt	aggaaaatta	ggagatcgat	ttggcaatca	tcggttattg	840
ttagccgctt	tgtgttatag	ctttatcatg	tatttttagca	gtgccttagc	gcagaccagt	900
tttcaattag	gagtactacg	ctttgcttat	gggtttggtg	tgggcgcttt	gatgccaaagt	960
attaactcct	tactaactaa	gttaacacca	aaagaaggta	tttctagagt	atttgcctat	1020
aatcaaatgt	ttagtaacct	tggtaagtc	attggccctt	ttattggatc	aaatgtggct	1080
gtagtgttag	gctaccgttc	tgttttttat	gtgactagtt	tgatttgtgt	tgttaattta	1140
atatggagtt	tgattatatt	tcgaaaatat	attaaagtta	aggatattgt	gtga	1194

<210> SEQ ID NO 494

<211> LENGTH: 397

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 494

Met	Asn	Trp	Arg	Gln	Asn	Leu	Lys	Val	Ala	Trp	Leu	Gly	Asn	Phe	Phe
1				5					10					15	
Thr	Gly	Ala	Ser	Phe	Ser	Leu	Val	Met	Pro	Phe	Met	Ala	Leu	Tyr	Val
			20					25					30		
Glu	Asn	Leu	Gly	Thr	Pro	Thr	Glu	Leu	Val	Glu	Tyr	Tyr	Ala	Gly	Leu
	35					40					45				
Ala	Val	Ala	Val	Thr	Ala	Leu	Ala	Ser	Ala	Leu	Phe	Ala	Pro	Val	Trp
	50					55					60				
Gly	Lys	Leu	Ala	Asp	Arg	Tyr	Gly	Arg	Lys	Pro	Met	Met	Leu	Arg	Ala
65				70					75					80	
Ser	Phe	Val	Met	Thr	Phe	Thr	Met	Gly	Gly	Leu	Ala	Ile	Ile	Pro	Asn
			85					90						95	
Val	Phe	Trp	Leu	Leu	Ile	Leu	Arg	Leu	Leu	Thr	Gly	Val	Ser	Ala	Gly

			100					105				110				
Tyr	Val	Pro	Asn	Ala	Thr	Ala	Leu	Ile	Ala	Ser	Gln	Ala	Pro	Lys	Glu	
		115					120					125				
Glu	Ser	Gly	Tyr	Ala	Leu	Gly	Thr	Leu	Ala	Thr	Gly	Val	Thr	Ala	Gly	
		130					135					140				
Ala	Leu	Ile	Gly	Pro	Leu	Leu	Gly	Gly	Ile	Leu	Ala	Glu	Leu	Leu	Gly	
145					150					155					160	
Ile	Arg	Gln	Val	Phe	Leu	Leu	Val	Gly	Val	Ile	Leu	Phe	Leu	Cys	Ser	
			165						170					175		
Leu	Met	Thr	Ala	Val	Tyr	Val	Lys	Glu	Glu	Phe	Lys	Pro	Val	Arg	Arg	
		180						185					190			
Phe	Glu	Met	Ile	Pro	Thr	Lys	Val	Ile	Leu	Lys	Gln	Val	Lys	Ser	Pro	
		195					200					205				
Gln	Ile	Met	Leu	Gly	Leu	Phe	Val	Thr	Ser	Met	Ile	Ile	Gln	Ile	Ser	
210						215					220					
Ala	Gln	Ser	Val	Ala	Pro	Ile	Leu	Ser	Leu	Tyr	Ile	Arg	His	Leu	Gly	
225				230						235					240	
Gln	Thr	His	Asn	Leu	Met	Phe	Thr	Ser	Gly	Leu	Val	Val	Ser	Ala	Met	
			245						250					255		
Gly	Phe	Ser	Ser	Leu	Phe	Ser	Ser	Ser	Tyr	Leu	Gly	Lys	Leu	Gly	Asp	
			260					265					270			
Arg	Phe	Gly	Asn	His	Arg	Leu	Leu	Leu	Ala	Ala	Leu	Cys	Tyr	Ser	Phe	
		275				280					285					
Ile	Met	Tyr	Phe	Ser	Ser	Ala	Leu	Ala	Gln	Thr	Ser	Phe	Gln	Leu	Gly	
290						295					300					
Val	Leu	Arg	Phe	Ala	Tyr	Gly	Phe	Gly	Val	Gly	Ala	Leu	Met	Pro	Ser	
305				310					315					320		
Ile	Asn	Ser	Leu	Leu	Thr	Lys	Leu	Thr	Pro	Lys	Glu	Gly	Ile	Ser	Arg	
			325					330						335		
Val	Phe	Ala	Tyr	Asn	Gln	Met	Phe	Ser	Asn	Leu	Gly	Gln	Val	Ile	Gly	
		340						345					350			
Pro	Phe	Ile	Gly	Ser	Asn	Val	Ala	Val	Val	Leu	Gly	Tyr	Arg	Ser	Val	
		355				360					365					
Phe	Tyr	Val	Thr	Ser	Leu	Ile	Val	Phe	Val	Asn	Leu	Ile	Trp	Ser	Leu	
370					375						380					
Ile	Ile	Phe	Arg	Lys	Tyr	Ile	Lys	Val	Lys	Asp	Ile	Val				
385					390					395						

<210> SEQ ID NO 495

<211> LENGTH: 855

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 495

atgtctatga	aattttttga	gggcttgatg	tcataccact	ttttacaaaa	tgcactgata	60
acggctgtag	tcattggtat	cgtctcaggt	gctgtagggg	gttttattat	ccttaggtca	120
atgtctctta	tgggtgatgc	catctcacac	gctgttttac	caggggttgc	tttgtcattt	180
attttaggag	tcaatttttt	tattggagcg	attatttttg	ggttattagc	ttctgttatt	240
attacttata	tcaaggaaaa	ctctgtcatt	aaaggagata	cggctattgg	tatcaccttt	300
agctcttttt	tggcactggg	agtcattctg	ataggggtag	ccaatagttc	gacggactta	360
tttcatattt	tgtttgggaa	tatttttagct	gtgcaagata	gcgataagtg	gattactatt	420
gggtgtttcga	tttttgtttt	agtggttatt	agtccttttt	tcaaagaact	attattaaca	480
tcatttgatc	ctatcttagc	caaatcaatg	ggtgtgaagg	tcaatgcgta	tcattatttg	540
ttgatggccc	tattaacttt	agtggctgtt	acggcgatgc	aaagcgtggg	tactatcttg	600
attgttgcc	tattgattac	gccagcagcg	acagcttatt	tatatgctaa	tagcttaaaa	660
gtaatgtag	tgatgtcatc	tttactaggc	gcttttagcat	cggtttttagg	gctttatttg	720
ggctatacct	ttaatgttgc	cgcagggtca	agtatcgtag	tgacttctgc	gatgatgttt	780
ttgatcagtt	tctttgtttc	acccaagcaa	ggctacctta	aaagatggat	gcaaaaaaaaa	840

gaaaaaacac cttaa

855

<210> SEQ ID NO 496

<211> LENGTH: 284

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 496

```
Met Ser Met Lys Phe Phe Glu Gly Leu Met Ser Tyr His Phe Leu Gln
 1          5          10          15
Asn Ala Leu Ile Thr Ala Val Val Ile Gly Ile Val Ser Gly Ala Val
 20          25          30
Gly Cys Phe Ile Ile Leu Arg Ser Met Ser Leu Met Gly Asp Ala Ile
 35          40          45
Ser His Ala Val Leu Pro Gly Val Ala Leu Ser Phe Ile Leu Gly Val
 50          55          60
Asn Phe Phe Ile Gly Ala Ile Ile Phe Gly Leu Leu Ala Ser Val Ile
 65          70          75          80
Ile Thr Tyr Ile Lys Glu Asn Ser Val Ile Lys Gly Asp Thr Ala Ile
 85          90          95
Gly Ile Thr Phe Ser Ser Phe Leu Ala Leu Gly Val Ile Leu Ile Gly
100          105          110
Val Ala Asn Ser Ser Thr Asp Leu Phe His Ile Leu Phe Gly Asn Ile
115          120          125
Leu Ala Val Gln Asp Ser Asp Lys Trp Ile Thr Ile Gly Val Ser Ile
130          135          140
Phe Val Leu Val Val Ile Ser Leu Phe Phe Lys Glu Leu Leu Leu Thr
145          150          155          160
Ser Phe Asp Pro Ile Leu Ala Lys Ser Met Gly Val Lys Val Asn Ala
165          170          175
Tyr His Tyr Leu Leu Met Val Leu Leu Thr Leu Val Ala Val Thr Ala
180          185          190
Met Gln Ser Val Gly Thr Ile Leu Ile Val Ala Leu Leu Ile Thr Pro
195          200          205
Ala Ala Thr Ala Tyr Leu Tyr Ala Asn Ser Leu Lys Val Met Leu Val
210          215          220
Met Ser Ser Leu Leu Gly Ala Leu Ala Ser Val Leu Gly Leu Tyr Leu
225          230          235          240
Gly Tyr Thr Phe Asn Val Ala Ala Gly Ser Ser Ile Val Leu Thr Ser
245          250          255
Ala Met Met Phe Leu Ile Ser Phe Phe Val Ser Pro Lys Gln Gly Tyr
260          265          270
Leu Lys Arg Trp Met Gln Lys Lys Glu Lys Thr Pro
275          280
```

<210> SEQ ID NO 497

<211> LENGTH: 342

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 497

```
atgacactaa aaaaacacta ttatcttctc agcctgctag ctcttgtaac gggttggtgct      60
gcctttaaca caagccagag tgtcagtgca caagtttata gcaatgaagg gtatcaccag      120
catttgactg atgaaaaatc acacctgcaa tatagtaaag acaacgcaca acttcaattg      180
agaaatatcc ttgacggcta ccaaaatgac ctagggagac actactctag ctattattac      240
tacaacctaa gaaccgttat gggactatca agtgagcaag acattgaaaa acatatgaa      300
gagcttaaga acaagttaca tgatatgtac aatcattatt aa      342
```

<210> SEQ ID NO 498

<211> LENGTH: 113

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 498

```
Met Thr Leu Lys Lys His Tyr Tyr Leu Leu Ser Leu Leu Ala Leu Val
1          5          10          15
Thr Val Gly Ala Ala Phe Asn Thr Ser Gln Ser Val Ser Ala Gln Val
20          25          30
Tyr Ser Asn Glu Gly Tyr His Gln His Leu Thr Asp Glu Lys Ser His
35          40          45
Leu Gln Tyr Ser Lys Asp Asn Ala Gln Leu Gln Leu Arg Asn Ile Leu
50          55          60
Asp Gly Tyr Gln Asn Asp Leu Gly Arg His Tyr Ser Ser Tyr Tyr Tyr
65          70          75          80
Tyr Asn Leu Arg Thr Val Met Gly Leu Ser Ser Glu Gln Asp Ile Glu
85          90          95
Lys His Tyr Glu Glu Leu Lys Asn Lys Leu His Asp Met Tyr Asn His
100         105         110
Tyr
```

<210> SEQ ID NO 499

<211> LENGTH: 1383

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 499

```
atgacaaatt atgccattat tttagcagcg ggcaaaggga ctcgcatgac ttctgatctc 60
ccaaaagttc ttcataaagt atctggacta accatgcttg agcatgtttt tcgtagtgta 120
aaagcgatta gtcctgaaaa atccgtgacg gttattggtc acaaatcaga aatggtacgt 180
gctgtccttag cagatcaatc agcctttgtc catcaaacag agcagttagg aactggccat 240
gccgtgatga tggcagaaac acaactagaa ggactagaag ggcatacctt ggtgattgca 300
ggagatactc ccttgatcac tggagaaagc ctgaagagtc tgattgattt tcatgtgaat 360
cataaaaatg tcgccactat tttaacagct acggctcaag atccatttgg ttatggtcgt 420
attgttcgca acaaagatgg cgaagtgatc aagattgttg agcaaaaaga cgccaatgag 480
tatgagcaac aattaaaaga aatcaatata ggaacctatg tgtttgataa caagcgtctc 540
tttgaagcgc tcaaattgcat cactaccaac aatgctcaag gagagtatta cctgactgac 600
gttgtggcta tttttagagc aaacaaagaa aaggtaggag cctatatcct gagagacttc 660
aatgaaagtc tgggagtaaa tgatcgtgtg gccttagcaa tagctgaaac agtgatgcgt 720
cagcgcatta cccaaaaaca tatggtcaat ggggtgactt tccaaaatcc tgaaactgtt 780
tatattgaaa gcgatgttga gattgctcca gacgtcctta tcgaaggaaa tgtgacctta 840
aaagggcgta cacatatcgg ctcaggaact gtcttgacga atggtactta tattgtggat 900
tctgaaattg gtgataactg tgttgttacc aattcgatga tcgaatcatc tgtttttagct 960
gcaggagtta cggttgccc ttacgcccac cttcgaccgg gaacgacctt agatagggaa 1020
gtccatatcg gtaactttgt cgagggtcaag ggttctcaca ttggtgaaaa aacaaaggct 1080
gggcatctga cttatattgg aaacgctcag gttgggtcct cagtcaatgt tggggctgga 1140
accatcactg tcaactacga cggccaaaac aaatatgaaa cagtcattgg agatcacgct 1200
tttattggga gcaactcgac tctcattgca cttttggaag ttggggatca cgctttaaca 1260
gcagcagggt caacgatctt aaaaacagtt cctatcgata gcattgctat tggctcgtagc 1320
cgccaagtca caaaagaagg ttatgccaaag cgctagcgc atcacccaag tcgaagcaaa 1380
taa 1383
```

<210> SEQ ID NO 500

<211> LENGTH: 460

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 500

```
Met Thr Asn Tyr Ala Ile Ile Leu Ala Ala Gly Lys Gly Thr Arg Met
1          5          10          15
```

Thr	Ser	Asp	Leu	Pro	Lys	Val	Leu	His	Lys	Val	Ser	Gly	Leu	Thr	Met
			20					25					30		
Leu	Glu	His	Val	Phe	Arg	Ser	Val	Lys	Ala	Ile	Ser	Pro	Glu	Lys	Ser
		35					40					45			
Val	Thr	Val	Ile	Gly	His	Lys	Ser	Glu	Met	Val	Arg	Ala	Val	Leu	Ala
	50				55					60					
Asp	Gln	Ser	Ala	Phe	Val	His	Gln	Thr	Glu	Gln	Leu	Gly	Thr	Gly	His
65					70					75					80
Ala	Val	Met	Met	Ala	Glu	Thr	Gln	Leu	Glu	Gly	Leu	Glu	Gly	His	Thr
				85					90					95	
Leu	Val	Ile	Ala	Gly	Asp	Thr	Pro	Leu	Ile	Thr	Gly	Glu	Ser	Leu	Lys
			100					105					110		
Ser	Leu	Ile	Asp	Phe	His	Val	Asn	His	Lys	Asn	Val	Ala	Thr	Ile	Leu
		115					120					125			
Thr	Ala	Thr	Ala	Gln	Asp	Pro	Phe	Gly	Tyr	Gly	Arg	Ile	Val	Arg	Asn
	130					135					140				
Lys	Asp	Gly	Glu	Val	Ile	Lys	Ile	Val	Glu	Gln	Lys	Asp	Ala	Asn	Glu
145					150					155					160
Tyr	Glu	Gln	Gln	Leu	Lys	Glu	Ile	Asn	Thr	Gly	Thr	Tyr	Val	Phe	Asp
				165					170					175	
Asn	Lys	Arg	Leu	Phe	Glu	Ala	Leu	Lys	Cys	Ile	Thr	Thr	Asn	Asn	Ala
			180					185					190		
Gln	Gly	Glu	Tyr	Tyr	Leu	Thr	Asp	Val	Val	Ala	Ile	Phe	Arg	Ala	Asn
		195					200					205			
Lys	Glu	Lys	Val	Gly	Ala	Tyr	Ile	Leu	Arg	Asp	Phe	Asn	Glu	Ser	Leu
	210					215					220				
Gly	Val	Asn	Asp	Arg	Val	Ala	Leu	Ala	Ile	Ala	Glu	Thr	Val	Met	Arg
225					230					235					240
Gln	Arg	Ile	Thr	Gln	Lys	His	Met	Val	Asn	Gly	Val	Thr	Phe	Gln	Asn
				245					250					255	
Pro	Glu	Thr	Val	Tyr	Ile	Glu	Ser	Asp	Val	Glu	Ile	Ala	Pro	Asp	Val
			260					265					270		
Leu	Ile	Glu	Gly	Asn	Val	Thr	Leu	Lys	Gly	Arg	Thr	His	Ile	Gly	Ser
		275					280					285			
Gly	Thr	Val	Leu	Thr	Asn	Gly	Thr	Tyr	Ile	Val	Asp	Ser	Glu	Ile	Gly
	290					295					300				
Asp	Asn	Cys	Val	Val	Thr	Asn	Ser	Met	Ile	Glu	Ser	Ser	Val	Leu	Ala
305					310					315					320
Ala	Gly	Val	Thr	Val	Gly	Pro	Tyr	Ala	His	Leu	Arg	Pro	Gly	Thr	Thr
				325					330					335	
Leu	Asp	Arg	Glu	Val	His	Ile	Gly	Asn	Phe	Val	Glu	Val	Lys	Gly	Ser
			340					345					350		
His	Ile	Gly	Glu	Lys	Thr	Lys	Ala	Gly	His	Leu	Thr	Tyr	Ile	Gly	Asn
		355					360					365			
Ala	Gln	Val	Gly	Ser	Ser	Val	Asn	Val	Gly	Ala	Gly	Thr	Ile	Thr	Val
						375					380				
Asn	Tyr	Asp	Gly	Gln	Asn	Lys	Tyr	Glu	Thr	Val	Ile	Gly	Asp	His	Ala
385					390					395					400
Phe	Ile	Gly	Ser	Asn	Ser	Thr	Leu	Ile	Ala	Pro	Leu	Glu	Val	Gly	Asp
				405					410					415	
His	Ala	Leu	Thr	Ala	Ala	Gly	Ser	Thr	Ile	Ser	Lys	Thr	Val	Pro	Ile
			420					425					430		
Asp	Ser	Ile	Ala	Ile	Gly	Arg	Ser	Arg	Gln	Val	Thr	Lys	Glu	Gly	Tyr
		435					440					445			
Ala	Lys	Arg	Leu	Ala	His	His	Pro	Ser	Arg	Ser	Lys				
	450					455					460				

<210> SEQ ID NO 501
 <211> LENGTH: 1344
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 501

```

ttgtttatgg aagaggatta taacaaaaga gaacctgaga agtttacgca atttctgcgc      60
cgtcaaaagg tcgctctttt tgctcgcatth tttggttatg tgtgtgctta cttggtagcg      120
aacaatttca aactaatgtc aaacactatt atggtgcaaa atggttgga caaggctcaa      180
attgcatct tggtatcggt tttgaccgtt tcttatggct tagcaaaatt ctatatggga      240
gccttagggg atcggtgtag cttgaggaag ctcttttcaa tcagcttggg tgcaagcgct      300
ttgatttgta ttttaattgg ttttttcaat agttcaatgg tggtagtagg aatactgcta      360
gtcttggtgt gtgtcgtaga aggtgccttg gcacctgcct cacaagccat gattgccaat      420
tattttccaa ataaaacacg cggcggagcc atcgctggat ggaacatttc tcaaaacatg      480
ggatcagccc tcttgccatt aaccatcgcc ttgctcacca gtatgggctt ggtggtacca      540
gctaattggca atattttact tgccttttta atccctggcg ttttagtggt cttgtttgct      600
ttgtgttgct ggaagcttgg cggtgataac cctgagtctg agggacttga ctctcttcga      660
acgatgtatg gtgatgcggg cgagtcagct gttgccagtg aagaagaaaa gcataacctg      720
tcttattggc aactcatctg gaaatacgtt ttttgtaacc cgtcgctctt acttgttgct      780
gctgtcaatg tggcccttta ttttgttcgt tttgggattg aagactggat gccgatctac      840
ttgtcacaag tagccaatat gtcagaggct catatccatt ttgcatcttc aatgtagtag      900
tgggtcgcta ttccaggctc gctggtatth gcgtggttag cggttcgta tcctaataaa      960
atggccaagg ttggggctat tgggcttttt gtgttagcgg ctattgtctt tgtctatgaa     1020
cgcttgactg ccacaggtgc tccaaattat ttctgtgtgc ttgttattgc aggtatttta     1080
gggtcattga tttatggccc acagttgatc gtgaatattt taacaatcaa ctttgttcct     1140
ttaaatgttg caggaacagc gattggtttt gtaggagtaa cagcttatct catcggaat     1200
atgggagcaa actggctgat gccgattttg gcagatgggt ttggctgggt ttggtcatat     1260
attgtcgttg cagccttatc tgctttttca gcggttggtt atttgatttt agccaaacgt     1320
gaggaagaaa tcatcaaaga ttag                                     1344

```

<210> SEQ ID NO 502
 <211> LENGTH: 447
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 502

```

Met Phe Met Glu Glu Asp Tyr Asn Lys Arg Glu Pro Glu Lys Phe Thr
1          5          10          15
Gln Phe Leu Arg Arg Gln Lys Val Val Phe Phe Val Ala Phe Phe Gly
20          25          30
Tyr Val Cys Ala Tyr Leu Val Arg Asn Asn Phe Lys Leu Met Ser Asn
35          40          45
Thr Ile Met Val Gln Asn Gly Trp Asp Lys Ala Gln Ile Ala Ile Leu
50          55          60
Leu Ser Cys Leu Thr Val Ser Tyr Gly Leu Ala Lys Phe Tyr Met Gly
65          70          75          80
Ala Leu Gly Asp Arg Val Ser Leu Arg Lys Leu Phe Ser Ile Ser Leu
85          90          95
Gly Ala Ser Ala Leu Ile Cys Ile Leu Ile Gly Phe Phe Asn Ser Ser
100         105         110
Met Val Val Leu Gly Ile Leu Leu Val Leu Cys Gly Val Val Gln Gly
115         120         125
Ala Leu Ala Pro Ala Ser Gln Ala Met Ile Ala Asn Tyr Phe Pro Asn
130         135         140
Lys Thr Arg Gly Gly Ala Ile Ala Gly Trp Asn Ile Ser Gln Asn Met
145         150         155         160
Gly Ser Ala Leu Leu Pro Leu Thr Ile Ala Leu Leu Thr Ser Met Gly
165         170         175
Leu Val Val Pro Ala Asn Gly Asn Ile Leu Leu Ala Phe Leu Ile Pro

```


			180					185				190					
Gly	Val	Leu	Val	Phe	Leu	Phe	Ala	Leu	Cys	Cys	Trp	Lys	Leu	Gly	Gly		
		195					200					205					
Asp	Asn	Pro	Glu	Ser	Glu	Gly	Leu	Asp	Ser	Leu	Arg	Thr	Met	Tyr	Gly		
		210				215					220						
Asp	Ala	Gly	Glu	Ser	Ala	Val	Ala	Ser	Glu	Glu	Glu	Lys	His	Asn	Leu		
225					230					235					240		
Ser	Tyr	Trp	Gln	Leu	Ile	Trp	Lys	Tyr	Val	Phe	Cys	Asn	Pro	Ser	Leu		
			245						250					255			
Leu	Leu	Val	Ala	Ala	Val	Asn	Val	Ala	Leu	Tyr	Phe	Val	Arg	Phe	Gly		
		260						265					270				
Ile	Glu	Asp	Trp	Met	Pro	Ile	Tyr	Leu	Ser	Gln	Val	Ala	Asn	Met	Ser		
		275					280					285					
Glu	Ala	His	Ile	His	Phe	Ala	Ile	Ser	Met	Leu	Glu	Trp	Val	Ala	Ile		
	290					295					300						
Pro	Gly	Ser	Leu	Val	Phe	Ala	Trp	Leu	Ala	Val	Arg	Tyr	Pro	Asn	Lys		
305					310					315					320		
Met	Ala	Lys	Val	Gly	Ala	Ile	Gly	Leu	Phe	Val	Leu	Ala	Ala	Ile	Val		
			325					330						335			
Phe	Val	Tyr	Glu	Arg	Leu	Thr	Ala	Thr	Gly	Ala	Pro	Asn	Tyr	Phe	Leu		
		340						345					350				
Leu	Leu	Val	Ile	Ala	Gly	Ile	Leu	Gly	Ser	Leu	Ile	Tyr	Gly	Pro	Gln		
	355					360					365						
Leu	Ile	Val	Asn	Ile	Leu	Thr	Ile	Asn	Phe	Val	Pro	Leu	Asn	Val	Ala		
	370					375					380						
Gly	Thr	Ala	Ile	Gly	Phe	Val	Gly	Val	Thr	Ala	Tyr	Leu	Ile	Gly	Asn		
385				390				395						400			
Met	Gly	Ala	Asn	Trp	Leu	Met	Pro	Ile	Leu	Ala	Asp	Gly	Phe	Gly	Trp		
			405					410					415				
Phe	Trp	Ser	Tyr	Ile	Val	Val	Ala	Ala	Leu	Ser	Ala	Phe	Ser	Ala	Val		
		420						425				430					
Gly	Tyr	Leu	Ile	Leu	Ala	Lys	Arg	Glu	Glu	Glu	Ile	Ile	Lys	Asp			
	435					440					445						

<210> SEQ ID NO 503

<211> LENGTH: 615

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 503

atgaaaaaaaa	cattaacctt	gctactggca	ctctttgcc	tcggggtaac	tagtagcgct	60
agagcggagg	atgaacagaa	taagtttata	cttgatggat	tacaggaaaa	agtaaaagaa	120
gtagtgtag	cagatttttc	tggtggagaa	tctaaaatca	aagtctggct	tcctcaagct	180
tggtcgggtca	aaattttctag	agaacattca	ccaaaatcaa	gcattttctaa	ttctggagaa	240
caaaaacctt	taagcaatag	ctcagagaat	aaagaaggct	aatttttctaa	aagattacct	300
tatggtaccc	aacatactat	taaattatca	tcccaactta	caaaagggtga	gagagtcact	360
ttgacattca	gagatgaaga	tttttgggga	gcaggttact	gcttctatag	agattcacta	420
tccataaaaag	aagacaaaaca	atacgaagaa	gaaattaaga	aaattgagga	tgacctagag	480
agacaagatc	ttgaaaaatga	tgactagag	atgttttaaaa	aacaaaccga	aagagaggct	540
aataaacctt	ggcatcagcg	gttaagcgaa	aacatccaag	atcagtgggtg	gaactttaag	600
ggactgtttc	agtga					615

<210> SEQ ID NO 504

<211> LENGTH: 204

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 504

Met Lys Lys Thr Leu Thr Leu Leu Leu Ala Leu Phe Ala Ile Gly Val

1				5					10					15			
Thr	Ser	Ser	Val	Arg	Ala	Glu	Asp	Glu	Gln	Asn	Lys	Phe	Ile	Leu	Asp		
			20					25					30				
Gly	Leu	Gln	Glu	Lys	Val	Lys	Glu	Val	Ser	Val	Ser	Asp	Phe	Ser	Val		
		35					40					45					
Gly	Glu	Ser	Lys	Ile	Lys	Val	Trp	Leu	Pro	Gln	Ala	Trp	Ser	Val	Lys		
	50				55					60							
Ile	Ser	Arg	Glu	His	Ser	Pro	Lys	Ser	Ser	Ile	Ser	Asn	Ser	Gly	Glu		
65				70				75						80			
Gln	Lys	Pro	Leu	Ser	Asn	Ser	Ser	Glu	Asn	Lys	Glu	Gly	Gln	Phe	Ser		
			85					90					95				
Lys	Arg	Leu	Pro	Tyr	Gly	Thr	Gln	His	Thr	Ile	Lys	Leu	Ser	Ser	Gln		
		100					105						110				
Leu	Thr	Lys	Gly	Glu	Arg	Val	Thr	Leu	Thr	Phe	Arg	Asp	Glu	Asp	Phe		
	115						120					125					
Trp	Gly	Ala	Gly	Tyr	Cys	Phe	Tyr	Arg	Asp	Ser	Leu	Ser	Ile	Lys	Glu		
	130					135				140							
Asp	Lys	Gln	Tyr	Glu	Glu	Glu	Ile	Lys	Lys	Ile	Glu	Asp	Asp	Leu	Glu		
145				150				155						160			
Arg	Gln	Asp	Leu	Glu	Asn	Asp	Ala	Leu	Glu	Met	Phe	Lys	Lys	Gln	Thr		
			165					170						175			
Glu	Arg	Glu	Ala	Asn	Lys	Pro	Trp	His	Gln	Arg	Leu	Ser	Glu	Asn	Ile		
		180					185						190				
Gln	Asp	Gln	Trp	Trp	Asn	Phe	Lys	Gly	Leu	Phe	Gln						
	195						200										

<210> SEQ ID NO 505

<211> LENGTH: 321

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 505

atgaaaaaaaa	cactattatt	aagtactgct	gttttgacgc	tagccggtac	tgtcgccccta	60
ttaactcatt	ctgtagatgc	atcgacttat	tcttactaca	gcactagtca	ttttttaaga	120
caagatggaa	gagagactct	tagagaagct	aaatatgcgg	cagagttaca	aattagaaac	180
ttgttaagtc	agtatcatat	taatggaaaa	gaatataata	attatttcag	atattattat	240
agacaagcta	tgcaagctag	aaatatagac	gaagttaata	aaatcattga	agatttagaa	300
aaaaaacttgc	aagcacaata	a				321

<210> SEQ ID NO 506

<211> LENGTH: 106

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 506

Met	Lys	Lys	Thr	Leu	Leu	Leu	Ser	Thr	Ala	Val	Leu	Thr	Leu	Ala	Gly
1				5				10					15		
Thr	Val	Ala	Leu	Leu	Thr	His	Ser	Val	Asp	Ala	Ser	Thr	Tyr	Ser	Tyr
		20					25					30			
Tyr	Ser	Thr	Ser	His	Phe	Leu	Arg	Gln	Asp	Gly	Arg	Glu	Thr	Leu	Arg
	35					40				45					
Glu	Ala	Lys	Tyr	Ala	Ala	Glu	Leu	Gln	Ile	Arg	Asn	Leu	Leu	Ser	Gln
	50					55				60					
Tyr	His	Ile	Asn	Gly	Lys	Glu	Tyr	Asn	Asn	Tyr	Phe	Arg	Tyr	Tyr	Tyr
65				70				75					80		
Arg	Gln	Ala	Met	Gln	Ala	Arg	Asn	Ile	Asp	Glu	Val	Asn	Lys	Ile	Ile
			85				90						95		
Glu	Asp	Leu	Glu	Lys	Asn	Leu	Gln	Ala	Gln						
	100						105								

```

<210> SEQ ID NO 507
<211> LENGTH: 633
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 507
atgaaaaaga cattaacttt gctactggca ctctttgcc a tcggggtaac tagtagcgtc      60
agagcgggagg atgaacaaaag tagtacacaa aagccagtaa aatttgattt ggatggacct      120
caacaaaaaaa ttaaagatta tagtggcaac acaatcactc tagaagactt atatgttggg      180
agtaaagtag taaaaatata tatccctcaa ggatgggtggg tatactcttta cagacaatgt      240
gatcataaca gtaaagaacg aggaatttta gctagtccta ttctcgaaaa aaatataaca      300
aaaacagatc cttatcgtca atattataca ggagtacctt atattcttaa cttaggagaa      360
gatcctttga agaaaggaga aaaattaact ttctcattta aaggagaaga cggattttat      420
gtcggtagct atatctatag agactctgat actataaaaa aagaaaaaga agctgaagaa      480
gcacttcaaa aaaaggaaga ggaaaagcaa caaaaacagc tagaagaaag catgctaaag      540
cagataagag aagaagacca taaaccttgg catcagcggc taagtgaag catccaagat      600
cagtgggtgga actttaaggg actgtttcag tga                                     633

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<210> SEQ ID NO 508
<211> LENGTH: 210
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 508
Met Lys Lys Thr Leu Thr Leu Leu Leu Ala Leu Phe Ala Ile Gly Val
1          5          10          15
Thr Ser Ser Val Arg Ala Glu Asp Glu Gln Ser Ser Thr Gln Lys Pro
20          25          30
Val Lys Phe Asp Leu Asp Gly Pro Gln Gln Lys Ile Lys Asp Tyr Ser
35          40          45
Gly Asn Thr Ile Thr Leu Glu Asp Leu Tyr Val Gly Ser Lys Val Val
50          55          60
Lys Ile Tyr Ile Pro Gln Gly Trp Trp Val Tyr Leu Tyr Arg Gln Cys
65          70          75          80
Asp His Asn Ser Lys Glu Arg Gly Ile Leu Ala Ser Pro Ile Leu Glu
85          90          95
Lys Asn Ile Thr Lys Thr Asp Pro Tyr Arg Gln Tyr Tyr Thr Gly Val
100         105         110
Pro Tyr Ile Leu Asn Leu Gly Glu Asp Pro Leu Lys Lys Gly Glu Lys
115         120         125
Leu Thr Phe Ser Phe Lys Gly Glu Asp Gly Phe Tyr Val Gly Ser Tyr
130         135         140
Ile Tyr Arg Asp Ser Asp Thr Ile Lys Lys Glu Lys Glu Ala Glu Glu
145         150         155         160
Ala Leu Gln Lys Lys Glu Glu Glu Lys Gln Gln Lys Gln Leu Glu Glu
165         170         175
Ser Met Leu Lys Gln Ile Arg Glu Glu Asp His Lys Pro Trp His Gln
180         185         190
Arg Leu Ser Glu Ser Ile Gln Asp Gln Trp Trp Asn Phe Lys Gly Leu
195         200         205
Phe Gln
210

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```

<210> SEQ ID NO 509
<211> LENGTH: 384
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 509

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```

gtgttgagca gtcccactgt tttaaaacaa ttttctgcta taattgggat aatcccttta      60
gtagtcaggc cacctctgat aggggtggct tttttgggtt ttagtgaccc gtgtgttgag      120
aaaggagcat ttatgccaga aaagaaagtg ttgcccgctc taagcatagt ggtgagtttt      180
gtctgcctgc ttgatcata cttctttttt gctacttata gttatctcta cttaccgctt      240
gtagcaagta gtctagctct tatcggtctg gtgcaaaaca aaggcaggca aaaggtgtgg      300
tcgctagctg gactcgtcct agctgctcta gccgtggcag tagtggccta tgcctactat      360
gacccaaccg tcatccccta ctaa                                     384

```

<210> SEQ ID NO 510
 <211> LENGTH: 127
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 510

```

Met Leu Ser Ser Pro Thr Val Leu Lys Gln Phe Ser Ala Ile Ile Gly
1           5           10           15
Ile Ile Pro Leu Val Val Arg Pro Pro Leu Ile Gly Val Ala Phe Leu
20          25          30
Gly Phe Ser Asp Pro Cys Val Glu Lys Gly Ala Phe Met Pro Glu Lys
35          40          45
Lys Val Leu Pro Val Leu Ser Ile Val Val Ser Phe Val Cys Leu Leu
50          55          60
Asp His Ile Phe Phe Phe Ala Thr Tyr Ser Tyr Leu Tyr Leu Pro Leu
65          70          75          80
Val Ala Ser Ser Leu Ala Leu Ile Gly Leu Val Gln Asn Lys Gly Arg
85          90          95
Gln Lys Val Trp Ser Leu Ala Gly Leu Val Leu Ala Ala Leu Ala Val
100         105         110
Ala Val Val Ala Tyr Ala Tyr Tyr Asp Pro Thr Val Ile Pro Tyr
115         120         125

```

<210> SEQ ID NO 511
 <211> LENGTH: 555
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 511

```

atgaaatgga gtgggttttat gaaaacaaaa tcaaaacgct ttttaaacct agcaaccctt      60
tgcttgggccc tactaggaac aacttttgcta atggcacatc ccgtacaggc ggaggtgata      120
tcaaaaagag actatatgac tcgcttcggg ttaggcgatt tagaagatga ttcagctaac      180
tatccttcaa atttagaagc tagatataaa ggatatttag agggatatga aaaaggctta      240
aaaggagatg atatacccgga acggcccaag attcagggttc ctgaggatgt tcagccatct      300
gaccatggcg actatagaga tggttatgag gaaggatttg gagaaggaca acataaacgt      360
gatccattag aaacagaagc agaagatgat tctcaaggag gacgtcaaga aggacgtcaa      420
ggacatcaag aaggagcaga ttctagtgat ttgaacgttg aagaaagcga cggtttgtct      480
gttattgatg aagtagttgg agtaatttat caagcattta gtactatttg gacataactta      540
agcggtttgt tctaa                                     555

```

<210> SEQ ID NO 512
 <211> LENGTH: 184
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 512

```

Met Lys Trp Ser Gly Phe Met Lys Thr Lys Ser Lys Arg Phe Leu Asn
1           5           10           15
Leu Ala Thr Leu Cys Leu Ala Leu Leu Gly Thr Thr Leu Leu Met Ala
20          25          30
His Pro Val Gln Ala Glu Val Ile Ser Lys Arg Asp Tyr Met Thr Arg
35          40          45

```

Phe	Gly	Leu	Gly	Asp	Leu	Glu	Asp	Asp	Ser	Ala	Asn	Tyr	Pro	Ser	Asn	
50						55					60					
Leu	Glu	Ala	Arg	Tyr	Lys	Gly	Tyr	Leu	Glu	Gly	Tyr	Glu	Lys	Gly	Leu	
65					70					75					80	
Lys	Gly	Asp	Asp	Ile	Pro	Glu	Arg	Pro	Lys	Ile	Gln	Val	Pro	Glu	Asp	
				85					90					95		
Val	Gln	Pro	Ser	Asp	His	Gly	Asp	Tyr	Arg	Asp	Gly	Tyr	Glu	Glu	Gly	
			100					105					110			
Phe	Gly	Glu	Gly	Gln	His	Lys	Arg	Asp	Pro	Leu	Glu	Thr	Glu	Ala	Glu	
		115					120					125				
Asp	Asp	Ser	Gln	Gly	Gly	Arg	Gln	Glu	Gly	Arg	Gln	Gly	His	Gln	Glu	
	130					135					140					
Gly	Ala	Asp	Ser	Ser	Asp	Leu	Asn	Val	Glu	Glu	Ser	Asp	Gly	Leu	Ser	
145					150					155					160	
Val	Ile	Asp	Glu	Val	Val	Gly	Val	Ile	Tyr	Gln	Ala	Phe	Ser	Thr	Ile	
				165					170						175	
Trp	Thr	Tyr	Leu	Ser	Gly	Leu	Phe									
						180										

<210> SEQ ID NO 513
 <211> LENGTH: 1635
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 513

atgtcgacag	aaaaaaaaaca	actgacacaa	gaagaattga	tggttcaggg	agcagcctgg	60
tccacagctg	gtaatttcat	tagccgactt	ttgggagtgt	tatacattat	tccctgggtac	120
atttggtatg	ggcaatacgc	gattcaagcc	aacgctcttt	tcaatatggg	gtataatggt	180
tatgcttatt	ttttattgat	ttcaaccaca	ggactcaatg	ttgcgattgc	taagcagggt	240
gccaaagtaca	attccatggg	acaaactgag	catagctatc	aattaatccg	aagtacccta	300
aaactcatgc	ttggtctggg	ccttatTTTT	tcagccatta	tgtatctggg	ctctccttta	360
tttgcgagct	tatctggtgg	tgatgacaca	cttgttccca	ttatgcacag	cctttccttta	420
gcagttttta	tttttcctgt	aatgagtgtg	attcgaggca	tctttcaagg	ccacaataat	480
atcaagcctt	atgcagttag	tcagattgct	gagcaactca	ttcgggttat	ctggatgctt	540
ttgaccacct	tttttatcat	gaagtgggt	tctggtgatt	acgcttcagc	agtgactcag	600
tcaacttttg	cagcctttat	cgggatgggt	gctagtatgg	gtgttctggg	gtactatcct	660
tggaaacagg	gacttctagc	agctattttt	agtaagccag	atcatactgt	ttctattgat	720
atcaagggtc	tggtgcttga	aaccttaaaa	gaatccatcc	cctttatcgt	aacaggaagt	780
gccattcaag	cctttcaatt	gattgatcaa	tggacttttg	tcaatacgat	gactcttttt	840
acagattata	gccgttctca	attgcttggt	ttatttggtt	actttaacgc	aaaccagacc	900
aaaattacaa	tggtcttaat	tgcagtagca	gcatctattg	gtggtgtagg	tattgccttg	960
ttaactgaaa	attatgtcaa	aaaagacatg	aaagcagctg	ctcgtttaat	cattaacaac	1020
attgaaatgt	tagtgatgtt	tttgttacct	gctcttactg	gggcaattat	tttagcaaga	1080
cctctatatt	ctgtttttta	cggagctagc	gaggagcgtg	ccattcacct	ccttggtggcg	1140
gttctctttc	aaaccttgct	actggcgctt	tacaccctct	tttcaccgat	gcttcaagct	1200
ctttttgaaa	atcgaaaagc	gatttactac	tttgcctatg	gtatcttgat	taagttagtt	1260
ttacagatac	cgcttattta	tttgctacat	gcttatgggtc	ccttactagc	gacgacgatt	1320
gcttttagtg	tgccgattta	tttgatgtat	cgacgcctat	atcagggttac	tcatttttaac	1380
cgcaaaactgt	tgcaaaaacg	tttattatta	accttaattg	aaaccttatt	aatgggactg	1440
gtcgtgtttg	tggccaactg	gctattgggc	tatgccttta	aaccgacagg	ccgcttgacc	1500
agccttcttt	acctcctcat	tattggtggc	ttgggaatga	cgttttacac	ggcactcacc	1560
ttgctgacgc	atcaactgga	taaattaatt	ggtagcaaag	ctagtcgcct	tcgtcagaaa	1620
ttaggctggc	attaa					1635

<210> SEQ ID NO 514
 <211> LENGTH: 544
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 514

Met	Ser	Thr	Glu	Lys	Lys	Gln	Leu	Thr	Gln	Glu	Glu	Leu	Met	Val	Gln	1	5	10	15
Gly	Ala	Ala	Trp	Ser	Thr	Ala	Gly	Asn	Phe	Ile	Ser	Arg	Leu	Leu	Gly	20	25	30	
Val	Leu	Tyr	Ile	Ile	Pro	Trp	Tyr	Ile	Trp	Met	Gly	Gln	Tyr	Ala	Ile	35	40	45	
Gln	Ala	Asn	Ala	Leu	Phe	Asn	Met	Gly	Tyr	Asn	Val	Tyr	Ala	Tyr	Phe	50	55	60	
Leu	Leu	Ile	Ser	Thr	Thr	Gly	Leu	Asn	Val	Ala	Ile	Ala	Lys	Gln	Val	65	70	75	80
Ala	Lys	Tyr	Asn	Ser	Met	Gly	Gln	Thr	Glu	His	Ser	Tyr	Gln	Leu	Ile	85	90	95	
Arg	Ser	Thr	Leu	Lys	Leu	Met	Leu	Gly	Leu	Gly	Leu	Ile	Phe	Ser	Ala	100	105	110	
Ile	Met	Tyr	Leu	Gly	Ser	Pro	Leu	Phe	Ala	Ser	Leu	Ser	Gly	Gly	Asp	115	120	125	
Asp	Thr	Leu	Val	Pro	Ile	Met	His	Ser	Leu	Ser	Leu	Ala	Val	Phe	Ile	130	135	140	
Phe	Pro	Val	Met	Ser	Val	Ile	Arg	Gly	Ile	Phe	Gln	Gly	His	Asn	Asn	145	150	155	160
Ile	Lys	Pro	Tyr	Ala	Val	Ser	Gln	Ile	Ala	Glu	Gln	Leu	Ile	Arg	Val	165	170	175	
Ile	Trp	Met	Leu	Leu	Thr	Thr	Phe	Phe	Ile	Met	Lys	Leu	Gly	Ser	Gly	180	185	190	
Asp	Tyr	Ala	Ser	Ala	Val	Thr	Gln	Ser	Thr	Phe	Ala	Ala	Phe	Ile	Gly	195	200	205	
Met	Val	Ala	Ser	Met	Gly	Val	Leu	Gly	Tyr	Tyr	Leu	Trp	Lys	Gln	Gly	210	215	220	
Leu	Leu	Ala	Ala	Ile	Phe	Ser	Lys	Pro	Asp	His	Thr	Val	Ser	Ile	Asp	225	230	235	240
Ile	Lys	Gly	Leu	Leu	Glu	Thr	Leu	Lys	Glu	Ser	Ile	Pro	Phe	Ile		245	250	255	
Val	Thr	Gly	Ser	Ala	Ile	Gln	Ala	Phe	Gln	Leu	Ile	Asp	Gln	Trp	Thr	260	265	270	
Phe	Val	Asn	Thr	Met	Thr	Leu	Phe	Thr	Asp	Tyr	Ser	Arg	Ser	Gln	Leu	275	280	285	
Leu	Val	Leu	Phe	Gly	Tyr	Phe	Asn	Ala	Asn	Pro	Ala	Lys	Ile	Thr	Met	290	295	300	
Val	Leu	Ile	Ala	Val	Ala	Ala	Ser	Ile	Gly	Gly	Val	Gly	Ile	Ala	Leu	305	310	315	320
Leu	Thr	Glu	Asn	Tyr	Val	Lys	Lys	Asp	Met	Lys	Ala	Ala	Ala	Arg	Leu	325	330	335	
Ile	Ile	Asn	Asn	Ile	Glu	Met	Leu	Val	Met	Phe	Leu	Leu	Pro	Ala	Leu	340	345	350	
Thr	Gly	Ala	Ile	Ile	Leu	Ala	Arg	Pro	Leu	Tyr	Ser	Val	Phe	Tyr	Gly	355	360	365	
Ala	Ser	Glu	Glu	Arg	Ala	Ile	His	Leu	Phe	Val	Ala	Val	Leu	Phe	Gln	370	375	380	
Thr	Leu	Leu	Leu	Ala	Leu	Tyr	Thr	Leu	Phe	Ser	Pro	Met	Leu	Gln	Ala	385	390	395	400
Leu	Phe	Glu	Asn	Arg	Lys	Ala	Ile	Tyr	Tyr	Phe	Ala	Tyr	Gly	Ile	Leu	405	410	415	
Ile	Lys	Leu	Val	Leu	Gln	Ile	Pro	Leu	Ile	Tyr	Leu	Leu	His	Ala	Tyr	420	425	430	
Gly	Pro	Leu	Leu	Ala	Thr	Thr	Ile	Ala	Leu	Val	Val	Pro	Ile	Tyr	Leu	435	440	445	

Met	Tyr	Arg	Arg	Leu	Tyr	Gln	Val	Thr	His	Phe	Asn	Arg	Lys	Leu	Leu
450						455					460				
Gln	Lys	Arg	Leu	Leu	Leu	Thr	Leu	Ile	Glu	Thr	Leu	Leu	Met	Gly	Leu
465						470					475				480
Val	Val	Phe	Val	Ala	Asn	Trp	Leu	Leu	Gly	Tyr	Ala	Phe	Lys	Pro	Thr
				485						490				495	
Gly	Arg	Leu	Thr	Ser	Leu	Leu	Tyr	Leu	Leu	Ile	Ile	Gly	Gly	Leu	Gly
			500					505					510		
Met	Thr	Val	Tyr	Thr	Ala	Leu	Thr	Leu	Leu	Thr	His	Gln	Leu	Asp	Lys
		515					520					525			
Leu	Ile	Gly	Ser	Lys	Ala	Ser	Arg	Leu	Arg	Gln	Lys	Leu	Gly	Trp	His
	530					535					540				

<210> SEQ ID NO 515

<211> LENGTH: 1053

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 515

gtgaaaacta	agcatccctt	tttgtgtctc	gagcgttttt	gcttaaaaaa	aacgcagata	60
atcactaagt	cacatatctt	ttggcttgct	tttgtgctac	ttagttttag	cttatgtgtt	120
gctattttact	gtcatctgcg	ctttggagcc	gttgctttat	cacatcagga	tcttaactct	180
attttatttg	gaaagcaaaa	cggccataaa	gccaatgttt	tactcgctat	acgattaccg	240
agactttttg	gtgctacctt	aactggctct	gcgttagctg	tttctggaac	tatcatgcaa	300
gcaatcacac	gtaatcctat	cgctgagcct	ggccttttag	gcattaatgc	tggagcagga	360
ctagccttgg	tactggctta	tgcgtttgta	cctcacttgc	actattccct	cattattctg	420
ctttcgttgt	tagggctctag	cctggcagca	accttagtct	ttggcctttc	ttatcaatct	480
ggcaaaggct	accatcagct	ccgccttgct	ttagcaggag	ctatggtttc	catactgcta	540
tcagcattag	gtcaagggtat	taccaattac	tatcatctgg	caaagtctgt	tatcggtctg	600
caagcaggag	gtcttgtcgg	ggtcaattgg	caaagtatcg	gctatattgc	tcctcttatt	660
attcttagtc	tttgttttagc	ccagctatta	tcttatcacc	tgaccgtcct	tagtctaagt	720
gagtctcagg	caaaagctct	tgggcaaaaa	accaacttga	tcagtgcagt	ctttatgatt	780
ttggttctta	ttttatcatc	agcagctgta	gccattgctg	gaagcatttc	ttttatcggc	840
ttagtcattc	ctcatcttat	gaaacatttt	acacctcatc	attaccgata	ccttttgccg	900
ctttgtgcag	tttctggcgc	tagtttcatg	gtatgggttg	atattgcttg	tcgtaatctc	960
aatccgcctt	atgaaaacccc	tcttggggca	ttgggttagct	taattggttt	tccatgcttt	1020
ttatgggttaa	taagaagagg	aggccgctat	tga			1053

<210> SEQ ID NO 516

<211> LENGTH: 350

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 516

Met	Lys	Thr	Lys	His	Pro	Phe	Leu	Cys	Leu	Glu	Arg	Phe	Cys	Leu	Lys
1				5					10					15	
Lys	Thr	Gln	Ile	Ile	Thr	Lys	Ser	His	Ile	Phe	Trp	Leu	Val	Phe	Val
			20					25					30		
Leu	Leu	Ser	Phe	Ser	Leu	Cys	Val	Ala	Ile	Tyr	Cys	His	Leu	Arg	Phe
		35					40					45			
Gly	Ala	Val	Ala	Leu	Ser	His	Gln	Asp	Leu	Asn	Ser	Ile	Leu	Phe	Gly
	50					55					60				
Lys	Gln	Asn	Gly	His	Lys	Ala	Asn	Val	Leu	Leu	Ala	Ile	Arg	Leu	Pro
65					70					75				80	
Arg	Leu	Phe	Gly	Ala	Thr	Leu	Thr	Gly	Ser	Ala	Leu	Ala	Val	Ser	Gly
			85					90					95		
Thr	Ile	Met	Gln	Ala	Ile	Thr	Arg	Asn	Pro	Ile	Ala	Glu	Pro	Gly	Leu
		100						105					110		
Leu	Gly	Ile	Asn	Ala	Gly	Ala	Gly	Leu	Ala	Leu	Val	Leu	Ala	Tyr	Ala

	115		120		125										
Phe	Val	Pro	His	Leu	His	Tyr	Ser	Leu	Ile	Ile	Leu	Leu	Ser	Leu	Leu
	130					135					140				
Gly	Ser	Ser	Leu	Ala	Ala	Thr	Leu	Val	Phe	Gly	Leu	Ser	Tyr	Gln	Ser
145					150					155				160	
Gly	Lys	Gly	Tyr	His	Gln	Leu	Arg	Leu	Val	Leu	Ala	Gly	Ala	Met	Val
				165					170					175	
Ser	Ile	Leu	Leu	Ser	Ala	Leu	Gly	Gln	Gly	Ile	Thr	Asn	Tyr	Tyr	His
			180					185					190		
Leu	Ala	Asn	Ala	Val	Ile	Gly	Trp	Gln	Ala	Gly	Gly	Leu	Val	Gly	Val
	195					200					205				
Asn	Trp	Gln	Met	Ile	Gly	Tyr	Ile	Ala	Pro	Leu	Ile	Ile	Leu	Ser	Leu
	210				215						220				
Cys	Leu	Ala	Gln	Leu	Leu	Ser	Tyr	His	Leu	Thr	Val	Leu	Ser	Leu	Ser
225				230						235					240
Glu	Ser	Gln	Ala	Lys	Ala	Leu	Gly	Gln	Lys	Thr	Asn	Leu	Ile	Ser	Ala
			245					250						255	
Val	Phe	Met	Ile	Leu	Val	Leu	Ile	Leu	Ser	Ser	Ala	Ala	Val	Ala	Ile
			260				265						270		
Ala	Gly	Ser	Ile	Ser	Phe	Ile	Gly	Leu	Val	Ile	Pro	His	Leu	Met	Lys
	275						280					285			
His	Phe	Thr	Pro	His	His	Tyr	Arg	Tyr	Leu	Leu	Pro	Leu	Cys	Ala	Val
	290					295					300				
Ser	Gly	Ala	Ser	Phe	Met	Val	Trp	Val	Asp	Ile	Ala	Cys	Arg	Asn	Leu
305				310					315					320	
Asn	Pro	Pro	Tyr	Glu	Thr	Pro	Leu	Gly	Ala	Leu	Val	Ser	Leu	Ile	Gly
			325					330					335		
Phe	Pro	Cys	Phe	Leu	Trp	Leu	Ile	Arg	Arg	Gly	Gly	Arg	Tyr		
			340					345					350		

<210> SEQ ID NO 517

<211> LENGTH: 1038

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 517

atgcttttta	tggtaataa	gaagaggagg	ccgctattga	aatctcaaag	acacctttta	60
aggttatata	ctagcctgat	cctgctactt	gtaagtctta	tgggattagc	tttgtccctt	120
ggagaatctc	atctatcttt	tttggacctt	gtccatgtgt	ttttgggaaa	atctagccat	180
gccatatctt	tcatcgttat	taacattcgt	ctgccaaaga	ttctagctgc	ttgtctagga	240
ggcggttctc	ttgctttatc	agggctatta	ttacaacggt	taacacgaaa	tcccttagct	300
gactctgggtg	tattaggtat	tactatagga	gcaggatatct	ctttggctat	tgtgggtctcc	360
ttttctttct	ttgagcaagc	tcatatcagc	cattacttgc	ctttatttgc	catgcttggt	420
gctattgtaa	caacctttag	cgtttattgg	ctatctttga	caaaacaagg	acaaattgat	480
cctacacggt	taattcttac	tgggtgtagct	gttactacca	tgctttcaag	tctaattggt	540
gctcttggtg	gtcatattaa	tcgctacaaa	gtcgatttgg	tcataaattg	gcttagcggc	600
caattaatag	gagacgactg	gcctactctg	agtgtcatcg	ctcctttggt	attgtgtttt	660
tggctattga	cttatagtca	agcccatttc	cttaatatta	tgggattagc	tgataatact	720
gctattgggc	taggactccc	tttaaaccgt	aagcgtcggt	tgatacttgt	cttagcagct	780
ggcttaggtg	ctttgagtgt	tcttttggtt	ggtaatatta	gttttatcgg	cttaatagct	840
ggacacttta	gtacatactt	ggtagggagt	aatcataaaa	taacaatacc	cattagtatt	900
ttaatcgga	tgatcctact	tcttggtgca	gatacagtag	gacgagtcta	tctgggtggc	960
agtaatatcc	agacagggat	tttagtgtcg	cttatcgga	ccccttattt	tctttactta	1020
atggcaaaaa	caaaaataa					1038

<210> SEQ ID NO 518

<211> LENGTH: 345

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 518

```
Met Leu Phe Met Val Asn Lys Lys Arg Arg Pro Leu Leu Lys Ser Gln
1           5           10           15
Arg His Leu Leu Arg Leu Tyr Thr Ser Leu Ile Leu Leu Leu Val Ser
20           25           30
Leu Met Gly Leu Ala Leu Ser Leu Gly Glu Ser His Leu Ser Phe Leu
35           40           45
Asp Leu Val His Val Phe Leu Gly Lys Ser Ser His Ala Ile Ser Phe
50           55           60
Ile Val Ile Asn Ile Arg Leu Pro Arg Ile Leu Ala Ala Cys Leu Gly
65           70           75           80
Gly Gly Ser Leu Ala Leu Ser Gly Leu Leu Leu Gln Arg Leu Thr Arg
85           90           95
Asn Pro Leu Ala Asp Ser Gly Val Leu Gly Ile Thr Ile Gly Ala Gly
100          105          110
Ile Ser Leu Ala Ile Val Val Ser Phe Ser Phe Phe Glu Gln Ala His
115          120          125
Ile Ser His Tyr Leu Pro Leu Phe Ala Met Leu Gly Ala Ile Val Thr
130          135          140
Thr Phe Ser Val Tyr Trp Leu Ser Leu Thr Lys Gln Gly Gln Ile Asp
145          150          155          160
Pro Thr Arg Leu Ile Leu Thr Gly Val Ala Val Thr Thr Met Leu Ser
165          170          175
Ser Leu Met Val Ala Leu Val Gly His Ile Asn Arg Tyr Lys Val Asp
180          185          190
Leu Val Ile Asn Trp Leu Ser Gly Gln Leu Ile Gly Asp Asp Trp Pro
195          200          205
Thr Leu Ser Val Ile Ala Pro Leu Leu Leu Cys Phe Trp Leu Leu Thr
210          215          220
Tyr Ser Gln Ala His Phe Leu Asn Ile Met Gly Leu Ala Asp Asn Thr
225          230          235          240
Ala Ile Gly Leu Gly Leu Pro Leu Asn Arg Lys Arg Arg Leu Ile Leu
245          250          255
Val Leu Ala Ala Gly Leu Gly Ala Leu Ser Val Leu Leu Val Gly Asn
260          265          270
Ile Ser Phe Ile Gly Leu Ile Ala Gly His Phe Ser Thr Tyr Leu Val
275          280          285
Gly Ser Asn His Lys Ile Thr Ile Pro Ile Ser Ile Leu Ile Gly Met
290          295          300
Ile Leu Leu Leu Val Ala Asp Thr Val Gly Arg Val Tyr Leu Val Gly
305          310          315          320
Ser Asn Ile Gln Thr Gly Ile Leu Val Ser Leu Ile Gly Ala Pro Tyr
325          330          335
Phe Leu Tyr Leu Met Ala Lys Thr Lys
340          345
```

<210> SEQ ID NO 519

<211> LENGTH: 1374

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 519

```
atgaagtcac tatattat ttttaggagt tacattaaca tggaagaccc tgtgagtcag      60
tccttagtga ttcaattttt attgttagtt gttttaacct tgtaaagtgc ttttttttca      120
gccagtga aaa tggccttagt ttctctcaat cgttctcggg tggaacaaaa agcagcagac      180
gggtgataaaa aatacgctcg tttgttcgcg gtttagagg aacctaata ttttttatca      240
acgattcaag ttgggattac ctttattagt ttactatcag gagcaagttt atcagcttct      300
```

```

ttgggtaagg tgatctcagg ttggctaggt aattcagcga ccgcaaggac agctgggtact 360
atcatctcct tggttttctt gacttatgtc tctattgttt taggagaatt gtatccaaaa 420
cggattgcca tgaacctcaa agacaagttg gcgattgttt cagcccctat tatcattggg 480
ttagggagac tggtagtcc ctttgtatgg ctcttatcag cttctactaa tttactgagc 540
cgacttacc cttatgacctt tgatgatgca gatgagcaaa tgacacgtga tgaaatcgag 600
tatatgttat caaaaagtga ggcgaccctt gatgctgaag aaattgagat gttgcaagga 660
gttttctcac ttgatgaaat gatggcgcgt gaagtcatgg tccaaggac cgatgctttc 720
atgattgaca ttaacgatga tccgcttgaa aatattcagg aaatcttaaa acaaagtttt 780
tcacgcattc ctgtttatga tgtggataaa gataaaatta tcggtctcat ccacactaag 840
cgtctcttgg agtcagggtt ccgccaggga tttgatcaga ttaacatgcg aaaaatgtta 900
caagaacctc tttttgttcc cgaaaccatt tttgtagatg atctcttacg ccagctgcgc 960
aatacccaaa atcagatggc tatttttgcta gatgaatag gtgggtgtggc aggacttgtg 1020
actttggaag acttgcttga agaaatcgct ggtgaaatcg atgatgaaac cgataaagca 1080
gaacaatttg ttcatgagat tggagacaat acctatattg ttgttggtac tatgacttta 1140
aatgagttta atgactattt tgataccgaa ctagaatcag atgatgtaga taccattgct 1200
ggtttttatt tgacagggtat cggaaccatt ccaagccagg agcaaaaaga agcctacgaa 1260
atagataaca aagacaaaaca tttagttcta atcaacgata aagtcaaaga tggccgtatt 1320
acgaaattaa aattaatcct gtctaataa gaacagatta ttgaggaaga ctag 1374

```

<210> SEQ ID NO 520

<211> LENGTH: 457

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 520

```

Met Lys Ser Leu Tyr Tyr Phe Phe Arg Ser Tyr Ile Asn Met Glu Asp
1          5          10          15
Pro Val Ser Gln Ser Leu Val Ile Gln Phe Leu Leu Leu Val Val Leu
20          25          30
Thr Leu Leu Asn Ala Phe Phe Ser Ala Ser Glu Met Ala Leu Val Ser
35          40          45
Leu Asn Arg Ser Arg Val Glu Gln Lys Ala Ala Asp Gly Asp Lys Lys
50          55          60
Tyr Ala Arg Leu Leu Arg Val Leu Glu Glu Pro Asn His Phe Leu Ser
65          70          75          80
Thr Ile Gln Val Gly Ile Thr Phe Ile Ser Leu Leu Ser Gly Ala Ser
85          90          95
Leu Ser Ala Ser Leu Gly Lys Val Ile Ser Gly Trp Leu Gly Asn Ser
100         105         110
Ala Thr Ala Arg Thr Ala Gly Thr Ile Ile Ser Leu Val Phe Leu Thr
115         120         125
Tyr Val Ser Ile Val Leu Gly Glu Leu Tyr Pro Lys Arg Ile Ala Met
130         135         140
Asn Leu Lys Asp Lys Leu Ala Ile Val Ser Ala Pro Ile Ile Ile Gly
145         150         155         160
Leu Gly Arg Leu Val Ser Pro Phe Val Trp Leu Leu Ser Ala Ser Thr
165         170         175
Asn Leu Leu Ser Arg Leu Thr Pro Met Thr Phe Asp Asp Ala Asp Glu
180         185         190
Gln Met Thr Arg Asp Glu Ile Glu Tyr Met Leu Ser Lys Ser Glu Ala
195         200         205
Thr Leu Asp Ala Glu Glu Ile Glu Met Leu Gln Gly Val Phe Ser Leu
210         215         220
Asp Glu Met Met Ala Arg Glu Val Met Val Pro Arg Thr Asp Ala Phe
225         230         235         240
Met Ile Asp Ile Asn Asp Asp Pro Leu Glu Asn Ile Gln Glu Ile Leu
245         250         255
Lys Gln Ser Phe Ser Arg Ile Pro Val Tyr Asp Val Asp Lys Asp Lys

```

				260					265					270					
Ile	Ile	Gly	Leu	Ile	His	Thr	Lys	Arg	Leu	Leu	Glu	Ser	Gly	Phe	Arg				
		275					280					285							
Gln	Gly	Phe	Asp	Gln	Ile	Asn	Met	Arg	Lys	Met	Leu	Gln	Glu	Pro	Leu				
	290					295					300								
Phe	Val	Pro	Glu	Thr	Ile	Phe	Val	Asp	Asp	Leu	Leu	Arg	Gln	Leu	Arg				
305					310					315					320				
Asn	Thr	Gln	Asn	Gln	Met	Ala	Ile	Leu	Leu	Asp	Glu	Tyr	Gly	Gly	Val				
			325						330					335					
Ala	Gly	Leu	Val	Thr	Leu	Glu	Asp	Leu	Leu	Glu	Glu	Ile	Val	Gly	Glu				
		340						345					350						
Ile	Asp	Asp	Glu	Thr	Asp	Lys	Ala	Glu	Gln	Phe	Val	His	Glu	Ile	Gly				
	355					360					365								
Asp	Asn	Thr	Tyr	Ile	Val	Val	Gly	Thr	Met	Thr	Leu	Asn	Glu	Phe	Asn				
	370				375						380								
Asp	Tyr	Phe	Asp	Thr	Glu	Leu	Glu	Ser	Asp	Asp	Val	Asp	Thr	Ile	Ala				
385				390					395						400				
Gly	Phe	Tyr	Leu	Thr	Gly	Ile	Gly	Thr	Ile	Pro	Ser	Gln	Glu	Gln	Lys				
			405				410							415					
Glu	Ala	Tyr	Glu	Ile	Asp	Asn	Lys	Asp	Lys	His	Leu	Val	Leu	Ile	Asn				
		420				425						430							
Asp	Lys	Val	Lys	Asp	Gly	Arg	Ile	Thr	Lys	Leu	Lys	Leu	Ile	Leu	Ser				
	435				440						445								
Asn	Ile	Glu	Gln	Ile	Ile	Glu	Glu	Asp											
	450				455														

<210> SEQ ID NO 521

<211> LENGTH: 564

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 521

atgtcaaaaa	cacataaaat	gattatgatt	ggtatacttt	ctgcgatatc	atttctattg	60
atgctagtta	gctttgcat	tattccaggc	gcagcttttt	taaaaattga	atttagtatt	120
attcctgttt	tatttggttt	aatgattatg	gacttaaaga	gtgcttactt	aattttgtta	180
ttgaggtcct	tattgaaact	ctttttgaac	aatcgtgggg	ttaatgattt	tattggtctc	240
ccaatgaata	ttatcgctat	cgctttat	gtgacggctt	ttgccttagt	ttggaaccgt	300
caaaaaacgc	ttagtcaata	tgtatttgct	agcttactag	gcacagggtt	attaacgttt	360
ggcatgggtt	ttcttaatta	tacttttgcc	attcctttat	atgctatatt	tgcaaattatt	420
gatatcagag	cttatattgg	tgttactaag	tatatgatga	ctatgggttat	tccgtttaat	480
cttggtgaag	ggttgatatt	tgcaattacc	ttttattttg	tgtatattgc	aagtaaacca	540
attttagaaa	gatacttaca	ctaa				564

<210> SEQ ID NO 522

<211> LENGTH: 187

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 522

Met	Ser	Lys	Thr	His	Lys	Met	Ile	Met	Ile	Gly	Ile	Leu	Ser	Ala	Ile				
1			5					10			15								
Ser	Phe	Leu	Leu	Met	Leu	Val	Ser	Phe	Ala	Ile	Ile	Pro	Gly	Ala	Ala				
		20					25				30								
Phe	Leu	Lys	Ile	Glu	Phe	Ser	Ile	Pro	Val	Leu	Phe	Gly	Leu	Met					
	35				40				45										
Ile	Met	Asp	Leu	Lys	Ser	Ala	Tyr	Leu	Ile	Leu	Leu	Arg	Ser	Leu					
	50				55			60											
Leu	Lys	Leu	Phe	Leu	Asn	Asn	Arg	Gly	Val	Asn	Asp	Phe	Ile	Gly	Leu				
65				70				75					80						

Pro	Met	Asn	Ile	Ile	Ala	Ile	Ala	Leu	Phe	Val	Thr	Ala	Phe	Ala	Leu
				85					90					95	
Val	Trp	Asn	Arg	Gln	Lys	Thr	Leu	Ser	Gln	Tyr	Val	Phe	Ala	Ser	Leu
		100						105					110		
Leu	Gly	Thr	Gly	Leu	Leu	Thr	Phe	Gly	Met	Val	Val	Leu	Asn	Tyr	Thr
	115					120					125				
Phe	Ala	Ile	Pro	Leu	Tyr	Ala	Ile	Phe	Ala	Asn	Ile	Asp	Ile	Arg	Ala
	130					135					140				
Tyr	Ile	Gly	Val	Thr	Lys	Tyr	Met	Met	Thr	Met	Val	Ile	Pro	Phe	Asn
	145				150					155				160	
Leu	Val	Glu	Gly	Leu	Ile	Phe	Ala	Ile	Thr	Phe	Tyr	Phe	Val	Tyr	Ile
			165						170					175	
Ala	Ser	Lys	Pro	Ile	Leu	Glu	Arg	Tyr	Leu	His					
			180					185							

<210> SEQ ID NO 523

<211> LENGTH: 375

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 523

atgtctaaca	tatcattaat	catgattgcc	atacggtcag	cctcatgcgc	tggtgctgtc	60
aagctttctt	caagaatatc	actgtcatct	ttaccccaac	gttgtaagag	accaatatgc	120
cctttaataa	tcgcaaccgg	tggtcgtaat	tcattggctga	catcactaat	aaaacgtgat	180
tgcaacttag	tatgtgtctc	caatttgtct	aacatattgt	caaagataac	agacaattct	240
tcgatttcac	ctcctgacga	aatatctgag	cgcagggtta	aattattagg	attttcagag	300
atattacgca	tcacttcacg	taaattgtgt	aaagggttca	aaaagcgccg	cgtagtaatt	360
aagatgatta	aatag					375

<210> SEQ ID NO 524

<211> LENGTH: 124

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 524

Met	Ser	Asn	Ile	Ser	Leu	Ile	Met	Ile	Ala	Ile	Arg	Ser	Ala	Ser	Cys
1			5						10				15		
Ala	Val	Ala	Val	Lys	Leu	Ser	Ser	Arg	Ile	Ser	Leu	Ser	Ser	Leu	Pro
			20					25					30		
Gln	Arg	Cys	Lys	Arg	Pro	Ile	Cys	Pro	Leu	Ile	Ile	Ala	Thr	Gly	Val
		35				40					45				
Arg	Asn	Ser	Trp	Leu	Thr	Ser	Leu	Ile	Lys	Arg	Asp	Cys	Asn	Leu	Val
	50				55					60					
Cys	Val	Ser	Asn	Leu	Ser	Asn	Ile	Leu	Ser	Lys	Ile	Thr	Asp	Asn	Ser
	65			70					75					80	
Ser	Ile	Ser	Ser	Pro	Asp	Glu	Ile	Ser	Glu	Arg	Arg	Phe	Lys	Leu	Leu
			85					90					95		
Gly	Phe	Ser	Glu	Ile	Leu	Arg	Ile	Thr	Ser	Cys	Lys	Leu	Cys	Lys	Gly
		100					105					110			
Phe	Lys	Lys	Arg	Arg	Val	Val	Ile	Lys	Met	Ile	Lys				
		115				120									

<210> SEQ ID NO 525

<211> LENGTH: 1503

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 525

atggaaaatc	agaaacaaaa	acagaagaaa	tataaaaatt	cgttaccaa	acgactatct	60
aatatctttt	ttgttctttt	tttctgcatt	ttctctgcct	ttacactgat	tgcttatagt	120

210	215	220
His Glu Val Met Arg Asn Ile Ser Glu Asn Pro Asn Asn Leu Asn Leu		
225	230	235
Arg Ser Asp Ile Ser Ser Gly Asp Glu Ile Glu Glu Leu Ser Val Ile		240
	245	250
Phe Asp Asn Met Leu Asp Lys Leu Glu Thr His Thr Lys Leu Gln Ser		255
	260	265
Arg Phe Ile Ser Asp Val Ser His Glu Leu Arg Thr Pro Val Ala Ile		270
	275	280
Ile Lys Gly His Ile Gly Leu Leu Gln Arg Trp Gly Lys Asp Asp Ser		285
	290	295
Asp Ile Leu Glu Glu Ser Leu Thr Ala Thr Ala His Glu Ala Asp Arg		300
305	310	315
Met Ala Ile Met Ile Asn Asp Met Leu Asp Met Ile Arg Val Gln Gly		320
	325	330
Ser Phe Glu Gly His Gln Asn Asp Met Thr Val Leu Glu Asp Ser Ile		335
	340	345
Glu Thr Val Val Gly Asn Phe Arg Val Leu Arg Glu Asp Phe Ile Phe		350
	355	360
Thr Trp Gln Ser Glu Asn Pro Lys Thr Ile Ala Arg Ile Tyr Lys Asn		365
	370	375
His Phe Glu Gln Ala Leu Met Ile Leu Ile Asp Asn Ala Val Lys Tyr		380
385	390	395
Ser Arg Lys Glu Lys Lys Ile Ala Ile Asn Leu Ser Val Thr Gly Lys		400
	405	410
Gln Glu Ala Ile Val Arg Val Gln Asp Lys Gly Glu Gly Ile Ser Lys		415
	420	425
Glu Asp Ile Glu His Ile Phe Glu Arg Phe Tyr Arg Thr Asp Lys Ser		430
	435	440
Arg Asn Arg Thr Ser Thr Gln Ala Gly Leu Gly Ile Gly Leu Ser Ile		445
	450	455
Leu Lys Gln Ile Val Asp Gly Tyr His Leu Gln Met Lys Val Glu Ser		460
465	470	475
Glu Leu Asn Glu Gly Ser Val Phe Ile Leu His Ile Pro Leu Ala Gln		480
	485	490
Ser Lys Glu Ser		495
	500	

<210> SEQ ID NO 527

<211> LENGTH: 297

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<220> FEATURE:

<221> NAME/KEY: Unsure

<222> LOCATION: (3)..(3)

<223> OTHER INFORMATION: unsure

<400> SEQUENCE: 527

ttntgtcgtt attatctttg ctttttagcg cccctagtag caagtttgat tcagttggct	60
atttctcgtc aaagagaata tctagctgat gctagttctg ttgaactaac aagaaatccc	120
caaggatga ttaaggctct tgaaaaattg cagttatctc agccaatgaa gcacccgtgtt	180
gatgatgcta gtgcggcctt gtatattaat gagcctcgca aaaaaaggag cttcagttca	240
ttattcagca cccatcctcc tattgaggag aggattgaaa ggttaaaaaa catgtga	297

<210> SEQ ID NO 528

<211> LENGTH: 98

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

```

<400> SEQUENCE: 528
Met Cys Arg Tyr Tyr Leu Cys Phe Leu Ala Pro Leu Val Ala Ser Leu
1           5           10           15
Ile Gln Leu Ala Ile Ser Arg Gln Arg Glu Tyr Leu Ala Asp Ala Ser
           20           25           30
Ser Val Glu Leu Thr Arg Asn Pro Gln Gly Met Ile Lys Ala Leu Glu
           35           40           45
Lys Leu Gln Leu Ser Gln Pro Met Lys His Pro Val Asp Asp Ala Ser
           50           55           60
Ala Ala Leu Tyr Ile Asn Glu Pro Arg Lys Lys Arg Ser Phe Ser Ser
65           70           75           80
Leu Phe Ser Thr His Pro Pro Ile Glu Glu Arg Ile Glu Arg Leu Lys
           85           90           95
Asn Met

```

```

<210> SEQ ID NO 529
<211> LENGTH: 630
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<220> FEATURE:
<221> NAME/KEY: Unsure
<222> LOCATION: (41)..(41)
<223> OTHER INFORMATION: unsure
<400> SEQUENCE: 529

```

```

atgctttatc aacagatttc acaaaataag caacgaacag ntgttttatt agttggtttc      60
ttcgctctct tagcacttat tggagcttca gcaggctatc tgctgttaga taattatgcc      120
atgggcttgg tccttgctct tgtcattggg gtgatttatg ctaccagtat gatttttcaa      180
tccaccagtc ttgtaatgag tatgaacaat gctagagaag ttacagaaaa agaggctcca      240
ggctttttcc atattgtcga ggatatggct atggtggccc agattccgat gccgagagtt      300
tttattattg aagatccttc tttaaatgct tttgcgacag gatctagccc tcaaaatgct      360
gctggtgcag caacgacagg tttacttgaa gtcatgaatc gtgaagaact tgaagggtgt      420
atcggccatg aaattagcca catccgaaat tatgatatcc gtatttcgac tattgctgta      480
gctttggcga gtgctgttac cgttatttct agtatcggtg ggcgtatgct atgggatggg      540
ggcggttctc gcaggcaaag agatgacgga gatgatgatg ttttaagaat cattacatta      600
cttntgtcgc ttattatctt tgctttttag                                     630

```

```

<210> SEQ ID NO 530
<211> LENGTH: 209
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<220> FEATURE:
<221> NAME/KEY: UNSURE
<222> LOCATION: (14)..(14)
<223> OTHER INFORMATION: unsure
<400> SEQUENCE: 530

```

```

Met Leu Tyr Gln Gln Ile Ser Gln Asn Lys Gln Arg Thr Xaa Val Leu
1           5           10           15
Leu Val Gly Phe Phe Ala Leu Leu Ala Leu Ile Gly Ala Ser Ala Gly
           20           25           30
Tyr Leu Leu Leu Asp Asn Tyr Ala Met Gly Leu Val Leu Ala Leu Val
           35           40           45
Ile Gly Val Ile Tyr Ala Thr Ser Met Ile Phe Gln Ser Thr Ser Leu
           50           55           60
Val Met Ser Met Asn Asn Ala Arg Glu Val Thr Glu Lys Glu Ala Pro
65           70           75           80
Gly Phe Phe His Ile Val Glu Asp Met Ala Met Val Ala Gln Ile Pro
           85           90           95

```

Met	Pro	Arg	Val	Phe	Ile	Ile	Glu	Asp	Pro	Ser	Leu	Asn	Ala	Phe	Ala
			100					105					110		
Thr	Gly	Ser	Ser	Pro	Gln	Asn	Ala	Ala	Val	Ala	Ala	Thr	Thr	Gly	Leu
		115					120					125			
Leu	Glu	Val	Met	Asn	Arg	Glu	Glu	Leu	Glu	Gly	Val	Ile	Gly	His	Glu
		130				135					140				
Ile	Ser	His	Ile	Arg	Asn	Tyr	Asp	Ile	Arg	Ile	Ser	Thr	Ile	Ala	Val
145					150					155					160
Ala	Leu	Ala	Ser	Ala	Val	Thr	Val	Ile	Ser	Ser	Ile	Gly	Gly	Arg	Met
			165						170					175	
Leu	Trp	Tyr	Gly	Gly	Gly	Ser	Arg	Arg	Gln	Arg	Asp	Asp	Gly	Asp	Asp
		180						185					190		
Asp	Val	Leu	Arg	Ile	Ile	Thr	Leu	Leu	Xaa	Val	Val	Ile	Ile	Phe	Ala
		195					200					205			
Phe															

<210> SEQ ID NO 531

<211> LENGTH: 558

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 531

atgccaacag	ttttgattat	cttagtcggt	ttaggagtg	ttgcgctatg	gttaatgatt	60
agttacaata	gcctgggttaa	atctcggatg	cacacaaaag	aagcttggag	tcagattgat	120
gtgcaattaa	agcgtcgtaa	tgacttgatt	ccaaatctta	ttgaaaccgt	aaagggatat	180
gctagctacg	agcaaaagac	atttgaaaaa	atcactgatt	tgctgctgcg	tgttgcgaa	240
gcctcaactc	ctcaagaaac	catggcggct	tctaacgaat	tgagtaaaca	agtgaccagt	300
ttgtttgccg	ttgctgaaaa	ttacccagac	ttaaaaagcta	acgaaaactt	cttgaaatta	360
caagaagagt	tgaccaatac	ggaaaaataaa	atctcatatt	ctcgtcaact	ctataattca	420
acaacgtcta	attacaacct	tcaattagaa	tctttcccaa	gcaatatcgc	tggtaaatta	480
tttggtttta	aaccaagtga	attccttaca	acaccagaag	ctgaaaaaga	agttccaaaa	540
gttgaattta	acttttaa					558

<210> SEQ ID NO 532

<211> LENGTH: 185

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 532

Met	Pro	Thr	Val	Leu	Ile	Ile	Leu	Val	Val	Leu	Gly	Val	Leu	Ala	Leu
1				5					10					15	
Trp	Leu	Met	Ile	Ser	Tyr	Asn	Ser	Leu	Val	Lys	Ser	Arg	Met	His	Thr
		20					25					30			
Lys	Glu	Ala	Trp	Ser	Gln	Ile	Asp	Val	Gln	Leu	Lys	Arg	Arg	Asn	Asp
		35				40					45				
Leu	Ile	Pro	Asn	Leu	Ile	Glu	Thr	Val	Lys	Gly	Tyr	Ala	Ser	Tyr	Glu
	50					55				60					
Gln	Lys	Thr	Phe	Glu	Lys	Ile	Thr	Asp	Leu	Arg	Ala	Arg	Val	Ala	Asn
65					70					75					80
Ala	Ser	Thr	Pro	Gln	Glu	Thr	Met	Ala	Ala	Ser	Asn	Glu	Leu	Ser	Lys
			85						90					95	
Gln	Val	Thr	Ser	Leu	Phe	Ala	Val	Ala	Glu	Asn	Tyr	Pro	Asp	Leu	Lys
		100					105					110			
Ala	Asn	Glu	Asn	Phe	Leu	Lys	Leu	Gln	Glu	Leu	Thr	Asn	Thr	Glu	
	115					120				125					
Asn	Lys	Ile	Ser	Tyr	Ser	Arg	Gln	Leu	Tyr	Asn	Ser	Thr	Thr	Ser	Asn
	130					135				140					
Tyr	Asn	Leu	Gln	Leu	Glu	Ser	Phe	Pro	Ser	Asn	Ile	Ala	Gly	Lys	Leu
145					150					155					160

Phe	Gly	Phe	Lys	Pro	Ser	Glu	Phe	Leu	Gln	Thr	Pro	Glu	Ala	Glu	Lys
				165					170					175	
Glu	Val	Pro	Lys	Val	Glu	Phe	Asn	Phe							
			180					185							

<210> SEQ ID NO 533
 <211> LENGTH: 1215
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 533

atgaaaaaaa	tatatgattt	atgggtagg	gttagtctaa	tcaaaaaaat	aggtatcgg	60
gttgtaatat	gagtcattgt	gggcattttg	gctcctgatc	ttacagggtt	tagtatttta	120
ggaaagttaa	ttgttggtgg	tttaaaggct	atcgacacct	tgcttgattt	tgctttgggt	180
tccaagcta	tctcccatca	gaaaaaagg	aaacagacta	atatgacatt	aatcattggt	240
ctgtatttat	ttgggtacct	tgcgtcagct	ttagtagcag	tactgacagc	ttatctattc	300
cctttgacgt	tagtggttaa	tacacctgta	aatacagaat	tatcaccacc	tcaagggtgt	360
gctgaagttt	ttcagtcact	tctattaaaa	ttagtggata	atccgatcaa	tgcttttagct	420
actgccaatt	atattggtgt	gctatcatgg	gcaattattt	ttggactagc	attaaaggct	480
gcaagtaaag	aaacaaagca	tcttataaaa	acagcggcag	aagttacttc	acaaatagtt	540
gtttggatca	tcaatctggc	acctattggg	attatgagtc	tggtgttcac	tacgatttct	600
gaaaacgggtg	ttggaatctt	atctgattat	gcttttttga	tactagtttt	agtaggaaca	660
atgctttttg	tcgccttagt	ggttaatcca	cttattgcgg	ttttgattac	acgacaaaat	720
ccttatcccc	ttgtcttgag	atgtttacgt	gagtcaggct	ttacagcatt	tttcacacga	780
agttctgcag	ccaatattcc	agtcaatatg	caattatgcc	aaaaaattgg	attgagtaaa	840
gatacttatt	cagtgtcaat	tccacttgga	gcaactatta	atatgggtgg	ggcagcaatt	900
accatcaatg	tcctaacgct	tgctgctgta	cacacttttg	gtattcctat	tgatttttcta	960
acagccctct	tacttagcgt	tgttgctgct	gtctctgctt	gtggtgcttc	tggtgttgct	1020
gggggatcgt	tgttacttat	tcctgtagca	tgtagtttgt	ttggcatttc	aaatgatctt	1080
gcgatgcagg	tggttggtgt	tggttttatt	gttggtgtta	tccaggattc	ttgtgagaca	1140
gccttaaatt	cgtcaaccga	tggtcttttt	acagctattg	ctgaaaaatgc	tttttggaag	1200
cgtaaaaaag	catag					1215

<210> SEQ ID NO 534
 <211> LENGTH: 404
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 534

Met	Lys	Lys	Ile	Tyr	Asp	Leu	Trp	Val	Arg	Val	Ser	Leu	Ile	Lys	Lys
1				5					10					15	
Ile	Gly	Ile	Gly	Val	Val	Ile	Gly	Val	Met	Leu	Gly	Ile	Leu	Ala	Pro
			20					25					30		
Asp	Leu	Thr	Gly	Phe	Ser	Ile	Leu	Gly	Lys	Leu	Phe	Val	Gly	Gly	Leu
		35					40				45				
Lys	Ala	Ile	Ala	Pro	Leu	Leu	Val	Phe	Ala	Leu	Val	Ser	Gln	Ala	Ile
		50				55					60				
Ser	His	Gln	Lys	Lys	Gly	Lys	Gln	Thr	Asn	Met	Thr	Leu	Ile	Ile	Val
65				70					75					80	
Leu	Tyr	Leu	Phe	Gly	Thr	Phe	Ala	Ser	Ala	Leu	Val	Ala	Val	Leu	Thr
			85					90						95	
Ala	Tyr	Leu	Phe	Pro	Leu	Thr	Leu	Val	Leu	Asn	Thr	Pro	Val	Asn	Thr
		100						105					110		
Glu	Leu	Ser	Pro	Pro	Gln	Gly	Val	Ala	Glu	Val	Phe	Gln	Ser	Leu	Leu
		115					120					125			
Leu	Lys	Leu	Val	Asp	Asn	Pro	Ile	Asn	Ala	Leu	Ala	Thr	Ala	Asn	Tyr
		130				135					140				
Ile	Gly	Val	Leu	Ser	Trp	Ala	Ile	Ile	Phe	Gly	Leu	Ala	Leu	Lys	Ala
145					150					155					160

Ala	Ser	Lys	Glu	Thr	Lys	His	Leu	Ile	Lys	Thr	Ala	Ala	Glu	Val	Thr
				165					170					175	
Ser	Gln	Ile	Val	Val	Trp	Ile	Ile	Asn	Leu	Ala	Pro	Ile	Gly	Ile	Met
			180					185					190		
Ser	Leu	Val	Phe	Thr	Thr	Ile	Ser	Glu	Asn	Gly	Val	Gly	Ile	Leu	Ser
		195					200				205				
Asp	Tyr	Ala	Phe	Leu	Ile	Leu	Val	Leu	Val	Gly	Thr	Met	Leu	Phe	Val
	210				215					220					
Ala	Leu	Val	Val	Asn	Pro	Leu	Ile	Ala	Val	Leu	Ile	Thr	Arg	Gln	Asn
225					230					235					240
Pro	Tyr	Pro	Leu	Val	Leu	Arg	Cys	Leu	Arg	Glu	Ser	Gly	Leu	Thr	Ala
			245						250					255	
Phe	Phe	Thr	Arg	Ser	Ser	Ala	Ala	Asn	Ile	Pro	Val	Asn	Met	Gln	Leu
			260					265					270		
Cys	Gln	Lys	Ile	Gly	Leu	Ser	Lys	Asp	Thr	Tyr	Ser	Val	Ser	Ile	Pro
		275					280					285			
Leu	Gly	Ala	Thr	Ile	Asn	Met	Gly	Gly	Ala	Ala	Ile	Thr	Ile	Asn	Val
	290					295					300				
Leu	Thr	Leu	Ala	Ala	Val	His	Thr	Phe	Gly	Ile	Pro	Ile	Asp	Phe	Leu
305					310					315					320
Thr	Ala	Leu	Leu	Leu	Ser	Val	Val	Ala	Ala	Val	Ser	Ala	Cys	Gly	Ala
			325					330						335	
Ser	Gly	Val	Ala	Gly	Gly	Ser	Leu	Leu	Leu	Ile	Pro	Val	Ala	Cys	Ser
			340				345						350		
Leu	Phe	Gly	Ile	Ser	Asn	Asp	Leu	Ala	Met	Gln	Val	Val	Gly	Val	Gly
		355				360					365				
Phe	Ile	Val	Gly	Val	Ile	Gln	Asp	Ser	Cys	Glu	Thr	Ala	Leu	Asn	Ser
	370					375					380				
Ser	Thr	Asp	Val	Leu	Phe	Thr	Ala	Ile	Ala	Glu	Asn	Ala	Phe	Trp	Lys
385				390						395					400
Arg	Lys	Lys	Ala												

<210> SEQ ID NO 535

<211> LENGTH: 1371

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 535

atgaaacaaa	aaaatgtata	tatcgtcatt	ggattcatgc	tatttgcgct	atTTTTtggga	60
gcagcaaacc	tcattttacc	agcttttttta	ggcatctact	cagggtcatca	gatttctatgg	120
tctatcattg	gtttttgttt	aactgggtgtc	tccttgccct	tactcgggtgt	cattgctgtt	180
gctaaatctg	gatcaggcga	tggtgaaagt	ttggcacgcc	ccatctctaa	atgggatgca	240
atcttctatt	cttccatttt	gtatttatct	attggcccat	tttttgctat	tccaagaaca	300
ggagccactt	ctttttcagt	cggtatcgct	cctatccttag	gagataatac	aaccaataaa	360
gctattttatg	ctatactatt	ttttgggtctg	tcctacttcc	ttgctatcaa	acctagttaa	420
ctagctgaaa	atatcggaaa	atTTTTtaacg	ccaacgttgt	tagttgttat	ttctatTTTTg	480
gttatcgcg	cctttgtcca	tcctgctgga	aattacgggtg	atgcttttta	cgctgggggtc	540
ggtgttaata	atgcctttta	agattttcct	tttatagcag	gattaattca	aggttatggc	600
actatggatg	cactagcttc	tcttgTTTTt	gctatttttag	tcattgaggc	taccaaacaa	660
tttggcgcta	agacggacaa	agaaatgacc	aaaataaacac	ttattttctgg	ggctattgcc	720
atTTtgctat	tagcacttgt	ctatatcttt	gtcggtcgta	ttggagcaac	atcacaatca	780
ttatttcctt	ttattgatgg	cagctttacc	cttcatggta	atccagttaa	tggcgggtcaa	840
atcctaagtc	atgcttctcg	tttttaccta	ggtggcatcg	gacaagcatt	tctagctgtt	900
gtgattttcc	tggcctgtct	aaccacttca	acaggcttaa	tcacgtcaag	tgctgaatac	960
ttccataaat	ttagtcctgc	tttatctcat	attgcttggg	caactatctt	tactttacta	1020
tcagctttct	tttatTTTtg	tggtttatca	gtcattatca	actggtcagc	tcctgtttta	1080
ttccttttat	acccattaac	agtcgattta	atTTTtccttg	ttttggcaca	aaaatgcttc	1140
aataatgatc	ctattgtcta	tcgaactaca	attgggtctaa	cctttatttc	tgccatattt	1200

gatgcactcc	taacactatc	acaaatgact	ggattatttc	atttaccaga	agccgttgta	1260
acttttttcc	aaaaaactgt	tccactaggg	caattctcaa	tgggatggat	tatctttgct	1320
gctattgggt	ttttaatagg	gcttatacta	agtaaaacga	agaaaagcta	a	1371

<210> SEQ ID NO 536

<211> LENGTH: 456

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 536

Met	Lys	Gln	Lys	Asn	Val	Tyr	Ile	Val	Ile	Gly	Phe	Met	Leu	Phe	Ala	
1				5					10					15		
Leu	Phe	Phe	Gly	Ala	Ala	Asn	Leu	Ile	Tyr	Pro	Ala	Phe	Leu	Gly	Ile	
			20					25					30			
Tyr	Ser	Gly	His	Gln	Ile	Leu	Trp	Ser	Ile	Ile	Gly	Phe	Cys	Leu	Thr	
		35					40					45				
Gly	Val	Ser	Leu	Pro	Leu	Leu	Gly	Val	Ile	Ala	Val	Ala	Lys	Ser	Gly	
	50					55					60					
Ser	Gly	Asp	Val	Glu	Ser	Leu	Ala	Arg	Pro	Ile	Ser	Lys	Trp	Tyr	Ala	
65				70						75					80	
Ile	Phe	Tyr	Ser	Ser	Ile	Leu	Tyr	Leu	Ser	Ile	Gly	Pro	Phe	Phe	Ala	
				85					90					95		
Ile	Pro	Arg	Thr	Gly	Ala	Thr	Ser	Phe	Ser	Val	Gly	Ile	Ala	Pro	Ile	
			100					105					110			
Leu	Gly	Asp	Asn	Thr	Thr	Asn	Lys	Ala	Ile	Tyr	Ala	Ile	Leu	Phe	Phe	
		115				120						125				
Gly	Leu	Ser	Tyr	Phe	Leu	Ala	Ile	Lys	Pro	Ser	Lys	Leu	Ala	Glu	Asn	
	130					135					140					
Ile	Gly	Lys	Phe	Leu	Thr	Pro	Thr	Leu	Leu	Val	Val	Ile	Ser	Ile	Leu	
145				150						155					160	
Val	Ile	Ala	Ser	Phe	Val	His	Pro	Ala	Gly	Asn	Tyr	Gly	Asp	Ala	Phe	
				165					170					175		
Asn	Ala	Gly	Val	Gly	Val	Asn	Asn	Ala	Phe	Lys	Asp	Phe	Pro	Phe	Ile	
			180					185					190			
Ala	Gly	Leu	Ile	Gln	Gly	Tyr	Gly	Thr	Met	Asp	Ala	Leu	Ala	Ser	Leu	
		195					200					205				
Val	Phe	Ala	Ile	Leu	Val	Ile	Glu	Ala	Thr	Lys	Gln	Phe	Gly	Ala	Lys	
	210					215					220					
Thr	Asp	Lys	Glu	Met	Thr	Lys	Ile	Thr	Leu	Ile	Ser	Gly	Ala	Ile	Ala	
225				230						235					240	
Ile	Leu	Leu	Leu	Ala	Leu	Val	Tyr	Ile	Phe	Val	Gly	Arg	Ile	Gly	Ala	
				245					250					255		
Thr	Ser	Gln	Ser	Leu	Phe	Pro	Phe	Ile	Asp	Gly	Ser	Phe	Thr	Leu	His	
			260					265					270			
Gly	Asn	Pro	Val	Asn	Gly	Gly	Gln	Ile	Leu	Ser	His	Ala	Ser	Arg	Phe	
		275					280					285				
Tyr	Leu	Gly	Gly	Ile	Gly	Gln	Ala	Phe	Leu	Ala	Val	Val	Ile	Phe	Leu	
	290					295					300					
Ala	Cys	Leu	Thr	Thr	Ser	Thr	Gly	Leu	Ile	Thr	Ser	Ser	Ala	Glu	Tyr	
305					310					315					320	
Phe	His	Lys	Leu	Val	Pro	Ala	Leu	Ser	His	Ile	Ala	Trp	Ala	Thr	Ile	
				325					330					335		
Phe	Thr	Leu	Leu	Ser	Ala	Phe	Phe	Tyr	Phe	Gly	Gly	Leu	Ser	Val	Ile	
			340					345					350			
Ile	Asn	Trp	Ser	Ala	Pro	Val	Leu	Phe	Leu	Leu	Tyr	Pro	Leu	Thr	Val	
		355					360					365				
Asp	Leu	Ile	Phe	Leu	Val	Leu	Ala	Gln	Lys	Cys	Phe	Asn	Asn	Asp	Pro	
	370						375					380				

Ile	Val	Tyr	Arg	Thr	Thr	Ile	Gly	Leu	Thr	Phe	Ile	Pro	Ala	Ile	Phe
385					390					395					400
Asp	Ala	Leu	Leu	Thr	Leu	Ser	Gln	Met	Thr	Gly	Leu	Phe	His	Leu	Pro
				405					410					415	
Glu	Ala	Val	Val	Thr	Phe	Phe	Gln	Lys	Thr	Val	Pro	Leu	Gly	Gln	Phe
			420				425						430		
Ser	Met	Gly	Trp	Ile	Ile	Phe	Ala	Ala	Ile	Gly	Phe	Leu	Ile	Gly	Leu
		435					440					445			
Ile	Leu	Ser	Lys	Thr	Lys	Lys	Ser								
	450					455									

<210> SEQ ID NO 537

<211> LENGTH: 663

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 537

atgtttatga	actcggatgg	tcatggagat	gcaggttggg	gcttagcgat	ttggaatact	60
ttatacatga	ccattgtgcc	ttttattggt	gggggggcta	ttgggtctct	attaggcttg	120
ttattagttt	taacaggacc	ggacggtggt	attgaaaaca	aaacgatttg	ttgggttatt	180
gataaagtta	cctctatttt	tagagccatt	ccttttggtta	ttttgattgc	tatttttagct	240
agctttacct	atttgctttt	aagaacaact	ttaggagcaa	cagcggcctt	ggtaccttta	300
acctttgcga	cttttccttt	ttatgcccgt	caggtccaag	ttgttttttc	agaattagac	360
aaggggtgta	ttgaagcagc	acaagcttca	ggtgctactt	tctgggatat	tgtcaaagtg	420
tatctcagtg	aaggtttacc	agatcttatt	cgtgtttcta	cagtcacctt	aatttcttta	480
gttggggaaa	ctgccatggc	aggagctatc	ggtgctggag	gattaggaaa	tgtagcgatt	540
tcttatgggt	ataatcggtt	taacaatgat	gtgacttggg	tagcgactat	tattattcct	600
ttaattattt	ttgctatcca	atttattggt	gatagcttga	ctagaagggt	tagtcataaa	660
taa						663

<210> SEQ ID NO 538

<211> LENGTH: 220

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 538

Met	Phe	Met	Asn	Ser	Asp	Gly	His	Gly	Asp	Ala	Gly	Trp	Gly	Leu	Ala
1			5						10					15	
Ile	Trp	Asn	Thr	Leu	Tyr	Met	Thr	Ile	Val	Pro	Phe	Ile	Val	Gly	Gly
			20					25					30		
Ala	Ile	Gly	Leu	Leu	Leu	Gly	Leu	Leu	Leu	Val	Leu	Thr	Gly	Pro	Asp
		35				40					45				
Gly	Val	Ile	Glu	Asn	Lys	Thr	Ile	Cys	Trp	Val	Ile	Asp	Lys	Val	Thr
	50				55					60					
Ser	Ile	Phe	Arg	Ala	Ile	Pro	Phe	Val	Ile	Leu	Ile	Ala	Ile	Leu	Ala
65			70						75					80	
Ser	Phe	Thr	Tyr	Leu	Leu	Leu	Arg	Thr	Thr	Leu	Gly	Ala	Thr	Ala	Ala
			85					90					95		
Leu	Val	Pro	Leu	Thr	Phe	Ala	Thr	Phe	Pro	Phe	Tyr	Ala	Arg	Gln	Val
		100						105				110			
Gln	Val	Val	Phe	Ser	Glu	Leu	Asp	Lys	Gly	Val	Ile	Glu	Ala	Ala	Gln
	115					120					125				
Ala	Ser	Gly	Ala	Thr	Phe	Trp	Asp	Ile	Val	Lys	Val	Tyr	Leu	Ser	Glu
	130					135				140					
Gly	Leu	Pro	Asp	Leu	Ile	Arg	Val	Ser	Thr	Val	Thr	Leu	Ile	Ser	Leu
145				150					155					160	
Val	Gly	Glu	Thr	Ala	Met	Ala	Gly	Ala	Ile	Gly	Ala	Gly	Gly	Leu	Gly
			165					170					175		
Asn	Val	Ala	Ile	Ser	Tyr	Gly	Tyr	Asn	Arg	Phe	Asn	Asn	Asp	Val	Thr

			180					185				190					
Trp	Val	Ala	Thr	Ile	Ile	Ile	Leu	Leu	Ile	Ile	Phe	Ala	Ile	Gln	Phe		
		195					200					205					
Ile	Gly	Asp	Ser	Leu	Thr	Arg	Arg	Phe	Ser	His	Lys						
	210					215					220						

<210> SEQ ID NO 539
 <211> LENGTH: 927
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 539

atggaatcga	ttgataaatc	taaatttcga	tttgttgagc	gcgatagtga	agcctccgaa	60
gtgattgata	cccctgctta	ttcttactgg	aaatcagtg	ttcgtcagtt	tttttctaaa	120
aaatctacag	tctttatgct	cgtaatttta	gtgacagtct	tgatgatgag	ctttatttat	180
ccaatgtttg	ccaactacga	ctttaatgac	gttagtaata	tcaatgactt	ttcaaagcgt	240
tatatttggc	caaatgcaga	gtactgggtt	ggaaccgaca	aaaatgggca	atctctgttt	300
gatggtgttt	ggtagggggc	acgtaattct	attttaatct	cagttatagc	gacactaatt	360
aatatcacca	ttggggtagt	gttaggagcc	atatggggag	tttctaaagc	atttgataaa	420
gttatgattg	aaatttataa	cattatctca	aatatccctt	ctatgcttat	tatcattgtt	480
ttgacctatt	cattaggtgc	aggattttgg	aatttgattc	tagctttctg	tatcactgga	540
tggattggtg	tcgcctactc	catccgtgtt	caaatcttgc	gttaccgtga	tttagaatac	600
aaccttgcta	gtcaaacttt	gggaacacca	atgtacaaga	ttgctgttaa	gaacctcctg	660
cctcaattgg	tttcagttat	catgactatg	ttgtcacaaa	tgctaccagt	ttatgtatct	720
tctgaggcct	tcttatcctt	ctttgggatt	ggtttaccaa	ccaccactcc	aagttagga	780
cgttttattg	ctaattattc	aagcaactta	acaacaaaatg	cctacctctt	ttggattccc	840
ttagtaacat	tgattttagt	atcgttacca	ctatacattg	tcggacaaaa	cttggctgat	900
gccagtgacc	cacgttcaca	tagatag				927

<210> SEQ ID NO 540
 <211> LENGTH: 308
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 540

Met	Glu	Ser	Ile	Asp	Lys	Ser	Lys	Phe	Arg	Phe	Val	Glu	Arg	Asp	Ser
1			5					10						15	
Glu	Ala	Ser	Glu	Val	Ile	Asp	Thr	Pro	Ala	Tyr	Ser	Tyr	Trp	Lys	Ser
		20						25					30		
Val	Phe	Arg	Gln	Phe	Phe	Ser	Lys	Lys	Ser	Thr	Val	Phe	Met	Leu	Val
	35					40					45				
Ile	Leu	Val	Thr	Val	Leu	Met	Met	Ser	Phe	Ile	Tyr	Pro	Met	Phe	Ala
	50					55					60				
Asn	Tyr	Asp	Phe	Asn	Asp	Val	Ser	Asn	Ile	Asn	Asp	Phe	Ser	Lys	Arg
65				70					75					80	
Tyr	Ile	Trp	Pro	Asn	Ala	Glu	Tyr	Trp	Phe	Gly	Thr	Asp	Lys	Asn	Gly
			85					90					95		
Gln	Ser	Leu	Phe	Asp	Gly	Val	Trp	Tyr	Gly	Ala	Arg	Asn	Ser	Ile	Leu
		100						105					110		
Ile	Ser	Val	Ile	Ala	Thr	Leu	Ile	Asn	Ile	Thr	Ile	Gly	Val	Val	Leu
	115					120						125			
Gly	Ala	Ile	Trp	Gly	Val	Ser	Lys	Ala	Phe	Asp	Lys	Val	Met	Ile	Glu
	130					135					140				
Ile	Tyr	Asn	Ile	Ile	Ser	Asn	Ile	Pro	Ser	Met	Leu	Ile	Ile	Ile	Val
145				150						155					160
Leu	Thr	Tyr	Ser	Leu	Gly	Ala	Gly	Phe	Trp	Asn	Leu	Ile	Leu	Ala	Phe
			165					170						175	
Cys	Ile	Thr	Gly	Trp	Ile	Gly	Val	Ala	Tyr	Ser	Ile	Arg	Val	Gln	Ile
			180					185						190	

Leu	Arg	Tyr	Arg	Asp	Leu	Glu	Tyr	Asn	Leu	Ala	Ser	Gln	Thr	Leu	Gly
	195						200					205			
Thr	Pro	Met	Tyr	Lys	Ile	Ala	Val	Lys	Asn	Leu	Leu	Pro	Gln	Leu	Val
	210					215					220				
Ser	Val	Ile	Met	Thr	Met	Leu	Ser	Gln	Met	Leu	Pro	Val	Tyr	Val	Ser
225					230					235					240
Ser	Glu	Ala	Phe	Leu	Ser	Phe	Phe	Gly	Ile	Gly	Leu	Pro	Thr	Thr	Thr
			245					250						255	
Pro	Ser	Leu	Gly	Arg	Phe	Ile	Ala	Asn	Tyr	Ser	Ser	Asn	Leu	Thr	Thr
		260						265					270		
Asn	Ala	Tyr	Leu	Phe	Trp	Ile	Pro	Leu	Val	Thr	Leu	Ile	Leu	Val	Ser
	275						280					285			
Leu	Pro	Leu	Tyr	Ile	Val	Gly	Gln	Asn	Leu	Ala	Asp	Ala	Ser	Asp	Pro
	290					295					300				
Arg	Ser	His	Arg												
305															

<210> SEQ ID NO 541
 <211> LENGTH: 1182
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 541

ttgaccaaaa	gaattatact	aactatTTTT	acctttatTTT	gcttttcggt	gatgcctctt	60
gtccacgccg	aagatgtcat	ggatattaca	aggcaagcag	gctacacagt	tagtgagggt	120
aatcgaccaa	aatcttctat	tgtcgttgat	gcaaatagtt	cagatattct	ttggcaagat	180
aatattgata	ttcctaggga	tcttgctagt	atgtctaaga	tgtttacgct	ttacatttta	240
tttgaagagc	tcgctaaggg	aaaaattacg	atggacacta	ctattacggc	aactccaacc	300
gatcaagcta	tcgctaacat	ttatgagatt	agcaataata	atatcgtcgc	tggagtagct	360
tatcctattc	gtgatcttat	tactatgaca	gctgtgcctt	catcaaagtc	agcaactggt	420
atgattgcca	attatTTTatc	aaacaatgat	gcttctgcgt	ttatcgatcg	tgtaaatgcc	480
acagccaaac	aattaggcat	gactaacact	catttttcaa	acgctagtgg	tgcagcagca	540
caagcttttc	aaggttatta	taatcctact	aaatatgatt	tatctgcttc	aaatattacg	600
accgctcgag	atttgtccaa	gttactctat	gccttcttaa	aaaaatacc	tgaaattatc	660
tcctttacaa	ataaatctgt	tgtgcacact	atggtaggaa	cgccatatga	agaagaattt	720
cacacctata	accactctct	cccagataat	caatttggt	tgaaaggagt	tgatggatta	780
aaaacagggt	ctagtcccag	tgctgctttt	aacgccatga	taactgccaa	aagaggcaaa	840
actcgactca	ttactattgt	catgggggtc	ggagattggt	cagatcaaaa	cggggagttt	900
tatagacatc	ctttcgtaaa	tgcttgact	gagaaaggtt	ttaaagatag	taagacctta	960
tccaaaaaag	cacgcaaaaa	actcgaaaaa	ttagtgccac	aaaccaaaaa	agaaacatca	1020
tctaaacagc	agcacttcaa	agccactaaa	aagcaatcgt	acttggaag	agtcgaagat	1080
tttatgaatc	acaaccacac	tttcttgctt	atttgcttag	ctatctttat	aattactatc	1140
cttttactaa	gcctcgttgt	ctttgcaatg	ggacgccaat	aa		1182

<210> SEQ ID NO 542
 <211> LENGTH: 393
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 542

Met	Thr	Lys	Arg	Ile	Ile	Leu	Thr	Ile	Phe	Thr	Phe	Ile	Cys	Phe	Ser
1			5						10				15		
Val	Met	Pro	Leu	Val	His	Ala	Glu	Asp	Val	Met	Asp	Ile	Thr	Arg	Gln
		20						25				30			
Ala	Gly	Tyr	Thr	Val	Ser	Glu	Val	Asn	Arg	Pro	Lys	Ser	Ser	Ile	Val
	35						40				45				
Val	Asp	Ala	Asn	Ser	Ser	Asp	Ile	Leu	Trp	Gln	Asp	Asn	Ile	Asp	Ile
	50					55				60					
Pro	Arg	Asp	Pro	Ala	Ser	Met	Ser	Lys	Met	Phe	Thr	Leu	Tyr	Ile	Leu

65					70					75					80
Phe	Glu	Glu	Leu	Ala	Lys	Gly	Lys	Ile	Thr	Met	Asp	Thr	Thr	Ile	Thr
				85					90					95	
Ala	Thr	Pro	Thr	Asp	Gln	Ala	Ile	Ala	Asn	Ile	Tyr	Glu	Ile	Ser	Asn
			100					105					110		
Asn	Asn	Ile	Val	Ala	Gly	Val	Ala	Tyr	Pro	Ile	Arg	Asp	Leu	Ile	Thr
		115					120					125			
Met	Thr	Ala	Val	Pro	Ser	Ser	Asn	Ala	Ala	Thr	Val	Met	Ile	Ala	Asn
	130					135					140				
Tyr	Leu	Ser	Asn	Asn	Asp	Ala	Ser	Ala	Phe	Ile	Asp	Arg	Val	Asn	Ala
145					150					155					160
Thr	Ala	Lys	Gln	Leu	Gly	Met	Thr	Asn	Thr	His	Phe	Ser	Asn	Ala	Ser
				165					170					175	
Gly	Ala	Ala	Ala	Gln	Ala	Phe	Gln	Gly	Tyr	Tyr	Asn	Pro	Thr	Lys	Tyr
			180					185					190		
Asp	Leu	Ser	Ala	Ser	Asn	Ile	Thr	Thr	Ala	Arg	Asp	Leu	Ser	Lys	Leu
	195						200					205			
Leu	Tyr	Ala	Phe	Leu	Lys	Lys	Tyr	Pro	Glu	Ile	Ile	Ser	Phe	Thr	Asn
	210					215						220			
Lys	Ser	Val	Val	His	Thr	Met	Val	Gly	Thr	Pro	Tyr	Glu	Glu	Glu	Phe
225					230					235					240
His	Thr	Tyr	Asn	His	Ser	Leu	Pro	Asp	Asn	Gln	Phe	Gly	Met	Lys	Gly
			245						250					255	
Val	Asp	Gly	Leu	Lys	Thr	Gly	Ser	Ser	Pro	Ser	Ala	Ala	Phe	Asn	Ala
			260					265					270		
Met	Ile	Thr	Ala	Lys	Arg	Gly	Lys	Thr	Arg	Leu	Ile	Thr	Ile	Val	Met
	275						280					285			
Gly	Val	Gly	Asp	Trp	Ser	Asp	Gln	Asn	Gly	Glu	Phe	Tyr	Arg	His	Pro
	290					295					300				
Phe	Val	Asn	Ala	Leu	Thr	Glu	Lys	Gly	Phe	Lys	Asp	Ser	Lys	Thr	Leu
305					310					315					320
Ser	Lys	Lys	Ala	Arg	Gln	Lys	Leu	Glu	Lys	Leu	Val	Pro	Gln	Thr	Lys
			325						330					335	
Lys	Glu	Thr	Ser	Ser	Lys	Gln	Gln	His	Phe	Lys	Ala	Thr	Lys	Lys	Gln
			340					345					350		
Ser	Tyr	Leu	Glu	Arg	Val	Glu	Asp	Phe	Met	Asn	His	Asn	His	Thr	Phe
	355						360					365			
Leu	Leu	Ile	Cys	Leu	Ala	Ile	Phe	Ile	Ile	Thr	Ile	Leu	Leu	Leu	Ser
	370					375					380				
Leu	Val	Val	Phe	Ala	Met	Gly	Arg	Gln							
385						390									

<210> SEQ ID NO 543

<211> LENGTH: 1170

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 543

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ttcttaaccc	ctcttggtcg	cttttttagcc	tttcgtgtgg	gtgcagtaga	caatcccaat	120
gccagacggg	tcaataaggt	tccgatgcca	accagtgggt	gattagctat	ttttatgtct	180
tttttagtag	caagtttggg	acttattccg	attgcttcta	aaggcgccat	gttttttgggt	240
cagacctact	tcagttatat	tttacctgtc	gtgattgggt	ctacagtaat	tacccttact	300
ggtttttttag	atgatttgta	tgagttaagt	cctaaattaa	agatgtttgg	tattctaatt	360
ggtgcagtga	ttgtctgggc	ttttaccgac	tttaaatttg	atagcttcaa	aattcctttt	420
ggaggggcgt	tgtagtttt	tggtcctttc	ttaaccttat	tcttaacagt	cctgtggatt	480
gtttccatca	ctaagtctat	taacttgatt	gacggtttgg	atggtttgggt	tagtgggggtc	540
tctattatta	gttttagtgac	catggctatt	gtatcttatt	tcttttttacc	tcaaaaggat	600

ttctttttga	cgtaaccat	tttggctcttg	atttctgcta	ttgcaggatt	ttttccttat	660
aattaccatc	cagctatgat	ttatttgggt	gacacaggag	ccctctttat	tggctttatg	720
ataggggttt	tgtctcttca	aggattgaaa	aattcaacgg	ctgtggctgt	ggtgacacct	780
gttattattc	ttggtgtacc	cattatggat	accatcgtgg	ctattattcg	acgtagttta	840
tcagggtcaaa	aattctacga	gccggataag	atgcacctgc	atcatcgact	cttatcaatg	900
ggctttactc	atcgaggagc	tgtcttagta	gtttatggta	ttaccatgct	ttttccctt	960
atttctttac	ttttaaatgt	ttctagtcga	attggtggcg	tcctcttgat	gcttggactt	1020
ttatttgggt	tagaagtttt	tattgaagga	ttggagatct	ggggtgaaaa	gcgaacgcct	1080
ttgtttaact	tgttaaagtt	tattggtaat	agtgattatc	gtcaagcaat	gcttctgaaa	1140
tggaaagaaa	agaaggattt	gaaacactaa				1170

<210> SEQ ID NO 544

<211> LENGTH: 389

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 544

Met	Phe	Ser	Phe	Thr	Ile	Asp	Tyr	Val	Leu	Val	Leu	Ile	Gly	Ala	Leu
1				5					10					15	
Leu	Met	Ser	Leu	Phe	Leu	Thr	Pro	Leu	Val	Arg	Phe	Leu	Ala	Phe	Arg
			20					25					30		
Val	Gly	Ala	Val	Asp	Asn	Pro	Asn	Ala	Arg	Arg	Val	Asn	Lys	Val	Pro
			35				40					45			
Met	Pro	Thr	Ser	Gly	Gly	Leu	Ala	Ile	Phe	Met	Ser	Phe	Leu	Val	Ala
			50			55					60				
Ser	Leu	Gly	Leu	Ile	Pro	Ile	Ala	Ser	Lys	Gly	Ala	Met	Phe	Phe	Gly
65				70						75				80	
Gln	Thr	Tyr	Phe	Ser	Tyr	Ile	Leu	Pro	Val	Val	Ile	Gly	Ala	Thr	Val
			85						90					95	
Ile	Thr	Leu	Thr	Gly	Phe	Leu	Asp	Asp	Leu	Tyr	Glu	Leu	Ser	Pro	Lys
			100				105						110		
Leu	Lys	Met	Phe	Gly	Ile	Leu	Ile	Gly	Ala	Val	Ile	Val	Trp	Ala	Phe
			115			120						125			
Thr	Asp	Phe	Lys	Phe	Asp	Ser	Phe	Lys	Ile	Pro	Phe	Gly	Gly	Pro	Leu
			130			135					140				
Leu	Val	Phe	Gly	Pro	Phe	Leu	Thr	Leu	Phe	Leu	Thr	Val	Leu	Trp	Ile
145				150						155				160	
Val	Ser	Ile	Thr	Asn	Ala	Ile	Asn	Leu	Ile	Asp	Gly	Leu	Asp	Gly	Leu
			165						170					175	
Val	Ser	Gly	Val	Ser	Ile	Ile	Ser	Leu	Val	Thr	Met	Ala	Ile	Val	Ser
			180					185					190		
Tyr	Phe	Phe	Leu	Pro	Gln	Lys	Asp	Phe	Phe	Leu	Thr	Leu	Thr	Ile	Leu
			195			200						205			
Val	Leu	Ile	Ser	Ala	Ile	Ala	Gly	Phe	Phe	Pro	Tyr	Asn	Tyr	His	Pro
			210			215					220				
Ala	Met	Ile	Tyr	Leu	Gly	Asp	Thr	Gly	Ala	Leu	Phe	Ile	Gly	Phe	Met
225				230						235				240	
Ile	Gly	Val	Leu	Ser	Leu	Gln	Gly	Leu	Lys	Asn	Ser	Thr	Ala	Val	Ala
			245						250					255	
Val	Val	Thr	Pro	Val	Ile	Ile	Leu	Gly	Val	Pro	Ile	Met	Asp	Thr	Ile
			260					265					270		
Val	Ala	Ile	Arg	Arg	Ser	Leu	Ser	Gly	Gln	Lys	Phe	Tyr	Glu	Pro	
			275			280					285				
Asp	Lys	Met	His	Leu	His	His	Arg	Leu	Leu	Ser	Met	Gly	Phe	Thr	His
			290			295					300				
Arg	Gly	Ala	Val	Leu	Val	Val	Tyr	Gly	Ile	Thr	Met	Leu	Phe	Ser	Leu
305				310						315				320	
Ile	Ser	Leu	Leu	Leu	Asn	Val	Ser	Ser	Arg	Ile	Gly	Gly	Val	Leu	Leu

				325						330					335				
Met	Leu	Gly	Leu	Leu	Phe	Gly	Leu	Glu	Val	Phe	Ile	Glu	Gly	Leu	Glu				
				340															
Ile	Trp	Gly	Glu	Lys	Arg	Thr	Pro	Leu	Phe	Asn	Leu	Leu	Lys	Phe	Ile				
				355															
Gly	Asn	Ser	Asp	Tyr	Arg	Gln	Ala	Met	Leu	Leu	Lys	Trp	Lys	Glu	Lys				
				370															
Lys	Asp	Leu	Lys	His															
				385															

<210> SEQ ID NO 545
 <211> LENGTH: 1899
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 545

atgaaaaaaaa	ttttgatgac	gcttggtgctc	tgcttcagtc	ttttagggat	acgaataaaa	60
gcagctgatg	tagactatag	catcaccaac	tatgaaggctc	agttactgtt	atcaaaaagaa	120
aatactgctc	ggtttgagca	aaaagtaacc	tatcaatttg	acacttctta	taacggccag	180
tatatttcgc	tgggccggac	aggtcatttg	ccagcgggct	ttgctattga	ccaaaagcct	240
aaagttgagg	tatatcagaa	tggtcaacag	gtacctgtta	gtcaagagtt	tagtgacctt	300
ggagatggct	atcgtttaaa	actttataat	gctggccaag	ctggtgataa	ggttgacgtc	360
aaggttatct	ggcaactgca	ccacctttta	acagcttatc	aagacgtggc	agagctgaat	420
tggacaccga	ttagtgattg	ggacaaaaca	ttagaaaagg	tgagtttgac	cgctactacc	480
ccaactgata	ttcaggattc	taatctatgg	gctcacagag	gatattacca	aaagaaacct	540
caagtgttaa	aagaaggtaa	cagtcgctat	cagattaatg	ccaagaatgt	ctcagggcaa	600
ctggaattgc	atgcttattg	ggataaaaaa	gcattattgg	gaaaagagcc	agttgatgtt	660
tcaacgagta	aaaagaataa	aattgtagcg	ttagaaacta	agatttccag	acgaaggacc	720
ttgttacagc	tgctatttgg	caaagtcatt	cctctggtag	aggtaggttt	tcttctttgg	780
cagttaatac	agtttacaa	attaaagaaa	caattcaatc	gttatcattt	ggctaaccat	840
acagatcaca	gttacgaagt	ccctgaagat	ctttcgctc	ttgtgttgac	acaagcgatt	900
tatggacaga	gttttgccta	tttatcccct	acagcatcag	aaagccagaa	attattgatc	960
cctaaaggag	tgacctttga	ggcccttggt	caagctacct	tggtggatct	gatcgaccaa	1020
aagggtgctt	tattaacgaa	agaagaaggg	aaagcttatc	ttgaaatcag	tcagttagat	1080
cggtgtgacg	atgaggaagc	tgcccttcta	gatatggctt	ttggaaacaa	ggtgacattg	1140
ccggtggatc	aattgtttag	tcaataccat	tatgatgctg	ataccattaa	acaattaaag	1200
aaaacgtaca	aaggtaaaaa	gctcgagcaa	gaagtcgctc	aatcgtctga	gcaggtgatt	1260
aaggcgatga	aaaaagcgct	ggcagctatt	acaaacaatg	tcctagaaac	tatcaaaaag	1320
ttaaacttac	cagatactta	tcgtcaaagt	acccggcgag	agaaacgaaa	aagcaatagt	1380
gtccagggat	taggttggtt	gttgcttatt	ctaaatagtg	gtttattgat	ttacttggct	1440
attaaagaaa	gtgggttagc	cctcatttac	cttgctttaa	tggtgctaac	gatgtgcctt	1500
ggcttttaca	ttagcctgaa	gttagatcaa	tacaagaaat	tggttattga	aacacctgag	1560
gggggtgttc	ggttacatca	atggcagagc	tttaaaaaaca	tgatacgaga	cattgacaaa	1620
tttgaggatg	ttgctattga	aggtttggtt	gtttggaacc	gtgttttggt	ttatgccacc	1680
ttatttggtt	acgctaagaa	agtggaacgc	tatttgaaag	tccatcgtat	tgcccttacct	1740
gaggtttacc	aagctgttcg	accaggtgaa	ttatcaatgg	taatgtatgc	tacgacacca	1800
acctttgtgt	ctagcttgct	ttcagctaca	acttcctcaa	atttctcagt	ctcttcgga	1860
ggcgggatta	gtggtggtgg	cggcggcggt	gccttttaa			1899

<210> SEQ ID NO 546
 <211> LENGTH: 632
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 546

Met	Lys	Lys	Ile	Leu	Met	Thr	Leu	Val	Leu	Cys	Phe	Ser	Leu	Leu	Gly
1				5				10						15	
Ile	Arg	Ile	Lys	Ala	Ala	Asp	Val	Asp	Tyr	Ser	Ile	Thr	Asn	Tyr	Glu
				20				25						30	

Gly	Gln	Leu	Leu	Leu	Ser	Lys	Glu	Asn	Thr	Ala	Arg	Phe	Glu	Gln	Lys
		35					40					45			
Val	Thr	Tyr	Gln	Phe	Asp	Thr	Ser	Tyr	Asn	Gly	Gln	Tyr	Ile	Ser	Leu
	50					55				60					
Gly	Arg	Thr	Gly	His	Leu	Pro	Ala	Gly	Phe	Ala	Ile	Asp	Gln	Lys	Pro
65					70					75					80
Lys	Val	Glu	Val	Tyr	Gln	Asn	Gly	Gln	Gln	Val	Pro	Val	Ser	Gln	Glu
				85					90					95	
Phe	Ser	Asp	Leu	Gly	Asp	Gly	Tyr	Arg	Leu	Lys	Leu	Tyr	Asn	Ala	Gly
			100					105					110		
Gln	Ala	Gly	Asp	Lys	Val	Asp	Val	Lys	Val	Ile	Trp	Gln	Leu	His	His
		115					120					125			
Leu	Leu	Thr	Ala	Tyr	Gln	Asp	Val	Ala	Glu	Leu	Asn	Trp	Thr	Pro	Ile
	130					135					140				
Ser	Asp	Trp	Asp	Lys	Thr	Leu	Glu	Lys	Val	Ser	Leu	Thr	Val	Thr	Thr
145					150					155					160
Pro	Thr	Asp	Ile	Gln	Asp	Ser	Asn	Leu	Trp	Ala	His	Arg	Gly	Tyr	Tyr
			165						170					175	
Gln	Lys	Lys	Pro	Gln	Val	Leu	Lys	Glu	Gly	Asn	Ser	Arg	Tyr	Gln	Ile
			180					185					190		
Asn	Ala	Lys	Asn	Val	Ser	Gly	Gln	Leu	Glu	Leu	His	Ala	Tyr	Trp	Asp
		195					200					205			
Lys	Lys	Ala	Leu	Leu	Gly	Lys	Glu	Pro	Val	Asp	Val	Ser	Thr	Ser	Lys
	210					215					220				
Lys	Asn	Lys	Ile	Val	Ala	Leu	Glu	Thr	Lys	Ile	Ser	Arg	Arg	Arg	Thr
225					230					235					240
Leu	Leu	Gln	Leu	Leu	Phe	Gly	Lys	Val	Ile	Pro	Leu	Val	Glu	Val	Gly
			245						250					255	
Phe	Leu	Leu	Trp	Gln	Leu	Ile	Gln	Phe	Thr	Arg	Leu	Lys	Lys	Gln	Phe
			260					265						270	
Asn	Arg	Tyr	His	Leu	Ala	Asn	His	Thr	Asp	His	Ser	Tyr	Glu	Val	Pro
		275					280					285			
Glu	Asp	Leu	Ser	Pro	Leu	Val	Leu	Thr	Gln	Ala	Ile	Tyr	Gly	Gln	Ser
	290					295					300				
Phe	Ala	Tyr	Leu	Ser	Pro	Thr	Ala	Ser	Glu	Ser	Gln	Lys	Leu	Leu	Ile
305					310					315					320
Pro	Lys	Gly	Val	Thr	Phe	Glu	Ala	Leu	Val	Gln	Ala	Thr	Leu	Leu	Asp
			325						330					335	
Leu	Ile	Asp	Gln	Lys	Val	Leu	Leu	Leu	Thr	Lys	Glu	Glu	Gly	Lys	Ala
		340					345						350		
Tyr	Leu	Glu	Ile	Ser	Gln	Leu	Asp	Arg	Val	Thr	Asp	Glu	Glu	Ala	Ala
		355					360					365			
Phe	Leu	Asp	Met	Ala	Phe	Gly	Asn	Lys	Val	Thr	Leu	Pro	Val	Asp	Gln
	370					375					380				
Leu	Phe	Ser	Gln	Tyr	His	Tyr	Asp	Ala	Asp	Thr	Ile	Lys	Gln	Leu	Lys
385					390					395					400
Lys	Thr	Tyr	Lys	Gly	Lys	Lys	Leu	Glu	Gln	Glu	Val	Arg	Gln	Ser	Ser
			405						410					415	
Glu	Gln	Val	Ile	Lys	Ala	Met	Lys	Lys	Ala	Ser	Ala	Ala	Ile	Thr	Asn
		420						425					430		
Asn	Val	Leu	Glu	Thr	Ile	Lys	Lys	Leu	Asn	Leu	Pro	Asp	Thr	Tyr	Arg
		435					440					445			
Gln	Met	Thr	Pro	Ala	Glu	Lys	Arg	Lys	Ser	Asn	Ser	Val	Gln	Gly	Leu
	450					455					460				
Gly	Cys	Leu	Leu	Leu	Ile	Leu	Asn	Ser	Gly	Leu	Leu	Ile	Tyr	Leu	Ala
465					470					475					480
Ile	Lys	Glu	Ser	Gly	Leu	Ala	Leu	Ile	Tyr	Leu	Ala	Leu	Met	Val	Leu

				485					490					495			
Thr	Met	Cys	Leu	Gly	Phe	Tyr	Ile	Ser	Leu	Lys	Leu	Asp	Gln	Tyr	Lys		
			500					505					510				
Lys	Leu	Gly	Ile	Glu	Thr	Pro	Glu	Gly	Gly	Val	Arg	Leu	His	Gln	Trp		
		515					520					525					
Gln	Ser	Phe	Lys	Asn	Met	Ile	Arg	Asp	Ile	Asp	Lys	Phe	Glu	Asp	Val		
	530					535					540						
Ala	Ile	Glu	Gly	Leu	Val	Val	Trp	Asn	Arg	Val	Leu	Val	Tyr	Ala	Thr		
545					550					555					560		
Leu	Phe	Gly	Tyr	Ala	Lys	Lys	Val	Glu	Arg	Tyr	Leu	Lys	Val	His	Arg		
			565					570						575			
Ile	Ala	Leu	Pro	Glu	Val	Tyr	Gln	Ala	Val	Arg	Pro	Gly	Glu	Leu	Ser		
		580						585					590				
Met	Val	Met	Tyr	Ala	Thr	Thr	Pro	Thr	Phe	Val	Ser	Ser	Leu	Ser	Ser		
		595					600					605					
Ala	Thr	Thr	Ser	Ser	Asn	Phe	Ser	Val	Ser	Ser	Gly	Gly	Gly	Ile	Ser		
	610				615						620						
Gly	Gly	Gly	Gly	Gly	Gly	Ala	Phe										
625					630												

<210> SEQ ID NO 547

<211> LENGTH: 1587

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 547

ttgaaacagg	agacctatat	gaaaaagcta	atccttagct	gtttggtcgc	cttggccctt	60
ctgtttggag	gaatgagccg	ggctcaagca	aaccaatatt	taagagtcgg	aatggaagca	120
gcctatgctc	cttttaactg	gactcaagat	gacgcttcaa	acggggctgt	tccaattgaa	180
ggaactagcc	aatacgccaa	cggttacgat	gtccaagtcg	ctaaaaagt	cgctaaagct	240
atgaacaaag	aacttttagt	cgtaaagacc	tcttggtaccg	gtttaattcc	agcattaact	300
tctggaaaaa	tcatatgat	cgctgctggt	atgagtccta	ccaaagagcg	tagaaacgaa	360
attagcttct	caaacagcta	ctacactagc	caccatgttc	tagtcgtaac	tgccaatggc	420
aaatatgctg	atgcaacaag	cctcaaggat	ttttctggag	ctaaagtaac	tgcccagcaa	480
ggcgtttggc	atgtcaatct	cttaactcaa	ctaaaagggtg	ctaagttaca	aacaccaatg	540
ggagatttct	ctcaaatgcg	acaagccctt	acttcgggtg	ttatcgatgc	ctatatctt	600
gaacgacctg	aagccatgac	tgctgaagct	gctgatagcc	gtttgaaaat	gatcactctt	660
aaaaaagggg	ttgctgttgc	tgaatcagat	gctgctatcg	ctgtcggaat	gaaaaaaaat	720
gacgatcgta	tggcaactgt	caaccaagt	cttgaaggat	tttctcaaac	agatcgatatg	780
gccctgatgg	atgatatggt	taccaaacia	cccgtggaaa	agaaagccga	agatgctaaa	840
gcatcatttc	taggccaaat	gtgggctatt	tttaaaggta	actggaagca	attcttacgt	900
ggaactggaa	tgacccttct	gatttccatg	gtcggaacca	ttacaggtct	ctttattgga	960
ttattaatcg	gtattttccg	tacagctcct	aaagctaagc	ataaagtagc	tgctttggga	1020
caaaaactct	ttggttggtt	actcactatt	tatatcgaaa	tcttccgtgg	gacacctatg	1080
attgttcaat	ctatggttat	ctactacgga	acagcgcaag	cctttggtat	ttcgatcgac	1140
cgtaccctag	cggctatttt	tatcgatatct	atcaatacgg	gggcctatat	gagtgaat	1200
gttcgcgggg	gtattttcgc	tgctgacaaa	ggtcaattca	aagcagcaac	tgctcttggc	1260
tttactcacg	gacaaacat	gcgtaaaatc	gtgctaccac	aagttgttcg	aaacatttta	1320
ccagcaacag	gtaatgagtt	tgtcatcaat	atcaaagata	cttctgtctt	gaatgttatc	1380
tctgttgtgg	aactttactt	ctcaggtaat	accgtagcca	cacaaacct	ccaatatttc	1440
caaaccttta	cgattatcgc	cattatctac	ttgttcttta	ccttcacggg	gacacgtatc	1500
cttcgttata	ttgaacgccg	tttcgatgcc	gatacttaca	ccactggagc	aaaccaaatg	1560
cagattgcgg	aggtctcaaa	tgtctaa				1587

<210> SEQ ID NO 548

<211> LENGTH: 528

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 548

Met	Lys	Gln	Glu	Thr	Tyr	Met	Lys	Lys	Leu	Ile	Leu	Ser	Cys	Leu	Val
1				5					10					15	
Ala	Leu	Ala	Leu	Leu	Phe	Gly	Gly	Met	Ser	Arg	Ala	Gln	Ala	Asn	Gln
			20					25					30		
Tyr	Leu	Arg	Val	Gly	Met	Glu	Ala	Ala	Tyr	Ala	Pro	Phe	Asn	Trp	Thr
		35				40						45			
Gln	Asp	Asp	Ala	Ser	Asn	Gly	Ala	Val	Pro	Ile	Glu	Gly	Thr	Ser	Gln
	50					55					60				
Tyr	Ala	Asn	Gly	Tyr	Asp	Val	Gln	Val	Ala	Lys	Lys	Val	Ala	Lys	Ala
65					70					75					80
Met	Asn	Lys	Glu	Leu	Leu	Val	Val	Lys	Thr	Ser	Trp	Thr	Gly	Leu	Ile
			85						90					95	
Pro	Ala	Leu	Thr	Ser	Gly	Lys	Ile	Asp	Met	Ile	Ala	Ala	Gly	Met	Ser
			100					105						110	
Pro	Thr	Lys	Glu	Arg	Arg	Asn	Glu	Ile	Ser	Phe	Ser	Asn	Ser	Tyr	Tyr
		115					120						125		
Thr	Ser	His	His	Val	Leu	Val	Val	Thr	Ala	Asn	Gly	Lys	Tyr	Ala	Asp
	130					135						140			
Ala	Thr	Ser	Leu	Lys	Asp	Phe	Ser	Gly	Ala	Lys	Val	Thr	Ala	Gln	Gln
145					150					155					160
Gly	Val	Trp	His	Val	Asn	Leu	Leu	Thr	Gln	Leu	Lys	Gly	Ala	Lys	Leu
			165						170					175	
Gln	Thr	Pro	Met	Gly	Asp	Phe	Ser	Gln	Met	Arg	Gln	Ala	Leu	Thr	Ser
			180					185					190		
Gly	Val	Ile	Asp	Ala	Tyr	Ile	Ser	Glu	Arg	Pro	Glu	Ala	Met	Thr	Ala
	195						200					205			
Glu	Ala	Ala	Asp	Ser	Arg	Leu	Lys	Met	Ile	Thr	Leu	Lys	Lys	Gly	Phe
	210					215					220				
Ala	Val	Ala	Glu	Ser	Asp	Ala	Ala	Ile	Ala	Val	Gly	Met	Lys	Lys	Asn
225					230					235					240
Asp	Asp	Arg	Met	Ala	Thr	Val	Asn	Gln	Val	Leu	Glu	Gly	Phe	Ser	Gln
			245						250					255	
Thr	Asp	Arg	Met	Ala	Leu	Met	Asp	Asp	Met	Val	Thr	Lys	Gln	Pro	Val
			260					265					270		
Glu	Lys	Lys	Ala	Glu	Asp	Ala	Lys	Ala	Ser	Phe	Leu	Gly	Gln	Met	Trp
		275					280					285			
Ala	Ile	Phe	Lys	Gly	Asn	Trp	Lys	Gln	Phe	Leu	Arg	Gly	Thr	Gly	Met
	290					295					300				
Thr	Leu	Leu	Ile	Ser	Met	Val	Gly	Thr	Ile	Thr	Gly	Leu	Phe	Ile	Gly
305					310					315					320
Leu	Leu	Ile	Gly	Ile	Phe	Arg	Thr	Ala	Pro	Lys	Ala	Lys	His	Lys	Val
			325						330					335	
Ala	Ala	Leu	Gly	Gln	Lys	Leu	Phe	Gly	Trp	Leu	Leu	Thr	Ile	Tyr	Ile
			340					345					350		
Glu	Ile	Phe	Arg	Gly	Thr	Pro	Met	Ile	Val	Gln	Ser	Met	Val	Ile	Tyr
		355					360					365			
Tyr	Gly	Thr	Ala	Gln	Ala	Phe	Gly	Ile	Ser	Ile	Asp	Arg	Thr	Leu	Ala
	370					375					380				
Ala	Ile	Phe	Ile	Val	Ser	Ile	Asn	Thr	Gly	Ala	Tyr	Met	Ser	Glu	Ile
385					390					395					400
Val	Arg	Gly	Gly	Ile	Phe	Ala	Val	Asp	Lys	Gly	Gln	Phe	Lys	Ala	Ala
			405						410					415	
Thr	Ala	Leu	Gly	Phe	Thr	His	Gly	Gln	Thr	Met	Arg	Lys	Ile	Val	Leu
			420					425					430		
Pro	Gln	Val	Val	Arg	Asn	Ile	Leu	Pro	Ala	Thr	Gly	Asn	Glu	Phe	Val
		435					440						445		

Ile	Asn	Ile	Lys	Asp	Thr	Ser	Val	Leu	Asn	Val	Ile	Ser	Val	Val	Glu
450						455					460				
Leu	Tyr	Phe	Ser	Gly	Asn	Thr	Val	Ala	Thr	Gln	Thr	Tyr	Gln	Tyr	Phe
465					470					475					480
Gln	Thr	Phe	Thr	Ile	Ile	Ala	Ile	Ile	Tyr	Phe	Val	Leu	Thr	Phe	Thr
				485					490					495	
Val	Thr	Arg	Ile	Leu	Arg	Tyr	Ile	Glu	Arg	Arg	Phe	Asp	Ala	Asp	Thr
			500					505					510		
Tyr	Thr	Thr	Gly	Ala	Asn	Gln	Met	Gln	Ile	Ala	Glu	Val	Ser	Asn	Val
		515					520					525			

<210> SEQ ID NO 549

<211> LENGTH: 1038

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 549

ttgattttca	taaggaggaa	atcactaatg	gtagttaaaag	ttggtattaa	cggtttcggt	60
cgtatcggac	gtcttgcatt	ccgccgtatt	caaaacatcg	aagggtgtga	agtaactcgt	120
atcaatgacc	ttacagatcc	aaatatgctt	gcacacttgt	tgaaatacga	tacaactcaa	180
ggtcgttttg	atggaacagt	tgaagttaaa	gaagggtggat	ttgaagtaaa	cggaaacttc	240
atcaaagttt	ctgctgaacg	tgatccagaa	aacatcgact	gggcaactga	tgggggttgaa	300
atcgttcttg	aagcaactgg	tttctttgct	aaaaaagaag	cagctgaaaa	acacttacat	360
gctaacgggtg	ctaaaaaagt	tgttatcaca	gctcctgggtg	gaaacgatgt	taaaacagtt	420
gttttcaaca	ctaaccacga	cattcttgac	ggtactgaaa	cagttatctc	aggtgcttca	480
tgtactacaa	actgttttagc	tcctatggct	aaagctcttc	acgatgcatt	cggatttcaa	540
aaagggtctta	tgactacaat	ccacgcttac	actggtgacc	aaatgatcct	tgacggacca	600
caccgtgggtg	gtgaccttcg	tcgtgcacgc	gctgggtgctg	caaatatcgt	tcctaactca	660
actggtgctg	ctaaagctat	cggctcttgt	atcccagaac	ttaacggtaa	acttgacggg	720
gctgcacaac	gtgttcctgt	tccaactgga	tcagtaactg	agttggttgt	aactcttgac	780
aaaaacgttt	ctgttgacga	aatcaacgct	gctatgaaag	ctgcttcaaa	cgatagcttc	840
ggttacactg	aagatccaat	cgtttcttca	gatatcgtag	gcgtatcata	cgggttcattg	900
tttgacgcaa	ctcaaactaa	agtaatggaa	gttgacggat	cacaattggg	taaagttgta	960
tcatgggtatg	acaacgaaat	gtcttacact	gctcaacttg	tacgtactct	tgagtacttc	1020
gcaaaaattg	ctaaataa					1038

<210> SEQ ID NO 550

<211> LENGTH: 345

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 550

Met	Ile	Phe	Ile	Arg	Arg	Lys	Ser	Leu	Met	Val	Val	Lys	Val	Gly	Ile
1				5				10						15	
Asn	Gly	Phe	Gly	Arg	Ile	Gly	Arg	Leu	Ala	Phe	Arg	Arg	Ile	Gln	Asn
			20					25					30		
Ile	Glu	Gly	Val	Glu	Val	Thr	Arg	Ile	Asn	Asp	Leu	Thr	Asp	Pro	Asn
		35				40					45				
Met	Leu	Ala	His	Leu	Leu	Lys	Tyr	Asp	Thr	Thr	Gln	Gly	Arg	Phe	Asp
	50					55					60				
Gly	Thr	Val	Glu	Val	Lys	Glu	Gly	Gly	Phe	Glu	Val	Asn	Gly	Asn	Phe
65					70					75				80	
Ile	Lys	Val	Ser	Ala	Glu	Arg	Asp	Pro	Glu	Asn	Ile	Asp	Trp	Ala	Thr
			85					90						95	
Asp	Gly	Val	Glu	Ile	Val	Leu	Glu	Ala	Thr	Gly	Phe	Phe	Ala	Lys	Lys
		100						105					110		
Glu	Ala	Ala	Glu	Lys	His	Leu	His	Ala	Asn	Gly	Ala	Lys	Lys	Val	Val
		115					120					125			
Ile	Thr	Ala	Pro	Gly	Gly	Asn	Asp	Val	Lys	Thr	Val	Val	Phe	Asn	Thr

130	135	140
Asn His Asp Ile Leu Asp Gly Thr Glu Thr Val Ile Ser Gly Ala Ser		
145	150	155
Cys Thr Thr Asn Cys Leu Ala Pro Met Ala Lys Ala Leu His Asp Ala		160
	165	170
Phe Gly Ile Gln Lys Gly Leu Met Thr Thr Ile His Ala Tyr Thr Gly		175
	180	185
Asp Gln Met Ile Leu Asp Gly Pro His Arg Gly Gly Asp Leu Arg Arg		190
	195	200
Ala Arg Ala Gly Ala Ala Asn Ile Val Pro Asn Ser Thr Gly Ala Ala		205
	210	215
Lys Ala Ile Gly Leu Val Ile Pro Glu Leu Asn Gly Lys Leu Asp Gly		220
225	230	235
Ala Ala Gln Arg Val Pro Val Pro Thr Gly Ser Val Thr Glu Leu Val		240
	245	250
Val Thr Leu Asp Lys Asn Val Ser Val Asp Glu Ile Asn Ala Ala Met		255
	260	265
Lys Ala Ala Ser Asn Asp Ser Phe Gly Tyr Thr Glu Asp Pro Ile Val		270
	275	280
Ser Ser Asp Ile Val Gly Val Ser Tyr Gly Ser Leu Phe Asp Ala Thr		285
	290	295
Gln Thr Lys Val Met Glu Val Asp Gly Ser Gln Leu Val Lys Val Val		300
305	310	315
Ser Trp Tyr Asp Asn Glu Met Ser Tyr Thr Ala Gln Leu Val Arg Thr		320
	325	330
Leu Glu Tyr Phe Ala Lys Ile Ala Lys		335
	340	345

<210> SEQ ID NO 551

<211> LENGTH: 663

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 551

ttgacatcga	aaaaacaggg	actttttacac	tctctcttca	agcttgatag	taaatggatg	60
agggctagcg	cagcactggt	tgatttgctc	gtgtttaatc	tcttatttgt	cttgctcctgc	120
cttcccccttc	taacgattgg	ggttgctaaa	atggctttgt	atgcgagttt	gttggattgg	180
cgagaaggtc	aagttagtca	gcttgttact	acttatagct	ctcattttta	atattacttt	240
aaaagtgggc	tacgccttgg	ccttattgag	cttgggataa	tgactatttg	tctcttagat	300
cttttcttaa	ttcgaaacca	atcaggccta	gtttttcaag	ggtttaaagt	actttgcgtt	360
gctgttttat	ttttggtggt	tatactcttt	ttgtacgctt	atcctcaggc	cgtcaaaaga	420
gacctttccc	tatctacgct	gtttaagcga	agctttttat	tagcaggact	cttttttcca	480
tggagttttg	ctttcttggc	ttttatttgt	ctcacgatat	ttagcctaca	attgtctctg	540
ttaacgttat	ttggaggcgt	gtctttgcta	gctatcatcg	gcatcagtag	tctaacttat	600
ctctacttga	ttatcatgga	atctcttctt	aggcgattcc	cacttaataa	tgacattgaa	660
taa						663

<210> SEQ ID NO 552

<211> LENGTH: 220

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 552

Met Thr Ser Lys Lys Gln Gly Leu Leu His Ser Leu Phe Lys Leu Asp		
1	5	10
Ser Lys Trp Met Arg Ala Ser Ala Ala Leu Phe Asp Leu Leu Val Phe		
	20	25
Asn Leu Leu Phe Val Leu Ser Cys Leu Pro Leu Leu Thr Ile Gly Val		
	35	40
		45

Ala	Lys	Met	Ala	Leu	Tyr	Ala	Ser	Leu	Leu	Asp	Trp	Arg	Glu	Gly	Gln
50						55					60				
Val	Ser	Gln	Leu	Val	Thr	Thr	Tyr	Ser	Ser	His	Phe	Lys	Tyr	Tyr	Phe
65					70					75					80
Lys	Ser	Gly	Leu	Arg	Leu	Gly	Leu	Ile	Glu	Leu	Gly	Ile	Met	Thr	Ile
				85					90					95	
Cys	Leu	Leu	Asp	Leu	Phe	Leu	Ile	Arg	Asn	Gln	Ser	Gly	Leu	Val	Phe
			100					105					110		
Gln	Gly	Phe	Lys	Val	Leu	Cys	Val	Ala	Val	Leu	Phe	Leu	Val	Val	Ile
		115					120					125			
Leu	Phe	Leu	Tyr	Ala	Tyr	Pro	Gln	Ala	Val	Lys	Arg	Asp	Leu	Ser	Leu
		130				135					140				
Ser	Thr	Leu	Phe	Lys	Arg	Ser	Phe	Leu	Leu	Ala	Gly	Leu	Phe	Phe	Pro
145				150						155					160
Trp	Ser	Phe	Ala	Phe	Leu	Ala	Phe	Ile	Cys	Leu	Thr	Ile	Phe	Ser	Leu
				165					170					175	
Gln	Leu	Ser	Leu	Leu	Thr	Leu	Phe	Gly	Gly	Val	Ser	Leu	Leu	Ala	Ile
			180					185					190		
Ile	Gly	Ile	Ser	Ser	Leu	Thr	Tyr	Leu	Tyr	Leu	Ile	Ile	Met	Glu	Ser
		195					200					205			
Leu	Leu	Arg	Arg	Phe	Pro	Leu	Asn	Asn	Asp	Ile	Glu				
		210				215					220				

<210> SEQ ID NO 553

<211> LENGTH: 831

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 553

atgacgaaaa	agaaactaac	cgcatacagat	atcttaacca	ctgtgatgct	atgtgttttg	60
accatttttg	ttatttttcc	attttattgg	attatgacag	gagcatttaa	ggctcaagcc	120
gataaccatta	tgattccacc	gcaatggtgg	ccaaaggcgc	ctactattga	aaattttaag	180
gccttggtag	tgcaaaatcc	agccttaaaa	tggttgtgga	atagtgtcct	tatttcggtg	240
gcgaccatgt	tcttggtttg	tggaaacctcc	tcgttggctg	gctatgcttt	ggccaaaaag	300
cggttttatg	gacagcggct	tttgttttcg	atttttattg	ctgctatggc	cttgccaaaa	360
cagggtgttc	tagtgcctct	tgtgcggatt	gttaatttta	tgggaatcca	tgacactttg	420
gcggctgtta	ttttgcctct	tgtgggctgg	ccatttggtg	ttttccttat	gaaacagttc	480
tcagaaaaata	ttccaaccga	gttattggaa	tccgccaaga	ttgatggatg	tggcgaaatt	540
cgtacctttt	tcaatgtggc	tttccctatt	gtcaaaccag	gctttgcagc	gctagcgatt	600
tttaccttta	tcaatacttg	gaatgattat	tttatgcagt	tagtgatgtt	aacctctcga	660
gaaaatttaa	cgatttcact	tggggttgcc	actatgcaag	ctgaaatggc	tactaattat	720
ggcttgatta	tggcaggggc	tgccatggct	gcagtgccta	ttgtaacagt	ctttcttgtc	780
ttccaaaaat	catttaccca	aggcattact	atgggtgctg	tgaaagggtta	g	831

<210> SEQ ID NO 554

<211> LENGTH: 276

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 554

Met	Thr	Lys	Lys	Lys	Leu	Thr	Ala	Ser	Asp	Ile	Leu	Thr	Thr	Val	Met
1				5					10					15	
Leu	Cys	Val	Leu	Thr	Ile	Leu	Phe	Ile	Phe	Pro	Phe	Tyr	Trp	Ile	Met
			20					25					30		
Thr	Gly	Ala	Phe	Lys	Ala	Gln	Ala	Asp	Thr	Ile	Met	Ile	Pro	Pro	Gln
		35					40					45			
Trp	Trp	Pro	Lys	Ala	Pro	Thr	Ile	Glu	Asn	Phe	Lys	Ala	Leu	Val	Val
		50				55					60				
Gln	Asn	Pro	Ala	Leu	Lys	Trp	Leu	Trp	Asn	Ser	Val	Phe	Ile	Ser	Val

65		70		75		80									
Ala	Thr	Met	Phe	Leu	Val	Cys	Gly	Thr	Ser	Ser	Leu	Ala	Gly	Tyr	Ala
			85						90					95	
Leu	Ala	Lys	Lys	Arg	Phe	Tyr	Gly	Gln	Arg	Leu	Leu	Phe	Ser	Ile	Phe
			100					105					110		
Ile	Ala	Ala	Met	Ala	Leu	Pro	Lys	Gln	Val	Val	Leu	Val	Pro	Leu	Val
			115				120					125			
Arg	Ile	Val	Asn	Phe	Met	Gly	Ile	His	Asp	Thr	Leu	Ala	Ala	Val	Ile
			130			135					140				
Leu	Pro	Leu	Val	Gly	Trp	Pro	Phe	Gly	Val	Phe	Leu	Met	Lys	Gln	Phe
				150						155				160	
Ser	Glu	Asn	Ile	Pro	Thr	Glu	Leu	Leu	Glu	Ser	Ala	Lys	Ile	Asp	Gly
			165						170					175	
Cys	Gly	Glu	Ile	Arg	Thr	Phe	Phe	Asn	Val	Ala	Phe	Pro	Ile	Val	Lys
			180					185					190		
Pro	Gly	Phe	Ala	Ala	Leu	Ala	Ile	Phe	Thr	Phe	Ile	Asn	Thr	Trp	Asn
			195				200					205			
Asp	Tyr	Phe	Met	Gln	Leu	Val	Met	Leu	Thr	Ser	Arg	Glu	Asn	Leu	Thr
			210			215					220				
Ile	Ser	Leu	Gly	Val	Ala	Thr	Met	Gln	Ala	Glu	Met	Ala	Thr	Asn	Tyr
			225			230				235				240	
Gly	Leu	Ile	Met	Ala	Gly	Ala	Ala	Met	Ala	Ala	Val	Pro	Ile	Val	Thr
			245					250					255		
Val	Phe	Leu	Val	Phe	Gln	Lys	Ser	Phe	Thr	Gln	Gly	Ile	Thr	Met	Gly
			260					265					270		
Ala	Val	Lys	Gly												
			275												

<210> SEQ ID NO 555

<211> LENGTH: 990

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 555

gtgttcctaa	caagtggcctt	cttttcaatg	cacatgtcaa	atggtcactg	gaaagaagct	60
tttcttttta	gaaaagttga	acagaaaaaa	gaggtatttc	aagtgaacgt	caataaatta	120
aaaatgagag	agacgctcat	ctcatacgct	ttcttagctc	cggctcttgg	tttctttgtg	180
atttttgtct	tgataccgat	gattatgggc	tttgtgacga	gctttttcaa	ttattccatg	240
acagagttta	cctttgttgg	ttttgctaata	tatgctagga	tgtttcaaga	tcccattttc	300
atgaagtctc	ttattaacac	cttgattatt	gttattgggt	cggtagcctgt	tgtagttttc	360
ttttccctct	ttgtggcggc	taaaacctac	gacaaaaatg	tagtggcgcg	ttcgttttac	420
cgggcagttt	tctttctgcc	tgttggtacc	ggaagtgttg	cggtgacggg	ggtttggaaa	480
tggatctatg	atccaatgtc	agggattttg	aattatgtct	taaaatatgc	tcatgtgatt	540
gaacaaaata	ttagttggct	gggagataag	cactgggctt	tgttggctat	tattgttatt	600
ttattaacca	catctgttgg	gcagcctatt	attctatata	ttgctgctat	gggaaatatt	660
gataactctt	tggtagaagc	tgcgcgtgtg	gacggcgcca	cagaatttca	ggtgttttgg	720
aatatcaagt	ggccaagtct	gctgccaaca	accttatata	ttgctgtcat	aacaaccatt	780
aattccttcc	aatgttttgc	tttgattcaa	cttttgacgt	ctggaggggc	aaattattca	840
accagtaccc	tcatgtacta	tttgatgaa	aaggccttta	agctctctga	atacggctat	900
gccaacacaa	tgggtgtatt	cttggcagtc	atgattgcaa	tcacagctt	tgctcaattt	960
aaaattttag	gtaatgatgt	ggaatattag				990

<210> SEQ ID NO 556

<211> LENGTH: 329

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 556

Met Phe Leu Thr Ser Gly Phe Phe Ser Met His Met Ser Asn Gly His

1	5	10	15												
Trp	Lys	Glu	Ala	Phe	Leu	Phe	Arg	Lys	Val	Glu	Gln	Lys	Lys	Glu	Val
		20						25					30		
Phe	Gln	Val	Asn	Val	Asn	Lys	Leu	Lys	Met	Arg	Glu	Thr	Leu	Ile	Ser
		35					40					45			
Tyr	Ala	Phe	Leu	Ala	Pro	Val	Leu	Val	Phe	Phe	Val	Ile	Phe	Val	Leu
	50					55					60				
Ile	Pro	Met	Ile	Met	Gly	Phe	Val	Thr	Ser	Phe	Phe	Asn	Tyr	Ser	Met
65					70					75				80	
Thr	Glu	Phe	Thr	Phe	Val	Gly	Phe	Ala	Asn	Tyr	Ala	Arg	Met	Phe	Gln
				85					90					95	
Asp	Pro	Ile	Phe	Met	Lys	Ser	Leu	Ile	Asn	Thr	Leu	Ile	Ile	Val	Ile
			100					105					110		
Gly	Ser	Val	Pro	Val	Val	Val	Phe	Phe	Ser	Leu	Phe	Val	Ala	Ala	Lys
		115					120					125			
Thr	Tyr	Asp	Lys	Asn	Val	Val	Ala	Arg	Ser	Phe	Tyr	Arg	Ala	Val	Phe
	130					135					140				
Phe	Leu	Pro	Val	Val	Thr	Gly	Ser	Val	Ala	Val	Thr	Val	Val	Trp	Lys
145					150					155				160	
Trp	Ile	Tyr	Asp	Pro	Met	Ser	Gly	Ile	Leu	Asn	Tyr	Val	Leu	Lys	Tyr
			165					170					175		
Ala	His	Val	Ile	Glu	Gln	Asn	Ile	Ser	Trp	Leu	Gly	Asp	Lys	His	Trp
		180						185					190		
Ala	Leu	Leu	Ala	Ile	Ile	Val	Ile	Leu	Leu	Thr	Thr	Ser	Val	Gly	Gln
	195						200					205			
Pro	Ile	Ile	Leu	Tyr	Ile	Ala	Ala	Met	Gly	Asn	Ile	Asp	Asn	Ser	Leu
	210					215					220				
Val	Glu	Ala	Ala	Arg	Val	Asp	Gly	Ala	Thr	Glu	Phe	Gln	Val	Phe	Trp
225				230					235					240	
Asn	Ile	Lys	Trp	Pro	Ser	Leu	Leu	Pro	Thr	Thr	Leu	Tyr	Ile	Ala	Val
			245					250						255	
Ile	Thr	Thr	Ile	Asn	Ser	Phe	Gln	Cys	Phe	Ala	Leu	Ile	Gln	Leu	Leu
		260					265						270		
Thr	Ser	Gly	Gly	Pro	Asn	Tyr	Ser	Thr	Ser	Thr	Leu	Met	Tyr	Tyr	Leu
		275					280					285			
Tyr	Glu	Lys	Ala	Phe	Lys	Leu	Ser	Glu	Tyr	Gly	Tyr	Ala	Asn	Thr	Met
	290					295					300				
Gly	Val	Phe	Leu	Ala	Val	Met	Ile	Ala	Ile	Ile	Ser	Phe	Ala	Gln	Phe
305					310					315				320	
Lys	Ile	Leu	Gly	Asn	Asp	Val	Glu	Tyr							
				325											

<210> SEQ ID NO 557

<211> LENGTH: 1347

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 557

atggctaata	gcgaatatat	gtttttatta	ttatcaatta	ttgtctatta	tatgacaaaa	60
atztatattt	tttcctttct	atctgatatc	acattaccag	tttggaacaa	actaacgatt	120
ttggcttttag	ccctattttt	caatcagttc	ccgtatttgt	cgccattgct	aattgatcct	180
ctattatttt	tagttgtttt	aaggcaagaa	accaagcaat	tattttcttt	gaaagctctt	240
tttttggctg	ttgcacctag	tgttttggtg	gatttgctat	ctcgatttat	gggtacaatc	300
gttatcccct	atcttttttt	gtcgagtggg	atttatctgg	gtcatattat	ctttgacttg	360
cttgcttatc	tgctgatttt	tccaagtttt	gctattatta	attatatgat	tggaaaagat	420
tacaagatga	tatgccaatc	cggatattcg	aaacgatcgc	ataatttcta	tcaaacattg	480
ctgatgtttg	ttttggttta	ttatgtggac	atttttgtca	ttttaggatt	tacggacccc	540
tttttacatt	ttcatcattc	tctttttgtt	cccacacctt	ataagttatt	gtttttgatg	600

tttatacttc	ttttagttta	tcttctatct	tatttttaatc	atagttctaa	agaatacctt	660
aaaaatgagt	tgagaagaga	acaacaagct	tatatgacta	acttagagat	ttatgggaaa	720
catcttgaga	aactctatcg	agatgtaaga	gcttttcaaa	gtgattacct	gagccgtata	780
gagcgtttag	gtcaagccat	taagagtga	tccattactc	agattcaaga	tatttatgcc	840
caaacggttc	atgaagctaa	cgactactgg	gatgataaac	actataatat	ctcgaagctt	900
aggaaaatta	atatctcatc	gattaagagc	ttattgtcag	ctaaaattat	cagtgcggaa	960
aatcaggta	ttgatttgaa	tgtggaagtg	ccagataata	taaaagaaac	ttacattcct	1020
gagttggact	tactattggt	gatgtctatt	ttttgtgata	acgccattga	ggcagctctt	1080
gaagcacaa	aacctcatat	gtcaattgct	tactttttgt	taggtgacta	tcagatgttt	1140
gttgtagaaa	atacagctaa	aaaaaaggta	gacatttaaca	agatctttga	agaaggcttt	1200
tcttcaaaag	gttcagaacg	tggtatcggc	ctttctaattg	cgcagcgtat	tctcaaaaag	1260
tatccttatt	tatccttgcg	gactaaaagt	tttgataagg	aatttagcca	aaccttgacc	1320
atgccaaagg	aggaggtgga	tagatga				1347

Met	Ala	Asn	Ser	Glu	Tyr	Met	Phe	Leu	Leu	Leu	Ser	Ile	Ile	Val	Tyr
1				5				10						15	
Tyr	Met	Thr	Lys	Ile	Tyr	Ile	Phe	Ser	Phe	Leu	Ser	Asp	Ile	Thr	Leu
			20					25					30		
Pro	Val	Trp	Lys	Gln	Leu	Thr	Ile	Leu	Ala	Leu	Ala	Leu	Phe	Phe	Asn
			35					40					45		
Gln	Phe	Pro	Tyr	Leu	Ser	Pro	Leu	Leu	Ile	Asp	Pro	Leu	Leu	Phe	Leu
			50				55				60				
Val	Val	Leu	Arg	Gln	Glu	Thr	Lys	Gln	Leu	Phe	Ser	Leu	Lys	Ala	Leu
65					70					75					80
Phe	Leu	Ala	Val	Ala	Pro	Ser	Val	Leu	Val	Asp	Leu	Leu	Ser	Arg	Phe
				85					90					95	
Met	Gly	Thr	Ile	Val	Ile	Pro	Tyr	Leu	Phe	Leu	Ser	Ser	Gly	Ile	Tyr
			100					105					110		
Leu	Gly	His	Ile	Ile	Phe	Asp	Leu	Leu	Ala	Tyr	Leu	Leu	Ile	Phe	Pro
			115				120					125			
Ser	Phe	Ala	Ile	Ile	Asn	Tyr	Met	Ile	Gly	Lys	Asp	Tyr	Lys	Met	Ile
			130				135				140				
Cys	Gln	Ser	Gly	Tyr	Ser	Lys	Arg	Ser	His	Asn	Phe	Tyr	Gln	Thr	Leu
145					150					155					160
Leu	Met	Phe	Val	Leu	Val	Tyr	Tyr	Val	Asp	Ile	Phe	Val	Ile	Leu	Gly
				165					170					175	
Phe	Thr	Asp	Pro	Phe	Leu	His	Phe	His	His	Ser	Leu	Phe	Val	Pro	Thr
			180					185					190		
Pro	Tyr	Lys	Leu	Leu	Phe	Leu	Met	Phe	Ile	Leu	Leu	Leu	Val	Tyr	Leu
			195				200					205			
Leu	Ser	Tyr	Phe	Asn	His	Ser	Ser	Lys	Glu	Tyr	Leu	Lys	Asn	Glu	Leu
						215					220				
Arg	Arg	Glu	Gln	Gln	Ala	Tyr	Met	Thr	Asn	Leu	Glu	Ile	Tyr	Gly	Lys
225					230					235					240
His	Leu	Glu	Lys	Leu	Tyr	Arg	Asp	Val	Arg	Ala	Phe	Gln	Ser	Asp	Tyr
				245					250					255	
Leu	Ser	Arg	Ile	Glu	Arg	Leu	Gly	Gln	Ala	Ile	Lys	Ser	Glu	Ser	Ile
			260					265					270		
Thr	Gln	Ile	Gln	Asp	Ile	Tyr	Ala	Gln	Thr	Val	His	Glu	Ala	Asn	Asp
			275				280					285			
Tyr	Trp	Asp	Asp	Lys	His	Tyr	Asn	Ile	Ser	Lys	Leu	Arg	Lys	Ile	Asn
						295					300				

Ile	Ser	Ser	Ile	Lys	Ser	Leu	Leu	Ser	Ala	Lys	Ile	Ile	Ser	Ala	Glu
305				310					315						320
Lys	Ser	Gly	Ile	Asp	Leu	Asn	Val	Glu	Val	Pro	Asp	Asn	Ile	Lys	Glu
				325				330						335	
Thr	Tyr	Ile	Pro	Glu	Leu	Asp	Leu	Leu	Leu	Leu	Met	Ser	Ile	Phe	Cys
			340				345						350		
Asp	Asn	Ala	Ile	Glu	Ala	Ala	Leu	Glu	Ala	Gln	Gln	Pro	His	Met	Ser
		355					360					365			
Ile	Ala	Tyr	Phe	Leu	Leu	Gly	Asp	Tyr	Gln	Met	Phe	Val	Val	Thr	Asn
	370					375					380				
Thr	Thr	Lys	Lys	Lys	Val	Asp	Ile	Asn	Lys	Ile	Phe	Glu	Glu	Gly	Tyr
385					390					395					400
Ser	Ser	Lys	Gly	Ser	Glu	Arg	Gly	Ile	Gly	Leu	Ser	Asn	Ala	Gln	Arg
			405					410						415	
Ile	Leu	Lys	Lys	Tyr	Pro	Tyr	Leu	Ser	Leu	Arg	Thr	Lys	Ser	Phe	Asp
			420				425					430			
Lys	Glu	Phe	Ser	Gln	Thr	Leu	Thr	Met	Pro	Lys	Glu	Glu	Val	Asp	Arg
		435				440							445		

<210> SEQ ID NO 559

<211> LENGTH: 906

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 559

gtgctgatga	ccaaagtcag	aaaagctatt	attcccgcag	caggtttagg	cacacgtttt	60
ttacctgcaa	ccaaggccct	tgccaaggag	atgctaccta	ttgttgataa	accaactatt	120
caatttatcg	ttgaagaagc	tctaaaatca	ggtatcgaag	aaattccttat	cgttactgga	180
aaatccaaac	gctccataga	agatcatttt	gattcctaatt	ttgaattaga	atataattta	240
caggctaaag	gaaaaatcga	acttctaaag	ttagtagacg	agaccacttc	tattaatctt	300
cactttattc	gacagagtca	tccaagagga	ttaggagacg	cagttcttca	agcaaagacc	360
tttgttggca	atgaaccttt	tgttgtcatg	ctaggtgatg	atctgatgga	tattacaaat	420
ccaaatgtaa	aaccattaac	caaacaattg	atcgatgact	atgaagaaac	tcatgctgca	480
actattgccg	tcatgagggg	tcctcacgag	gatgtctcta	actacggtat	cattgctcct	540
caagcaaaag	cagtaaaagg	actctatagt	gtggatactt	ttgttgaaaa	accacaacct	600
caagatgcac	ctagtgattt	ggcaattatt	ggacgttact	tgctcacacc	agaaattttt	660
agtattttag	aaaaacaaga	acctgggtgca	ggcaatgaag	ttcaactgac	tgatgctatt	720
gataccctca	ataagacaca	gcgtgtcttt	gctcgtgagt	ttaaagggaa	acgctatgat	780
gttggcgata	aatttggggt	tatgaaaaact	tctttggatt	atgccctgaa	acaccctcaa	840
gtcaaagatg	acttgaaaagc	ctacatcatc	caactgggca	aagcactaga	gaagacaaaa	900
ccataa						906

<210> SEQ ID NO 560

<211> LENGTH: 301

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 560

Met	Leu	Met	Thr	Lys	Val	Arg	Lys	Ala	Ile	Ile	Pro	Ala	Ala	Gly	Leu
1				5				10						15	
Gly	Thr	Arg	Phe	Leu	Pro	Ala	Thr	Lys	Ala	Leu	Ala	Lys	Glu	Met	Leu
			20				25					30			
Pro	Ile	Val	Asp	Lys	Pro	Thr	Ile	Gln	Phe	Ile	Val	Glu	Glu	Ala	Leu
		35				40					45				
Lys	Ser	Gly	Ile	Glu	Glu	Ile	Leu	Ile	Val	Thr	Gly	Lys	Ser	Lys	Arg
	50					55				60					
Ser	Ile	Glu	Asp	His	Phe	Asp	Ser	Asn	Phe	Glu	Leu	Glu	Tyr	Asn	Leu
65				70					75					80	
Gln	Ala	Lys	Gly	Lys	Ile	Glu	Leu	Leu	Lys	Leu	Val	Asp	Glu	Thr	Thr

				85					90					95			
Ser	Ile	Asn	Leu	His	Phe	Ile	Arg	Gln	Ser	His	Pro	Arg	Gly	Leu	Gly		
			100					105					110				
Asp	Ala	Val	Leu	Gln	Ala	Lys	Thr	Phe	Val	Gly	Asn	Glu	Pro	Phe	Val		
		115					120					125					
Val	Met	Leu	Gly	Asp	Asp	Leu	Met	Asp	Ile	Thr	Asn	Pro	Asn	Val	Lys		
	130					135					140						
Pro	Leu	Thr	Lys	Gln	Leu	Ile	Asp	Asp	Tyr	Glu	Glu	Thr	His	Ala	Ala		
145				150					155						160		
Thr	Ile	Ala	Val	Met	Arg	Val	Pro	His	Glu	Asp	Val	Ser	Asn	Tyr	Gly		
			165						170					175			
Ile	Ile	Ala	Pro	Gln	Ala	Lys	Ala	Val	Lys	Gly	Leu	Tyr	Ser	Val	Asp		
		180					185						190				
Thr	Phe	Val	Glu	Lys	Pro	Gln	Pro	Gln	Asp	Ala	Pro	Ser	Asp	Leu	Ala		
	195					200						205					
Ile	Ile	Gly	Arg	Tyr	Leu	Leu	Thr	Pro	Glu	Ile	Phe	Ser	Ile	Leu	Glu		
210					215					220							
Lys	Gln	Glu	Pro	Gly	Ala	Gly	Asn	Glu	Val	Gln	Leu	Thr	Asp	Ala	Ile		
225				230					235					240			
Asp	Thr	Leu	Asn	Lys	Thr	Gln	Arg	Val	Phe	Ala	Arg	Glu	Phe	Lys	Gly		
			245				250						255				
Lys	Arg	Tyr	Asp	Val	Gly	Asp	Lys	Phe	Gly	Phe	Met	Lys	Thr	Ser	Leu		
		260				265						270					
Asp	Tyr	Ala	Leu	Lys	His	Pro	Gln	Val	Lys	Asp	Asp	Leu	Lys	Ala	Tyr		
	275					280						285					
Ile	Ile	Gln	Leu	Gly	Lys	Ala	Leu	Glu	Lys	Thr	Lys	Pro					
	290					295					300						

<210> SEQ ID NO 561

<211> LENGTH: 705

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 561

atgaaaaacaa	acatttttgac	aattatcata	ttatcatgtg	tttttagcta	tggaagtcaa	60
ttagcttatg	cagatgaaaa	tttaaaagat	ttaaaaagaa	gtttaagatt	tgccataaat	120
attaccccat	gcgattatga	aaatgtagaa	attgcatttg	ttactacaaa	tagcatacat	180
attaatacta	aacaaaaaag	atcggaatgt	attcttttat	ttgattctat	tgtatcttta	240
ggcattactg	atcagtttat	aaaaggggat	aaggtcgatg	tttttggtct	cccttataat	300
ttttcccccac	cttatgtaga	taatatttat	ggtggtattg	taaaacattc	gaatcaagga	360
aataaatcat	tacagtttgt	aggaatttta	aatcaagatg	ggaaagaaac	ttatttgccc	420
tctgaggctg	ttcgcataaa	aaagaaacag	tttactttac	aggaatttga	ttttaaaata	480
agaaaatttc	taatggaaaa	atacaatatc	tatgattcgg	aatcgcggtta	tacatcgggg	540
agccttttcc	ttgctactaa	agatagtaaa	cattatgaag	ttgatttatt	taataaggat	600
gataagcttt	taagtcgaga	cagtttcttt	aaaaggtata	aagataataa	gatttttaat	660
agtgaagaaa	ttagtcattt	tgatatctac	ttaaaaacgc	actag		705

<210> SEQ ID NO 562

<211> LENGTH: 234

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 562

Met	Lys	Thr	Asn	Ile	Leu	Thr	Ile	Ile	Ile	Leu	Ser	Cys	Val	Phe	Ser
1			5					10						15	
Tyr	Gly	Ser	Gln	Leu	Ala	Tyr	Ala	Asp	Glu	Asn	Leu	Lys	Asp	Leu	Lys
		20					25					30			
Arg	Ser	Leu	Arg	Phe	Ala	Tyr	Asn	Ile	Thr	Pro	Cys	Asp	Tyr	Glu	Asn
	35					40						45			

Val	Glu	Ile	Ala	Phe	Val	Thr	Thr	Asn	Ser	Ile	His	Ile	Asn	Thr	Lys
50						55					60				
Gln	Lys	Arg	Ser	Glu	Cys	Ile	Leu	Tyr	Val	Asp	Ser	Ile	Val	Ser	Leu
65					70					75					80
Gly	Ile	Thr	Asp	Gln	Phe	Ile	Lys	Gly	Asp	Lys	Val	Asp	Val	Phe	Gly
				85					90					95	
Leu	Pro	Tyr	Asn	Phe	Ser	Pro	Pro	Tyr	Val	Asp	Asn	Ile	Tyr	Gly	Gly
			100					105					110		
Ile	Val	Lys	His	Ser	Asn	Gln	Gly	Asn	Lys	Ser	Leu	Gln	Phe	Val	Gly
		115					120					125			
Ile	Leu	Asn	Gln	Asp	Gly	Lys	Glu	Thr	Tyr	Leu	Pro	Ser	Glu	Ala	Val
	130					135					140				
Arg	Ile	Lys	Lys	Lys	Gln	Phe	Thr	Leu	Gln	Glu	Phe	Asp	Phe	Lys	Ile
145					150					155					160
Arg	Lys	Phe	Leu	Met	Glu	Lys	Tyr	Asn	Ile	Tyr	Asp	Ser	Glu	Ser	Arg
				165					170					175	
Tyr	Thr	Ser	Gly	Ser	Leu	Phe	Leu	Ala	Thr	Lys	Asp	Ser	Lys	His	Tyr
			180					185						190	
Glu	Val	Asp	Leu	Phe	Asn	Lys	Asp	Asp	Lys	Leu	Leu	Ser	Arg	Asp	Ser
		195					200					205			
Phe	Phe	Lys	Arg	Tyr	Lys	Asp	Asn	Lys	Ile	Phe	Asn	Ser	Glu	Glu	Ile
	210					215					220				
Ser	His	Phe	Asp	Ile	Tyr	Leu	Lys	Thr	His						
225						230									

<210> SEQ ID NO 563

<211> LENGTH: 1311

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 563

atgattcatt	taataataat	tagcgccatt	gctctagcca	ttggaattgg	ttaccgcacc	60
aaaatcaata	ttggcctgct	ggctattgct	ttttcttacc	tcatcgcaac	cactctcatg	120
ggattaagcc	ccaaagaact	tcttcatttt	tggccaacct	cactcttttt	taccattttt	180
agcgtctctc	tcttttataa	cgttgcaaca	actaacggca	ctcttgatgt	tttggctcaa	240
cacattctct	accgcacacg	caccaccctt	aacgccctct	acatgatttt	atacctgata	300
gcaacccttt	tgtctgcttt	aggtgctgga	tttttacta	ctatggcctg	ttgctgtcct	360
ctagcgatta	ccctctgtca	aaaagcggac	aaacaccctt	tgattggagc	tcaagccgtc	420
aattggggag	cttcaggagg	ggctaatttg	ataaccagtg	gctcaggcat	tgtctttcaa	480
ggcctgttta	agcaaatggg	atgggaagag	caagcttttt	cacttggcaa	tcatatcttt	540
atcgctcagca	ttatctaccc	actcatcgtc	ttgcttttat	tatcttgta	catccgctac	600
agtaagggaa	gaacaaactc	atccttgact	attgaccaac	caccagtcct	cagcaaggctc	660
caaagacaaa	ccaccttgct	catgatcagc	agcatgggtt	tggtttggct	ttttcccttg	720
ttgcttctca	ttttcccaaa	catcgcatgg	atagctactt	atcgacaaac	atttgatatt	780
ggctttgtct	caatactcat	ggtctgcctc	gccttaaggc	tcaaattagg	gaagcaagaa	840
gccatttttg	ctaaggttcc	ctgggctata	attatcatgc	tctgcggtat	gagcttacta	900
atgtctctag	cggcaagtc	aggtttagtt	acactgatag	ggcacctcat	aacaacaacc	960
attcctcatt	tctggttacc	tctgttcttt	tgtgtgatag	ccggagtgat	gtcactcttt	1020
agttccaccc	tatccgtcgt	agccccaact	ctctttccca	tcattgctac	catcagtgtc	1080
caaagtcctc	acattgatat	tcgcttactc	acaacagcca	ctattattgg	cgctctatct	1140
actaatatct	ctcctttttc	atcagctggg	tccctcattc	aactctccct	tccccatata	1200
gaggaacgca	gtcttgcttt	caaaaaacaa	attcttctgg	gtgtgcccat	cagcttaagt	1260
ttggcactct	tgaccatctg	gattctcatg	ctgctagctt	ccttaagtta	g	1311

<210> SEQ ID NO 564

<211> LENGTH: 436

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 564

[illegible]

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<210> SEQ ID NO 565
<211> LENGTH: 327
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 565
gtgaaaaaca aattatTTTT agttgccctt gcgaccgtaa ctgtcctagg gccgtcttta      60
gcaacccttc atcaccagac cgtgcatgct agtgatgtaa cattaactga gacatgtgat      120
aaaaacggaa cagtatgttt tggctacgaa aacgtagatg gtgaagtatg taaattaaca      180
gctgacggaa agggaaccat ttgtgtgggt tacgaaaata gagacataaa agagagtgaa      240
acttctagca ccaaaaatga ttgttcta attggtttgggt gctttttaaa ttatctttgg      300
actacaataa aaagctgggt ttcgtaa                                     327

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<210> SEQ ID NO 566
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 566
Met Lys Asn Lys Leu Phe Leu Val Ala Leu Ala Thr Val Thr Val Leu
1      5      10      15
Gly Pro Ser Leu Ala Thr Pro His His Gln Thr Val His Ala Ser Asp
20      25      30
Val Thr Leu Thr Glu Thr Cys Asp Lys Asn Gly Thr Val Cys Phe Gly
35      40      45
Tyr Glu Asn Val Asp Gly Glu Val Cys Lys Leu Thr Ala Asp Gly Lys
50      55      60
Gly Thr Ile Cys Val Gly Tyr Glu Asn Arg Asp Ile Lys Glu Ser Glu
65      70      75      80
Thr Ser Ser Thr Lys Asn Asp Cys Ser Asn Trp Phe Trp Cys Phe Leu
85      90      95
Asn Tyr Leu Trp Thr Thr Ile Lys Ser Trp Val Ser
100      105

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<210> SEQ ID NO 567
<211> LENGTH: 429
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 567
atgaaacaac aatcttacca gcctctacgc ttcgtctacc tcttggtggc tctatttgct      60
gctctggtgc ttatagcaag acctgttatg gcagatgagg gaacaaatag tgctgatgcg      120
gcgtattata aagggaagag tgctggagaa gaagcagggg aaaaagctgg aaaagaagct      180
acttggactg atttgacccc aactgtccca actaatccag aaacacctag tgacatcgga      240
gagactacta ataaacagct ctataaagaa gggataaaag atgggtacaa agagggttat      300
aatgaaggct ggaaatctca gtatcccgtt ttgactccgg tcaagggttat atgggatttg      360
atctcttatt ggctacagcg attattcccc aataatcagt caagtaccgc agcacaaagc      420
atgtcataa                                     429

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<210> SEQ ID NO 568
<211> LENGTH: 142
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 568
Met Lys Gln Gln Ser Tyr Gln Pro Leu Arg Phe Val Tyr Leu Leu Val
1      5      10      15
Ala Leu Phe Ala Ala Leu Leu Leu Ile Ala Arg Pro Val Met Ala Asp
20      25      30
Glu Gly Thr Asn Ser Ala Asp Ala Ala Tyr Tyr Lys Gly Gln Ser Ala

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		35					40					45							
Gly	Glu	Glu	Ala	Gly	Lys	Lys	Ala	Gly	Lys	Glu	Ala	Thr	Trp	Thr	Asp				
	50					55					60								
Leu	Thr	Pro	Thr	Val	Pro	Thr	Asn	Pro	Glu	Thr	Pro	Ser	Asp	Ile	Gly				
65					70					75					80				
Glu	Thr	Thr	Asn	Lys	Gln	Leu	Tyr	Lys	Glu	Gly	Tyr	Lys	Asp	Gly	Tyr				
			85						90					95					
Lys	Glu	Gly	Tyr	Asn	Glu	Gly	Trp	Lys	Ser	Gln	Tyr	Pro	Val	Leu	Thr				
		100						105					110						
Pro	Val	Lys	Val	Ile	Trp	Asp	Leu	Ile	Ser	Tyr	Trp	Leu	Gln	Arg	Leu				
	115					120						125							
Phe	Pro	Asn	Asn	Gln	Ser	Ser	Thr	Ala	Ala	Gln	Ser	Met	Ser						
	130					135					140								

<210> SEQ ID NO 569

<211> LENGTH: 1353

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 569

gtggtttaca	tgagaaacaa	aaaagtaaca	ttagctcata	ttgtcgcaaa	gacaagtgtt	60
gctattgctt	tggctggagc	aatgggtagc	agttttattag	ctaatagcac	aacgtacgct	120
gttagtgcca	aagaaaataa	aaaaagcgat	gtcaaataatg	aaacgaccaa	agttatggaa	180
gctaacgcaa	cttcctctaa	agaagacaat	catgtcatgc	acacattaga	cggctcaatg	240
agtactgtct	gggaggaaaa	ttcacctggt	ggtggtgttg	gtgaagtact	ttcctacaag	300
tttgcgctccc	cgatgcatat	tgggagaatt	ttaattgtta	atggagatac	atctagcaag	360
gagaattact	acaagaaaaa	tagaattgca	aaggctgatg	ttaaatacta	taacaggaat	420
aaattgggcc	tctttcaaaa	aattgaatta	ggcgacacct	acactaaaaa	accgcatcac	480
attgagattg	ataaaaaaatt	agatgttgat	cgtattgata	ttgaggtaac	agaggtccat	540
cagggacaaa	acaaggatat	tttagccttg	tcagagggtca	cttttgcaa	tatagaacgc	600
gatatttttg	aaaaaaaagt	taaagaaatt	aaagataaat	gggtaacaga	taaacaagca	660
gatgagttaa	ttgaaactgc	cgacaagtat	gctgataaag	ctgttcagat	gtctgtctgt	720
gcgtcacgtg	ctgagtatta	tcggatgtac	gttagccgca	aataccacta	caaaaaagaa	780
ttgtttgaaa	aactaaaaca	agtctacaaa	gaaagcggag	cttcccacgt	tacaagcaaa	840
aaagatgtga	tgttagcttt	tgacgatgct	aaaaaaaaagt	caacgattgg	tcgacaagaa	900
aacggtcttt	ttgtgacaag	ttttgctgag	gatatggctt	tgctctttac	tgatcaaggt	960
aagttaaaat	cagctgacca	aattgaaaat	ataaaaagatg	tcgatagcgg	aaaatatagc	1020
gatgggggtt	atcaatatga	gtacgattct	gaactaacaa	aaaacattga	taagctaggc	1080
tatatccgaa	cagctagcgg	agatactcct	ggagcaaatt	cgctcaacgt	tcctggttgc	1140
caaacgtggt	caggaaaaca	cattgaaaat	tcagaaagtg	aattaatttt	cccatcgatt	1200
agtgttaaag	atctaaaatc	taaagctgtc	ttagcagaga	ttgatgccaa	aggctatttt	1260
gaaattattg	atcctaccat	cattgctcca	aatggtgacc	ataaaaaagt	aactggtcgc	1320
ttcaaaatta	agaaaatgca	agataggaag	taa			1353

<210> SEQ ID NO 570

<211> LENGTH: 450

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 570

Met	Val	Tyr	Met	Arg	Asn	Lys	Lys	Val	Thr	Leu	Ala	His	Ile	Val	Ala
1			5					10					15		
Lys	Thr	Ser	Val	Ala	Ile	Ala	Leu	Ala	Gly	Ala	Met	Gly	Ser	Ser	Leu
		20					25				30				
Leu	Ala	Asn	Ser	Thr	Thr	Tyr	Ala	Val	Ser	Gly	Lys	Glu	Asn	Lys	Lys
	35					40			45						
Ser	Asp	Val	Lys	Tyr	Glu	Thr	Thr	Lys	Val	Met	Glu	Ala	Asn	Ala	Thr
50					55				60						
Ser	Ser	Lys	Glu	Asp	Asn	His	Val	Met	His	Thr	Leu	Asp	Gly	Ser	Met

65					70					75				80	
Ser	Thr	Val	Trp	Glu	Glu	Asn	Ser	Pro	Gly	Gly	Gly	Val	Gly	Glu	Val
				85					90					95	
Leu	Ser	Tyr	Lys	Phe	Ala	Ser	Pro	Met	His	Ile	Gly	Arg	Ile	Leu	Ile
			100					105					110		
Val	Asn	Gly	Asp	Thr	Ser	Ser	Lys	Glu	Asn	Tyr	Tyr	Lys	Lys	Asn	Arg
		115					120					125			
Ile	Ala	Lys	Ala	Asp	Val	Lys	Tyr	Tyr	Asn	Arg	Asn	Lys	Leu	Val	Leu
	130					135					140				
Phe	Gln	Lys	Ile	Glu	Leu	Gly	Asp	Thr	Tyr	Thr	Lys	Lys	Pro	His	His
145					150					155				160	
Ile	Glu	Ile	Asp	Lys	Lys	Leu	Asp	Val	Asp	Arg	Ile	Asp	Ile	Glu	Val
			165						170					175	
Thr	Glu	Val	His	Gln	Gly	Gln	Asn	Lys	Asp	Ile	Leu	Ala	Leu	Ser	Glu
			180					185					190		
Val	Thr	Phe	Gly	Asn	Ile	Glu	Arg	Asp	Ile	Phe	Glu	Lys	Lys	Phe	Lys
	195						200					205			
Glu	Ile	Lys	Asp	Lys	Trp	Val	Thr	Asp	Lys	Gln	Ala	Asp	Glu	Phe	Ile
	210					215					220				
Glu	Thr	Ala	Asp	Lys	Tyr	Ala	Asp	Lys	Ala	Val	Gln	Met	Ser	Ala	Val
225					230					235				240	
Ala	Ser	Arg	Ala	Glu	Tyr	Tyr	Arg	Met	Tyr	Val	Ser	Arg	Lys	Tyr	His
			245						250				255		
Tyr	Lys	Lys	Glu	Phe	Val	Glu	Lys	Leu	Lys	Gln	Val	Tyr	Lys	Glu	Ser
			260					265					270		
Gly	Ala	Ser	His	Val	Thr	Ser	Lys	Lys	Asp	Val	Met	Leu	Ala	Phe	Asp
	275						280					285			
Asp	Ala	Lys	Lys	Lys	Ser	Thr	Ile	Gly	Arg	Gln	Glu	Asn	Gly	Leu	Phe
	290					295					300				
Val	Thr	Ser	Phe	Ala	Glu	Asp	Met	Ala	Leu	Leu	Phe	Thr	Asp	Gln	Gly
305					310					315				320	
Lys	Leu	Lys	Ser	Ala	Asp	Gln	Ile	Glu	Asn	Ile	Lys	Asp	Val	Asp	Ser
			325						330				335		
Gly	Lys	Tyr	Ser	Asp	Gly	Val	Tyr	Gln	Tyr	Glu	Tyr	Asp	Ser	Glu	Leu
			340					345					350		
Thr	Lys	Asn	Ile	Asp	Lys	Leu	Gly	Tyr	Ile	Arg	Thr	Ala	Ser	Gly	Asp
	355						360					365			
Thr	Pro	Gly	Ala	Asn	Ser	Leu	Asn	Val	Pro	Gly	Cys	Gln	Thr	Trp	Ser
	370					375					380				
Gly	Lys	His	Ile	Glu	Asn	Ser	Glu	Ser	Glu	Leu	Ile	Phe	Pro	Ser	Ile
385					390					395				400	
Ser	Val	Lys	Asp	Leu	Lys	Ser	Lys	Ala	Val	Leu	Ala	Glu	Ile	Asp	Ala
			405						410				415		
Lys	Gly	Tyr	Phe	Glu	Ile	Ile	Asp	Pro	Thr	Ile	Ile	Ala	Pro	Asn	Gly
			420					425				430			
Asp	His	Lys	Lys	Val	Thr	Gly	Arg	Phe	Lys	Ile	Lys	Lys	Met	Gln	Asp
		435					440					445			
Arg	Lys														
	450														

<210> SEQ ID NO 571

<211> LENGTH: 879

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 571

atgattagaa	agtatgaccg	cacgagcaca	aaaaagaaat	cactaaactg	gatttggcta	60
atcattgctt	tttttatgat	ttcaagcttt	ataggtggct	cttcttttac	tgagtcactt	120


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<210> SEQ ID NO 573
<211> LENGTH: 1416
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 573
atgagcgttc tcaaagaata tcggacgggt agcgaagtgg ttggcccttt gatgattggt      60
gatcaagttg caggagtgc ctacaacgaa ttggtagata ttactttgca taatggagaa      120
aggcgtaaag gtcaagtctt agaagtccaa ggtgacaagg ctatggtaca gctatttgaa      180
ggatcaactg gcatcaacct agccaaaacc aaggttcgat ttacagggca tcctttggaa      240
ttagccgtat cagaagatat ggtagggcgc atctttgatg gaatggggca gcccatagac      300
ggcgggccag aacttattcc cgaaaaatac cttgatattg atggtcaagc gatcaatcct      360
gtcgtcgtg attaccaga cgaatttatc cagacaggta tctcagctat tgatcacctc      420
aataccctcg ttcgtggtca aaagttacca gttttttcgg gctcagggtt acctcataat      480
gaattggccg cacagattgc tcgtcaggca actgttctaa actctgatga taactttgcg      540
gttggtgttg cagctatggg tattactttt gaagaggcag aattctttat gaatgacttg      600
cgtgaaacgg gtgccattga tcgatctgtt ttatttatca atttagctaa tgaccctgct      660
attgaacgca ttgcaacacc acgtatagct ctgacaacag ccgaataactt ggcttatgaa      720
aaaggatatg atgttttagt catcatgaca gatatgacaa attattgtga agccttacga      780
gaagtatcag ccgctcgcag agaagttcca ggcagacgag gttatcctgg ctatctctat      840
actaatctct ccaccttata tgaacgggct ggtcgttgta tcgggaaaaa agggtcagtg      900
actcaaattc ctattttaac catgccagaa gatgacatta cccaccctat ccccgatttg      960
acaggttata ttaccgaagg tcagattatt ttgtcgcaag aactatataa aaatgggttt      1020
agaccgccta ttaatgtctt gccatcgcta tctcgcttaa aagataaagg ctcaggtgaa      1080
ggtaagactc gacaagacca tgctgttaca atgaatcagc tctttgcagc ctatgcccaa      1140
ggaaaacaag ctaaggaatt ggctgttggt ctcggtgaat cagccctttc tgaaacggat      1200
aaactatatg tggcctttac caaccgggtt gaagaagaat acattaacca aggattttac      1260
accaaccgta gcattgaaga aagtcttgac ttgggttggg aattgttgtc gattttgccca      1320
cgtaccgaat taaaacgcat taaagatgat atgtagatc gttatttgcc taaagcagat      1380
accacgatga caaagggttt tgttgcaaat gattga      1416

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<210> SEQ ID NO 574
<211> LENGTH: 471
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 574
Met Ser Val Leu Lys Glu Tyr Arg Thr Val Ser Glu Val Val Gly Pro
1          5          10          15
Leu Met Ile Val Asp Gln Val Ala Gly Val His Tyr Asn Glu Leu Val
20        25        30
Asp Ile Thr Leu His Asn Gly Glu Arg Arg Lys Gly Gln Val Leu Glu
35        40        45
Val Gln Gly Asp Lys Ala Met Val Gln Leu Phe Glu Gly Ser Thr Gly
50        55        60
Ile Asn Leu Ala Lys Thr Lys Val Arg Phe Thr Gly His Pro Leu Glu
65        70        75        80
Leu Ala Val Ser Glu Asp Met Val Gly Arg Ile Phe Asp Gly Met Gly
85        90        95
Gln Pro Ile Asp Gly Gly Pro Glu Leu Ile Pro Glu Lys Tyr Leu Asp
100       105       110
Ile Asp Gly Gln Ala Ile Asn Pro Val Ala Arg Asp Tyr Pro Asp Glu
115       120       125
Phe Ile Gln Thr Gly Ile Ser Ala Ile Asp His Leu Asn Thr Leu Val
130       135       140
Arg Gly Gln Lys Leu Pro Val Phe Ser Gly Ser Gly Leu Pro His Asn
145       150       155       160
Glu Leu Ala Ala Gln Ile Ala Arg Gln Ala Thr Val Leu Asn Ser Asp

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				165					170				175				
Asp	Asn	Phe	Ala	Val	Val	Phe	Ala	Ala	Met	Gly	Ile	Thr	Phe	Glu	Glu		
			180					185					190				
Ala	Glu	Phe	Phe	Met	Asn	Asp	Leu	Arg	Glu	Thr	Gly	Ala	Ile	Asp	Arg		
		195					200					205					
Ser	Val	Leu	Phe	Ile	Asn	Leu	Ala	Asn	Asp	Pro	Ala	Ile	Glu	Arg	Ile		
	210					215					220						
Ala	Thr	Pro	Arg	Ile	Ala	Leu	Thr	Thr	Ala	Glu	Tyr	Leu	Ala	Tyr	Glu		
225					230					235					240		
Lys	Gly	Met	His	Val	Leu	Val	Ile	Met	Thr	Asp	Met	Thr	Asn	Tyr	Cys		
			245						250					255			
Glu	Ala	Leu	Arg	Glu	Val	Ser	Ala	Ala	Arg	Arg	Glu	Val	Pro	Gly	Arg		
		260						265					270				
Arg	Gly	Tyr	Pro	Gly	Tyr	Leu	Tyr	Thr	Asn	Leu	Ser	Thr	Leu	Tyr	Glu		
	275						280					285					
Arg	Ala	Gly	Arg	Leu	Ile	Gly	Lys	Lys	Gly	Ser	Val	Thr	Gln	Ile	Pro		
	290					295					300						
Ile	Leu	Thr	Met	Pro	Glu	Asp	Asp	Ile	Thr	His	Pro	Ile	Pro	Asp	Leu		
305					310					315					320		
Thr	Gly	Tyr	Ile	Thr	Glu	Gly	Gln	Ile	Ile	Leu	Ser	Gln	Glu	Leu	Tyr		
			325					330						335			
Lys	Asn	Gly	Phe	Arg	Pro	Pro	Ile	Asn	Val	Leu	Pro	Ser	Leu	Ser	Arg		
		340						345					350				
Leu	Lys	Asp	Lys	Gly	Ser	Gly	Glu	Gly	Lys	Thr	Arg	Gln	Asp	His	Ala		
	355					360						365					
Ala	Thr	Met	Asn	Gln	Leu	Phe	Ala	Ala	Tyr	Ala	Gln	Gly	Lys	Gln	Ala		
	370					375						380					
Lys	Glu	Leu	Ala	Val	Val	Leu	Gly	Glu	Ser	Ala	Leu	Ser	Glu	Thr	Asp		
385					390					395					400		
Lys	Leu	Tyr	Val	Ala	Phe	Thr	Asn	Arg	Phe	Glu	Glu	Glu	Tyr	Ile	Asn		
			405						410					415			
Gln	Gly	Phe	Tyr	Thr	Asn	Arg	Ser	Ile	Glu	Glu	Ser	Leu	Asp	Leu	Gly		
		420						425					430				
Trp	Glu	Leu	Leu	Ser	Ile	Leu	Pro	Arg	Thr	Glu	Leu	Lys	Arg	Ile	Lys		
	435						440					445					
Asp	Asp	Met	Leu	Asp	Arg	Tyr	Leu	Pro	Lys	Ala	Asp	Thr	Thr	Met	Thr		
	450					455					460						
Lys	Val	Phe	Val	Ala	Asn	Asp											
465					470												

<210> SEQ ID NO 575

<211> LENGTH: 1440

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 575

gtgcttttgg	acaatgtgaa	aggaattgac	aacatgaata	acatcaaaac	caaaaaaagg	60
tttatggatc	gctatataga	tggcttttatg	aaatggatgc	cagaatcgct	ttttatctgt	120
tttattttaa	ccttttttagt	cggtactatg	tctgtgttga	tgacggatag	tccctttatt	180
ggtagcgaaa	agacgggcgg	gattatctat	ggctgggtaa	atgggttttg	ggggctgttg	240
tcctttgcca	tgcatatgac	tattttactt	gcgacaggga	atgctgtagc	gagttctcca	300
cctgctcata	agatgtttaa	gtcccttgcc	aaactgcctc	aaaccaggac	tcagattttt	360
atcttttcca	ttgtagtagg	ctctatcttt	ggctttttac	actgggggtc	tggtatgatg	420
gttgctattg	tgtttgggaa	agagttgctt	gttcaggcta	ggcaaaaagg	gattaagggtg	480
catacgccct	tgtttgttgc	tactttattt	tttacctttt	taccagctac	ttctggtcta	540
tctggtgctg	cgggtgctta	ttcggtactt	ccagattatt	tgcgaaatag	tgtcgcagat	600
gcttataaac	agggtgttcc	tgaaagtgtt	cctctgacag	aatcagtttt	gaatcttcca	660
tttatcagtc	tttttagtgg	gtgtatgctg	gtaccgcttt	gctttgcttt	attggcgcac	720

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ccaaaagatg aaactaaaat catggaactt gatgatgaga tctatcacca tagtcttgat      780
accgcttcac atgttggtat tgcaagaaac acacctgctg aaaagatgaa cgcctctcgc      840
ttagtgatgt atcttggttg tggggccatt gttagctata gcctttatca tttttcgggtg      900
gtgggcttgt ctggtctaga tctcaattgt ttttaactttt tatttttagg cttaggcttg      960
cttctttgtg gtcaacaagg accagaatat tatggttcct tattcaaaga tggggtcattg     1020
tcatcttggg gcttggtgct tcagtttcca ttttacgctg gtatttttgg aatcattcaa     1080
agtacagggt taggattaga gatttcccat ttctttgtcg ctatttcaaa tgggacaaca     1140
tggccgggtc ttgcttatct ttactcggct ttgctgaata ttgcggtacc atcaggaggc     1200
tcaaaatttg tgattgaagc tccctatatc gtccctgcaa ctatcgaagt tggtaatgac     1260
ttaggtaaga ttttgcaggc ttatcaatta ggagatgccca caacaaactt gatagttcct     1320
ttttgggcct tatcttacct ctcaaaacttc aaactaaaat tcaatcaaat tgtggccttat     1380
actattcctt gtgtcttggt ggtcacagggt attgccatca tttacctatt tgtattttag     1440

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<210> SEQ ID NO 576
<211> LENGTH: 479
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 576

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Met Leu Leu Asp Asn Val Lys Gly Ile Asp Asn Met Asn Asn Ile Lys
 1             5             10            15
Thr Lys Lys Arg Phe Met Asp Arg Tyr Ile Asp Gly Phe Met Lys Trp
      20             25             30
Met Pro Glu Ser Leu Phe Ile Cys Phe Ile Leu Thr Phe Leu Val Val
      35             40             45
Thr Met Ser Val Leu Met Thr Asp Ser Pro Phe Ile Gly Thr Glu Lys
 50             55             60
Thr Gly Gly Ile Ile Tyr Gly Trp Val Asn Gly Phe Trp Gly Leu Leu
65             70             75             80
Ser Phe Ala Met Gln Met Thr Ile Leu Leu Ala Thr Gly Asn Ala Val
      85             90             95
Ala Ser Ser Pro Pro Ala His Lys Met Phe Lys Ser Leu Ala Lys Leu
      100            105            110
Pro Gln Thr Arg Thr Gln Ile Phe Ile Phe Ser Ile Val Val Gly Ser
      115            120            125
Ile Phe Gly Phe Leu His Trp Gly Leu Gly Met Met Val Ala Ile Val
      130            135            140
Phe Gly Lys Glu Leu Leu Val Gln Ala Arg Gln Lys Gly Ile Lys Val
145            150            155            160
His Thr Pro Leu Phe Val Ala Thr Leu Phe Phe Thr Phe Leu Pro Ala
      165            170            175
Thr Ser Gly Leu Ser Gly Ala Ala Val Leu Tyr Ser Ala Thr Pro Asp
      180            185            190
Tyr Leu Arg Asn Ser Val Ala Asp Ala Tyr Lys Gln Val Val Pro Glu
      195            200            205
Ser Val Pro Leu Thr Glu Ser Val Leu Asn Leu Pro Phe Ile Ser Leu
      210            215            220
Leu Val Val Cys Met Leu Val Pro Leu Cys Phe Ala Leu Leu Ala His
225            230            235            240
Pro Lys Asp Glu Thr Lys Ile Met Glu Leu Asp Asp Glu Ile Tyr His
      245            250            255
His Ser Leu Asp Thr Ala Ser His Val Val Ile Ala Arg Asn Thr Pro
      260            265            270
Ala Glu Lys Met Asn Ala Ser Arg Leu Val Met Tyr Leu Val Gly Gly
      275            280            285
Ala Ile Val Ser Tyr Ser Leu Tyr His Phe Ser Val Val Gly Leu Ser
      290            295            300
Gly Leu Asp Leu Asn Cys Phe Asn Phe Leu Phe Leu Gly Leu Gly Leu

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305		310		315		320									
Leu	Leu	Cys	Gly	Gln	Gln	Gly	Pro	Glu	Tyr	Tyr	Gly	Ser	Leu	Phe	Lys
		325		330		335									
Asp	Gly	Val	Met	Ser	Ser	Trp	Gly	Leu	Val	Leu	Gln	Phe	Pro	Phe	Tyr
		340		345		350									
Ala	Gly	Ile	Phe	Gly	Ile	Ile	Gln	Ser	Thr	Gly	Leu	Gly	Leu	Glu	Ile
		355		360		365									
Ser	His	Phe	Phe	Val	Ala	Ile	Ser	Asn	Gly	Thr	Thr	Trp	Pro	Val	Phe
	370			375		380									
Ala	Tyr	Leu	Tyr	Ser	Ala	Leu	Leu	Asn	Ile	Ala	Val	Pro	Ser	Gly	Gly
385				390		395									400
Ser	Lys	Phe	Val	Ile	Glu	Ala	Pro	Tyr	Ile	Val	Pro	Ala	Thr	Ile	Glu
			405		410									415	
Val	Gly	Asn	Asp	Leu	Gly	Lys	Ile	Leu	Gln	Ala	Tyr	Gln	Leu	Gly	Asp
		420		425		430									
Ala	Thr	Thr	Asn	Leu	Ile	Val	Pro	Phe	Trp	Ala	Leu	Ser	Tyr	Leu	Ser
	435			440		445									
Asn	Phe	Lys	Leu	Lys	Phe	Asn	Gln	Ile	Val	Ala	Tyr	Thr	Ile	Pro	Cys
	450			455		460									
Val	Leu	Val	Val	Thr	Gly	Ile	Ala	Ile	Ile	Tyr	Leu	Phe	Val	Phe	
465				470		475									

<210> SEQ ID NO 577

<211> LENGTH: 666

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 577

atgaaacgat	gtaataaata	tctcttcact	tcactactag	cagcttcgat	gctgttttagt	60
tcgtataaat	cagtacatgc	ccatgataac	attgatgaga	aaggtaaagt	gcacctttac	120
tggcagggaa	attactatgt	tgataactat	gtcgactata	ctaaaaaatt	ggtcgatagc	180
gataaaaaata	ttgaatggac	tgtaaccttt	aattcagcta	aagaacaatg	ggtttaccct	240
gattttctcag	tttttcttcc	taagggtgta	aaagctccta	cagagataac	ttatgagcat	300
cattattggg	acggtacagt	tcgttctgaa	acacgcaata	atacacaatg	gcattatgat	360
tggaaaagcc	aacaaacaaa	ttttaatcaa	gaatttgata	aattccctgg	tttactgggt	420
tggagtcctt	ctctagataa	attttacaaa	ctaaaaaacg	acggaaaatt	ttctcacggt	480
ttagtagata	cctatggccg	tcaatcacac	acttattttt	ctcataaaat	ggtttggaag	540
tttaaaactg	agcttgaaga	taattacaaa	aataaatggg	ataaattacc	gtttatagca	600
ggtattaaac	aaaacaaccc	attagcagca	tcattcccaa	gttataaagg	ggaattcggt	660
gagtaa						666

<210> SEQ ID NO 578

<211> LENGTH: 221

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 578

Met	Lys	Arg	Cys	Asn	Lys	Tyr	Leu	Phe	Thr	Ser	Leu	Leu	Ala	Ala	Ser
1				5					10					15	
Met	Leu	Phe	Ser	Ser	Tyr	Lys	Ser	Val	His	Ala	His	Asp	Asn	Ile	Asp
			20					25					30		
Glu	Lys	Gly	Lys	Val	His	Leu	Tyr	Trp	Gln	Gly	Asn	Tyr	Tyr	Val	Asp
	35					40					45				
Asn	Tyr	Val	Asp	Tyr	Thr	Lys	Lys	Leu	Val	Asp	Ser	Asp	Lys	Asn	Ile
	50					55				60					
Glu	Trp	Thr	Val	Thr	Phe	Asn	Ser	Ala	Lys	Glu	Gln	Trp	Val	Tyr	Pro
65				70					75					80	
Asp	Phe	Ser	Val	Phe	Leu	Pro	Lys	Gly	Val	Lys	Ala	Pro	Thr	Glu	Ile
				85					90					95	

Thr	Tyr	Glu	His	His	Tyr	Trp	Asp	Gly	Thr	Val	Arg	Ser	Glu	Thr	Arg
			100					105					110		
Asn	Asn	Thr	Gln	Trp	His	Tyr	Asp	Trp	Lys	Ser	Gln	Gln	Thr	Asn	Phe
		115					120				125				
Asn	Gln	Glu	Phe	Asp	Lys	Phe	Pro	Gly	Tyr	Thr	Gly	Trp	Ser	Pro	Ser
		130				135					140				
Leu	Asp	Lys	Phe	Tyr	Lys	Leu	Lys	Asn	Asp	Gly	Lys	Phe	Ser	His	Val
					150					155				160	
Leu	Val	Asp	Thr	Tyr	Gly	Arg	Gln	Ser	His	Thr	Tyr	Phe	Ser	His	Lys
				165					170					175	
Met	Val	Trp	Lys	Phe	Lys	Thr	Glu	Leu	Glu	Asp	Asn	Tyr	Lys	Asn	Lys
			180					185					190		
Trp	Asp	Lys	Leu	Pro	Phe	Ile	Ala	Gly	Ile	Lys	Gln	Asn	Asn	Pro	Leu
		195					200				205				
Ala	Ala	Ser	Phe	Pro	Ser	Tyr	Lys	Gly	Glu	Phe	Gly	Glu			
		210				215					220				

<210> SEQ ID NO 579

<211> LENGTH: 756

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 579

gtggaatgct	atcgatgacg	tcaattgcta	tcaacttata	acaaacaagt	gactcaaaaag	60
aagccctcag	aatggagga	ggtgtggcaa	aaggctaagg	cgtataacgc	taggcttggg	120
attcagcctg	ttccagatgc	tttttcattt	agggatggca	ttcatgataa	aaactacgaa	180
agcctacttc	aaattgaaaa	caatgatatt	atgggatatg	ttgaagtgcc	ctctattaaa	240
gtgacgttac	ccatatacca	ctatacgaca	gacgagggtc	taactaaaag	agcaggtcac	300
ttattttggaa	gtgccttacc	agttggtggt	gacgggactc	acacgggttat	ttctgctcat	360
agaggccttc	catcggcaga	aatgtttact	aatttgaatt	tagtgaaaaa	gggagatact	420
ttttactttc	gtgtgttaaa	taaagtattg	gcttataaaag	ttgatcagat	actaactggt	480
gaaccagatc	aagtcacatc	actttctgga	gtcatgggga	aagattatgc	tactttgggt	540
acctgcacac	catatggtgt	taacaccaag	cgtctattgg	tccgagggtca	tagaattgca	600
tatcattata	aaaagtatca	acaggctaaa	aaagcaatga	aactcgtgga	taaatcaaga	660
atgtgggcag	aagtagtggtg	tgctgctttc	ggggtgggta	tagctattat	tttagtggtt	720
atgtattcgc	gagtaagtgc	taagaaaagc	aagtga			756

<210> SEQ ID NO 580

<211> LENGTH: 251

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 580

Met	Glu	Cys	Tyr	Arg	Asp	Arg	Gln	Leu	Leu	Ser	Thr	Tyr	His	Lys	Gln
1			5					10					15		
Val	Thr	Gln	Lys	Lys	Pro	Ser	Glu	Met	Glu	Glu	Val	Trp	Gln	Lys	Ala
		20					25					30			
Lys	Ala	Tyr	Asn	Ala	Arg	Leu	Gly	Ile	Gln	Pro	Val	Pro	Asp	Ala	Phe
	35					40					45				
Ser	Phe	Arg	Asp	Gly	Ile	His	Asp	Lys	Asn	Tyr	Glu	Ser	Leu	Leu	Gln
	50				55					60					
Ile	Glu	Asn	Asn	Asp	Ile	Met	Gly	Tyr	Val	Glu	Val	Pro	Ser	Ile	Lys
	65			70					75					80	
Val	Thr	Leu	Pro	Ile	Tyr	His	Tyr	Thr	Thr	Asp	Glu	Val	Leu	Thr	Lys
			85					90					95		
Gly	Ala	Gly	His	Leu	Phe	Gly	Ser	Ala	Leu	Pro	Val	Gly	Gly	Asp	Gly
		100					105					110			
Thr	His	Thr	Val	Ile	Ser	Ala	His	Arg	Gly	Leu	Pro	Ser	Ala	Glu	Met
		115				120						125			

Phe	Thr	Asn	Leu	Asn	Leu	Val	Lys	Lys	Gly	Asp	Thr	Phe	Tyr	Phe	Arg
130						135					140				
Val	Leu	Asn	Lys	Val	Leu	Ala	Tyr	Lys	Val	Asp	Gln	Ile	Leu	Thr	Val
145					150					155					160
Glu	Pro	Asp	Gln	Val	Thr	Ser	Leu	Ser	Gly	Val	Met	Gly	Lys	Asp	Tyr
			165						170					175	
Ala	Thr	Leu	Val	Thr	Cys	Thr	Pro	Tyr	Gly	Val	Asn	Thr	Lys	Arg	Leu
			180					185					190		
Leu	Val	Arg	Gly	His	Arg	Ile	Ala	Tyr	His	Tyr	Lys	Lys	Tyr	Gln	Gln
		195				200					205				
Ala	Lys	Lys	Ala	Met	Lys	Leu	Val	Asp	Lys	Ser	Arg	Met	Trp	Ala	Glu
	210					215					220				
Val	Val	Cys	Ala	Ala	Phe	Gly	Val	Val	Ile	Ala	Ile	Ile	Leu	Val	Phe
225					230					235					240
Met	Tyr	Ser	Arg	Val	Ser	Ala	Lys	Lys	Ser	Lys					
				245					250						

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<210> SEQ ID NO 581
<211> LENGTH: 714
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 581
atgatagtaa gactgattaa gctccttgac aagttgataa acgtcattgt tctttgtttc      60
ttctttcttt gtttattgat tgcggcactt ggaatctacg atgctttaac agtttatcaa      120
ggagctaata ctactaacta tcaacaatat aagaaaaagg gtgttcagtt tgacgattta      180
ttagctatta attctgatgt tatggcatgg ctgactgtta aaggaacgca tattgattat      240
ccaattgtac agggagagaa taatttagaa tatatcaaca aatcagtaga aggagagtac      300
tccttatcag gaagtgtttt tctagattat cgtaataaag taacttttga agataaatac      360
tcattaatct atgcacatca tatggctgga aatgttatgt ttggcgaatt acctaacttt      420
aggaaaaaat cattttttta taaacacaaa gaatttagta ttgaaaccaa aacaaagcaa      480
aaactgaaaa tcaatatatt tgcatgtatc caaacagatg cttttgacag tttactgttt      540
aatccaattg atgttgatat ttctagtaaa aatgaatttt taaaccatat caagcaaaaa      600
tcggtacagt atcgtgaaat attgacaaca aatgaaagtc gttttgttgc cttatcaacc      660
tgtgaggata tgacaacaga tggtaggatt atcgttattg gacaaattga ataa          714

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<210> SEQ ID NO 582
<211> LENGTH: 237
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 582
Met Ile Val Arg Leu Ile Lys Leu Leu Asp Lys Leu Ile Asn Val Ile
1           5           10           15
Val Leu Cys Phe Phe Phe Leu Cys Leu Leu Ile Ala Ala Leu Gly Ile
20           25           30
Tyr Asp Ala Leu Thr Val Tyr Gln Gly Ala Asn Ala Thr Asn Tyr Gln
35           40           45
Gln Tyr Lys Lys Lys Gly Val Gln Phe Asp Asp Leu Leu Ala Ile Asn
50           55           60
Ser Asp Val Met Ala Trp Leu Thr Val Lys Gly Thr His Ile Asp Tyr
65           70           75           80
Pro Ile Val Gln Gly Glu Asn Asn Leu Glu Tyr Ile Asn Lys Ser Val
85           90           95
Glu Gly Glu Tyr Ser Leu Ser Gly Ser Val Phe Leu Asp Tyr Arg Asn
100          105          110
Lys Val Thr Phe Glu Asp Lys Tyr Ser Leu Ile Tyr Ala His His Met
115          120          125
Ala Gly Asn Val Met Phe Gly Glu Leu Pro Asn Phe Arg Lys Lys Ser

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130		135		140
Phe Phe Asn Lys His Lys Glu Phe Ser Ile Glu Thr Lys Thr Lys Gln				
145		150		155
Lys Leu Lys Ile Asn Ile Phe Ala Cys Ile Gln Thr Asp Ala Phe Asp				
	165		170	175
Ser Leu Leu Phe Asn Pro Ile Asp Val Asp Ile Ser Ser Lys Asn Glu				
	180		185	190
Phe Leu Asn His Ile Lys Gln Lys Ser Val Gln Tyr Arg Glu Ile Leu				
	195		200	205
Thr Thr Asn Glu Ser Arg Phe Val Ala Leu Ser Thr Cys Glu Asp Met				
	210		215	220
Thr Thr Asp Gly Arg Ile Ile Val Ile Gly Gln Ile Glu				
225		230		235

<210> SEQ ID NO 583

<211> LENGTH: 2289

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 583

ttgagaggag	agaaaaatgaa	aaaaacaagg	tttccaaata	agcttaatac	tcttaatact	60
caaagggat	taagtaaaaa	ctcaaaacga	tttactgtca	ctttagtggg	agtcttttta	120
atgatcttcg	cttttgtaac	ttccatgggt	gggtgctaaga	ctgttttttg	tttagtagaa	180
tctcgcacgc	caaacgcaat	aaatccagat	tcaagttcgg	aatacagatg	gtatggatat	240
gaatcttatg	taagagggca	tccatattat	aaacagttta	gagtagcaca	cgatttaagg	300
gttaacttag	aaggaagtag	aagttatcaa	gtttattgct	ttaatttaaa	gaaagcattt	360
cctctcggat	cagatagtag	tgtaaaaaag	tggtataaaa	aacatgatgg	aatctctaca	420
aaatttgaag	attatgcat	gagccctaga	attacgggag	atgagctaaa	tcagaagtta	480
cgagctgtta	tgtataatgg	acatccacaa	aatgccaatg	gtattatgga	aggcttggaa	540
cccttgaatg	ctatcagagt	tacacaagag	gcggtatggt	actattctga	taatgctcct	600
atttctaata	cagatgaaag	ttttaaaagg	gagtcagaaa	gtaacttggg	tagtacttct	660
caattatctt	tgatgcgtca	agctttgaag	caactgattg	atccgaattt	ggcaactaaa	720
atgccaaaac	aagttccgga	tgattttcag	ctaagtattt	ttgagctctga	ggacaaggga	780
gataaatata	ataaaaggata	ccaaaatctt	ttgagtgggt	gtttagtccc	tactaaacca	840
ccaactccag	gagaccacc	aatgcctcca	aatcaacctc	aaacgacttc	agtacttatt	900
agaaagtatg	ctataggtga	ttactctaaa	ttgcttgaag	gtgcaacatt	acagttgaca	960
ggggataacg	tgaatagttt	tcaagcgaga	gtgttttagca	gtaatgatat	tgagagaaga	1020
attgaactat	cagatggaac	ttatacttta	actgaattga	attctccagc	tggttatagt	1080
atcgagagc	caatcacttt	taagggtgaa	gctggcgaag	tgtatactat	tattgatgga	1140
aaacagattg	aaaatcccaa	taaagagata	gtagagcctt	actcagtaga	agcatataat	1200
gattttgaag	aatttagcgt	tttaactaca	caaaactatg	caaaatttta	ttatgcaaaa	1260
aataaaaaatg	gaagttcaca	ggttgtctat	tgctttaatg	cagatctaaa	atctccacca	1320
gactctgaag	atggtgggaa	aacaatgact	ccagacttta	caacaggaga	agtaaaatac	1380
actcatattg	caggtcgtga	cctctttaaa	tatactgtga	aaccaagaga	taccgatcct	1440
gacactttct	taaaacatat	caaaaaagta	attgagaagg	gttacaggga	aaaaggacaa	1500
gctattgagt	atagtgggtc	aactgagaca	caattgcgtg	cggctactca	gttagcaata	1560
tattatttca	ctgatagtgc	tgaattagat	aaggataaac	taaaagacta	tcattggtttt	1620
ggagacatga	atgatagtac	tttagcagtt	gctaaaatcc	ttgtagaata	cgctcaagat	1680
agtaatcctc	cacagctaac	tgaccttgat	ttctttattc	cgaataacaa	taaatatcaa	1740
tctcttattg	gaactcagtg	gcacccagaa	gatttagttg	atattattcg	tatggaagat	1800
aaaaaagaag	ttataacctgt	aactcataat	ttaacattga	gaaaaacggg	gactggttta	1860
gctggtgaca	gaactaaaaga	tttccatttt	gaaattgaat	taaaaaataa	taagcaagaa	1920
ttgctttctc	aaactgttaa	aacagataaa	acaaacctcg	aatttaaaga	tggtaaagca	1980
accattaatt	taaaacatgg	ggaaagttaa	acacttcaag	gtttaccaga	aggttattct	2040
taccttgta	aagaaacaga	ttctgaaggc	tataagggtta	aagttaatag	ccaagaagta	2100
gcaaatgcta	cagtttcaaa	aacaggaata	acaagtgatg	agacacttgc	ttttgaaaat	2160
aataaagagc	ctgttggtcc	tacaggagtt	gatcaaaaga	tcaatgggcta	tctagctttg	2220
atagttatcg	ctggtatcag	tttggggatc	tggggaattc	acacgataag	gataagaaaa	2280

<210> SEQ ID NO 584

<211> LENGTH: 762

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 584

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Met Arg Gly Glu Lys Met Lys Lys Thr Arg Phe Pro Asn Lys Leu Asn
1      5      10      15
Thr Leu Asn Thr Gln Arg Val Leu Ser Lys Asn Ser Lys Arg Phe Thr
20      25      30
Val Thr Leu Val Gly Val Phe Leu Met Ile Phe Ala Leu Val Thr Ser
35      40      45
Met Val Gly Ala Lys Thr Val Phe Gly Leu Val Glu Ser Ser Thr Pro
50      55      60
Asn Ala Ile Asn Pro Asp Ser Ser Ser Glu Tyr Arg Trp Tyr Gly Tyr
65      70      75      80
Glu Ser Tyr Val Arg Gly His Pro Tyr Tyr Lys Gln Phe Arg Val Ala
85      90      95
His Asp Leu Arg Val Asn Leu Glu Gly Ser Arg Ser Tyr Gln Val Tyr
100     105     110
Cys Phe Asn Leu Lys Lys Ala Phe Pro Leu Gly Ser Asp Ser Ser Val
115     120     125
Lys Lys Trp Tyr Lys Lys His Asp Gly Ile Ser Thr Lys Phe Glu Asp
130     135     140
Tyr Ala Met Ser Pro Arg Ile Thr Gly Asp Glu Leu Asn Gln Lys Leu
145     150     155     160
Arg Ala Val Met Tyr Asn Gly His Pro Gln Asn Ala Asn Gly Ile Met
165     170     175
Glu Gly Leu Glu Pro Leu Asn Ala Ile Arg Val Thr Gln Glu Ala Val
180     185     190
Trp Tyr Tyr Ser Asp Asn Ala Pro Ile Ser Asn Pro Asp Glu Ser Phe
195     200     205
Lys Arg Glu Ser Glu Ser Asn Leu Val Ser Thr Ser Gln Leu Ser Leu
210     215     220
Met Arg Gln Ala Leu Lys Gln Leu Ile Asp Pro Asn Leu Ala Thr Lys
225     230     235     240
Met Pro Lys Gln Val Pro Asp Asp Phe Gln Leu Ser Ile Phe Glu Ser
245     250     255
Glu Asp Lys Gly Asp Lys Tyr Asn Lys Gly Tyr Gln Asn Leu Leu Ser
260     265     270
Gly Gly Leu Val Pro Thr Lys Pro Pro Thr Pro Gly Asp Pro Pro Met
275     280     285
Pro Pro Asn Gln Pro Gln Thr Thr Ser Val Leu Ile Arg Lys Tyr Ala
290     295     300
Ile Gly Asp Tyr Ser Lys Leu Leu Glu Gly Ala Thr Leu Gln Leu Thr
305     310     315     320
Gly Asp Asn Val Asn Ser Phe Gln Ala Arg Val Phe Ser Ser Asn Asp
325     330     335
Ile Gly Glu Arg Ile Glu Leu Ser Asp Gly Thr Tyr Thr Leu Thr Glu
340     345     350
Leu Asn Ser Pro Ala Gly Tyr Ser Ile Ala Glu Pro Ile Thr Phe Lys
355     360     365
Val Glu Ala Gly Lys Val Tyr Thr Ile Ile Asp Gly Lys Gln Ile Glu
370     375     380
Asn Pro Asn Lys Glu Ile Val Glu Pro Tyr Ser Val Glu Ala Tyr Asn
385     390     395     400

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<210> SEQ ID NO 586
 <211> LENGTH: 94
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 586

Met	Gly	Ile	Ile	Lys	Lys	Gln	Val	Lys	Ala	Tyr	Ile	Ala	Leu	Glu	Ser
1				5					10					15	
Met	Ile	Ala	Thr	Gly	Ile	Leu	Phe	Ser	Ile	Val	Ile	Leu	Val	Leu	Ser
			20					25					30		
Ser	Leu	Gln	Gln	Ser	Gln	Ala	Ala	Leu	Thr	Tyr	Tyr	Arg	Lys	Gln	Gln
		35					40					45			
Glu	Lys	Leu	Asn	Leu	Ala	Leu	Met	Ala	Val	Gln	Thr	Arg	Thr	Lys	Glu
	50					55				60					
Met	Thr	Leu	Asn	Gly	Cys	His	Ile	Thr	Ile	Leu	Arg	Thr	Asp	Arg	Tyr
65					70					75					80
Ile	Ser	Ile	His	Asp	Asp	Glu	Gly	Glu	Val	Met	Lys	Ile	Glu		
				85					90						

<210> SEQ ID NO 587
 <211> LENGTH: 378
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 587

atgcggcaat	cctattacca	atttaccaaaa	atatgggagg	tatttttttaa	gatgattaat	60
caatggaaca	acttacgaca	caagaagcta	aaaggattta	ctcttctaga	aatgttattg	120
gtgattcttg	tcatcagtgt	tttgatgcta	ttattttgtgc	ctaatttaag	caagcaaaaa	180
gacagggtta	cagaaacagg	taatgccgct	gttggttaa	tagtggagaa	tcaagcagaa	240
ctatatgaat	tatctcaagg	ctcaaaaacca	agtttgagcc	agttaaaggc	agatggtagt	300
atcactgaga	aacaagaaaa	agcttatcaa	gactattatg	acaaacataa	aaatgaaaaa	360
gcccgtctta	gcaattaa					378

<210> SEQ ID NO 588
 <211> LENGTH: 125
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 588

Met	Arg	Gln	Ser	Tyr	Tyr	Gln	Phe	Thr	Lys	Ile	Trp	Glu	Val	Phe	Phe
1				5					10					15	
Lys	Met	Ile	Asn	Gln	Trp	Asn	Asn	Leu	Arg	His	Lys	Lys	Leu	Lys	Gly
			20					25					30		
Phe	Thr	Leu	Leu	Glu	Met	Leu	Leu	Val	Ile	Leu	Val	Ile	Ser	Val	Leu
		35					40					45			
Met	Leu	Leu	Phe	Val	Pro	Asn	Leu	Ser	Lys	Gln	Lys	Asp	Arg	Val	Thr
	50					55				60					
Glu	Thr	Gly	Asn	Ala	Ala	Val	Val	Lys	Leu	Val	Glu	Asn	Gln	Ala	Glu
65					70					75					80
Leu	Tyr	Glu	Leu	Ser	Gln	Gly	Ser	Lys	Pro	Ser	Leu	Ser	Gln	Leu	Lys
				85					90					95	
Ala	Asp	Gly	Ser	Ile	Thr	Glu	Lys	Gln	Glu	Lys	Ala	Tyr	Gln	Asp	Tyr
			100					105					110		
Tyr	Asp	Lys	His	Lys	Asn	Glu	Lys	Ala	Arg	Leu	Ser	Asn			
			115				120					125			

<210> SEQ ID NO 589
 <211> LENGTH: 939
 <212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 589

```
atggtacaag cattagcaaa agctattcta gcaaaagctg aacagggttca tgcacaagat      60
atttatattt tgccaagagc agatcaatat gatctttttt tacgaatagg agatgaaagg      120
agattagttg atgtttatca gagcgatcgg atgggtcctc ttattagtca ctttaaattc      180
gttgcaggaa tgatagttgg tgaaaagaga cgttgtcagg tgggttcattg tgattataag      240
cttagtaaaag ataagcagtt atctttgctc ttatctagcg tgggtgatta tcgcggggcaa      300
gaaagcttag tgattcgtct gcttcatcat caaaataaaa gtgtacatta ttggtttgat      360
ggattgacaa aagtagccaa tcagggtggc ggtagagggt tgtatttatt tgcaggacca      420
gttgggtctg ggaagacaac cttgatgtac cagctgattt cgaattatca tcaagaagca      480
caggttatta gtatagaaga tcctgtagaa attaaaaatc accaaatttt acaattacaa      540
gtgaatgatg atattgggtat gacttatgac aatttgatca aactgtcttt acgccatcga      600
ccagatattt tagttattgg tgagattcga gatagtcaaa cagcaagagc cgttattagg      660
gctagtctaa cagggtgccat gggttttttca acggttcacg ctaaaagtat ctcggtgtgt      720
tatgcaagat tgttagaact tgggtgtaacg aaagcagaac tgtctaattg cttagcatta      780
attgcttacc aaaggttact taatggagga gcattgattg actctactca aaacgaattt      840
gaatattatt cctcatcgaa ctggaatcaa caaattgatc agcttcttga ggcaggacat      900
ctcaatccca agcaagctaa gcttgaaaaa attatctag      939
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<210> SEQ ID NO 590

<211> LENGTH: 312

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 590

```
Met Val Gln Ala Leu Ala Lys Ala Ile Leu Ala Lys Ala Glu Gln Val
1      5      10      15
His Ala Gln Asp Ile Tyr Ile Leu Pro Arg Ala Asp Gln Tyr Asp Leu
20     25     30
Phe Leu Arg Ile Gly Asp Glu Arg Arg Leu Val Asp Val Tyr Gln Ser
35     40     45
Asp Arg Met Ala Pro Leu Ile Ser His Phe Lys Phe Val Ala Gly Met
50     55     60
Ile Val Gly Glu Lys Arg Arg Cys Gln Val Gly Ser Cys Asp Tyr Lys
65     70     75     80
Leu Ser Lys Asp Lys Gln Leu Ser Leu Arg Leu Ser Ser Val Gly Asp
85     90     95
Tyr Arg Gly Gln Glu Ser Leu Val Ile Arg Leu Leu His His Gln Asn
100    105    110
Lys Ser Val His Tyr Trp Phe Asp Gly Leu Thr Lys Val Ala Asn Gln
115    120    125
Val Gly Gly Arg Gly Leu Tyr Leu Phe Ala Gly Pro Val Gly Ser Gly
130    135    140
Lys Thr Thr Leu Met Tyr Gln Leu Ile Ser Asn Tyr His Gln Glu Ala
145    150    155    160
Gln Val Ile Ser Ile Glu Asp Pro Val Glu Ile Lys Asn His Gln Ile
165    170    175
Leu Gln Leu Gln Val Asn Asp Asp Ile Gly Met Thr Tyr Asp Asn Leu
180    185    190
Ile Lys Leu Ser Leu Arg His Arg Pro Asp Ile Leu Val Ile Gly Glu
195    200    205
Ile Arg Asp Ser Gln Thr Ala Arg Ala Val Ile Arg Ala Ser Leu Thr
210    215    220
Gly Ala Met Val Phe Ser Thr Val His Ala Lys Ser Ile Ser Gly Val
225    230    235    240
Tyr Ala Arg Leu Leu Glu Leu Gly Val Thr Lys Ala Glu Leu Ser Asn
245    250    255
Cys Leu Ala Leu Ile Ala Tyr Gln Arg Leu Leu Asn Gly Gly Ala Leu
```

			260					265					270				
Ile	Asp	Ser	Thr	Gln	Asn	Glu	Phe	Glu	Tyr	Tyr	Ser	Ser	Ser	Asn	Trp		
		275					280						285				
Asn	Gln	Gln	Ile	Asp	Gln	Leu	Leu	Glu	Ala	Gly	His	Leu	Asn	Pro	Lys		
	290					295					300						
Gln	Ala	Lys	Leu	Glu	Lys	Ile	Ile										
305						310											

<210> SEQ ID NO 591

<211> LENGTH: 855

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 591

atgaagctga	aacagatgac	gaaaaaggag	gtcatgggtca	tgcttgatat	tttattctat	60
gatttcacgc	aacggggcgg	aatggcggtta	gttgccatta	gtatttttgc	tccgatttta	120
gggtattttcc	ttatttttacg	tcgtcaaaagt	ttgatgagcg	atacccttag	tcatgtttct	180
ttggctgggg	tagcgcttgg	ggtagtcctt	ggtagttcac	caaccatcac	tactattatt	240
gttggtggtt	tagctgctat	tttgttagaa	tacctgcgtg	tagtttacia	acactacatg	300
gagatttcaa	cggcgatttt	gatgtcactt	ggcttggccc	tatctctgat	tattatgagt	360
aagtcgcata	gttcatcaag	catgagttta	gaacaatacc	tttttggatc	gatcatcacg	420
attagtagtg	aacaagttgt	cgccttggtt	gctattgctg	cgattatttt	aatcttgacc	480
gttctcttca	ttagaccgat	gtacattctg	acctttgatg	aagatactgc	ttttgtagat	540
ggtttgcccg	ttcgcttgat	gtctgttcta	ttcaatatcg	tcactggggg	tgctattgct	600
ttgaccattc	cagcagcagg	agcacttttg	gtttctacca	ttatggtcct	gccagcaagt	660
atcgcaatga	gattgggtaa	aaactttaaa	acagttatct	tactgggaat	tgatcatcgg	720
tttagcggta	tgttatctgg	tattttctta	tcttatttct	ttgaaacgcc	agctagtggc	780
actattacca	tgattttcat	tagtattttc	ctcttagtta	gtctaggtgg	aatgcttaaa	840
aaacggttat	tttaa					855

<210> SEQ ID NO 592

<211> LENGTH: 284

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 592

Met	Lys	Leu	Lys	Gln	Met	Thr	Lys	Lys	Glu	Val	Met	Val	Met	Leu	Asp
1				5					10					15	
Ile	Leu	Phe	Tyr	Asp	Phe	Met	Gln	Arg	Ala	Val	Met	Ala	Val	Val	Ala
			20					25					30		
Ile	Ser	Ile	Phe	Ala	Pro	Ile	Leu	Gly	Ile	Phe	Leu	Ile	Leu	Arg	Arg
		35					40					45			
Gln	Ser	Leu	Met	Ser	Asp	Thr	Leu	Ser	His	Val	Ser	Leu	Ala	Gly	Val
	50					55				60					
Ala	Leu	Gly	Val	Val	Leu	Gly	Ile	Ser	Pro	Thr	Ile	Thr	Thr	Ile	Ile
65					70				75					80	
Val	Val	Val	Leu	Ala	Ala	Ile	Leu	Leu	Glu	Tyr	Leu	Arg	Val	Val	Tyr
			85					90					95		
Lys	His	Tyr	Met	Glu	Ile	Ser	Thr	Ala	Ile	Leu	Met	Ser	Leu	Gly	Leu
			100					105					110		
Ala	Leu	Ser	Leu	Ile	Ile	Met	Ser	Lys	Ser	His	Ser	Ser	Ser	Ser	Met
	115					120					125				
Ser	Leu	Glu	Gln	Tyr	Leu	Phe	Gly	Ser	Ile	Ile	Thr	Ile	Ser	Met	Glu
	130					135					140				
Gln	Val	Val	Ala	Leu	Phe	Ala	Ile	Ala	Ala	Ile	Ile	Leu	Ile	Leu	Thr
145				150					155					160	
Val	Leu	Phe	Ile	Arg	Pro	Met	Tyr	Ile	Leu	Thr	Phe	Asp	Glu	Asp	Thr
			165					170				175			
Ala	Phe	Val	Asp	Gly	Leu	Pro	Val	Arg	Leu	Met	Ser	Val	Leu	Phe	Asn

Leu	Asp	Glu	Pro	Thr	Thr	Gly	Met	Asp	Ser	Gly	Thr	Thr	Asp	Thr	Phe
				165					170					175	
Tyr	Glu	Leu	Met	His	His	Ser	Ala	His	Gln	His	Gly	Lys	Ser	Val	Leu
		180					185						190		
Met	Ile	Thr	His	Asp	Pro	Glu	Glu	Val	Lys	Ala	Tyr	Ala	Asp	Arg	Asn
		195				200					205				
Ile	His	Leu	Val	Arg	Asn	Gln	Lys	Leu	Pro	Trp	Arg	Cys	Phe	Asn	Ile
	210				215					220					
His	Glu	Ala	Glu	Thr	Asp	Asp	Glu	Lys	Gly	Gly	His	Gly	His	Ala	
225					230					235					

<210> SEQ ID NO 595
 <211> LENGTH: 1353
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 595

ttgctaaagg	tggttcaatc	gaagtcactc	aatgagggga	tactcattat	gttcttaaaa	60
atactaaaag	acgcgttaaa	gataaagact	gtacggaata	aaattttctt	tactatattt	120
atcattcttg	tattccgaat	tgggacacat	attaccgtac	ctgggtgtaa	tgccaagagc	180
ttagagcaat	taagtgaact	ccctttctta	aatatgtaa	acttagttag	tggtaatgag	240
atgagaaatt	tctcagtatt	ttcaatgggg	gttagcccat	atattactgc	ttctatcggt	300
gttcagttat	tgcagatgga	tattttacct	aagtttggtg	agtggggcaa	acaaggtgag	360
gttggacgtc	gtaaattaaa	tcaagcgacg	cgctatattt	cacttgtttt	ggcttttgcc	420
caatccattg	gtatcactgc	agggtttaat	actttgtcga	acgttgcaat	tgtaaagaca	480
ccagacatca	aaacatattt	actgatcggg	gcattactga	caacaggtag	cgttattggt	540
acctggcttg	gagaacaaat	cacagataaa	ggatttggtg	atggcgtatc	aatgattatc	600
tttgcgggta	ttatttcgtc	tattccaagt	gcaattgcaa	caattcgtga	agactatttt	660
gtaaatgtta	aggcaagtga	tttacctcg	tcttatctca	ttgttgggat	tttaatcata	720
gctgttcttg	ctattgtttt	ctttacaaca	tatgtccaac	aagcggaata	taaaattcca	780
atccaataca	caaagcta	gcaaggtgca	cctacaagtt	catatcttcc	attaaaagta	840
aatccagccg	gcgttattcc	cggtatcttt	gctagctcga	ttacaactat	ccaagtacg	900
attattcctt	ttgttcaaaa	tggtagagat	ttaccgtggt	taaaccgttt	gcaagaaatt	960
tttaattatc	aaactccagt	cggaatgata	gtttacgcct	tggtgattat	attgttctca	1020
ttcttctata	cctttgtaca	agttaatcct	gagaagacag	cagaaaatct	tcagaagaat	1080
tcctcatata	taccaagtgt	tcgccctgga	cgtagagacag	aacaatttat	gtccgcattg	1140
ctaaaaaaac	tagcaaccgt	aggagctatc	ttcttagcat	ttatctcttt	agcgccaata	1200
gcagcacaac	aagctctcaa	cctttcttct	agtattgctt	taggtggaac	tagtttgctc	1260
attttgattt	caactgggat	cgaaggtatg	aaacagcttg	agggatatct	tctaaagaga	1320
aaatatgtcg	gatttatgaa	tacagcagaa	tag			1353

<210> SEQ ID NO 596
 <211> LENGTH: 450
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 596

Met	Leu	Lys	Val	Val	Gln	Ser	Lys	Ser	Ser	Asn	Glu	Gly	Ile	Leu	Ile
1			5					10					15		
Met	Phe	Leu	Lys	Ile	Leu	Lys	Asp	Ala	Leu	Lys	Ile	Lys	Thr	Val	Arg
		20					25					30			
Asn	Lys	Ile	Phe	Phe	Thr	Ile	Phe	Ile	Ile	Leu	Val	Phe	Arg	Ile	Gly
	35				40					45					
Thr	His	Ile	Thr	Val	Pro	Gly	Val	Asn	Ala	Lys	Ser	Leu	Glu	Gln	Leu
	50				55					60					
Ser	Glu	Leu	Pro	Phe	Leu	Asn	Met	Leu	Asn	Leu	Val	Ser	Gly	Asn	Ala
65				70					75					80	
Met	Arg	Asn	Phe	Ser	Val	Phe	Ser	Met	Gly	Val	Ser	Pro	Tyr	Ile	Thr
			85					90						95	

cctgtgaata	agacaccaag	cataggggct	atcgcttggt	ttgataaaaa	cgcttatcag	360
tcaaatgctg	cttacgggtca	tgtagcatgg	gtagctgata	tccgtggaga	cactgtcact	420
atcgaagagt	ataattacaa	cgctggacaa	ggccctgaaa	gataccataa	gcgtcaaatt	480
ccaaaatctc	aggtaagtgg	ttatatccat	tttaaagact	tatcatctca	gacaagtcac	540
tcctacccaa	gacaactaaa	acacatttct	caagcttcat	ttgacccttc	tggaacttat	600
cactttacaa	ccagattacc	agtcaaagga	caaaccagta	tcgatagccc	tgatcttgct	660
tactatgaag	caggtcaatc	tgtttattac	gataaagtcg	tgactgctgg	aggttataca	720
tggttagct	acctcagttt	ttctggaaac	cgacgctata	ttcccattaa	agagcccgca	780
cagtctgtgg	ttcaaaatga	caatacaaaa	ccttccatta	aggtcggtga	tactgttacc	840
ttccctggcg	tttttcgtgt	agatcagctt	gttaataaatt	tgatcgtaa	taaagaatta	900
gccggaggag	acccaactcc	actaaactgg	attgatccca	caccattaga	tgaacagat	960
aaccaaggaa	aagttttagg	agatcaaatt	ctccgtgtgg	gtgaatattt	tatcgtcact	1020
ggtagttata	aagtattaaa	aattgatcaa	ccaagtaatg	gtatttatgt	tcaaacgga	1080
tctcgtggaa	catgggtaaa	tgctgataaa	gctaacaaat	tatag		1125

<210> SEQ ID NO 598

<211> LENGTH: 374

<212> TYPE: PRT

<213> ORGANISM: *Streptococcus pyogenes*

<400> SEQUENCE: 598

Met	Lys	Lys	Phe	His	Arg	Phe	Leu	Val	Ser	Gly	Val	Ile	Leu	Leu	Gly
1				5					10					15	
Phe	Asn	Gly	Leu	Val	Pro	Thr	Met	Pro	Ser	Thr	Leu	Ile	Ser	Gln	Gln
			20					25					30		
Glu	Asn	Leu	Val	His	Ala	Ala	Val	Leu	Gly	Asp	Asn	Tyr	Pro	Ser	Lys
			35				40					45			
Trp	Lys	Lys	Gly	Asn	Gly	Ile	Asp	Ser	Trp	Asn	Met	Tyr	Ile	Arg	Gln
	50				55					60					
Cys	Thr	Ser	Phe	Ala	Ala	Phe	Arg	Leu	Ser	Ser	Ala	Asn	Gly	Phe	Gln
65				70					75				80		
Leu	Pro	Lys	Gly	Tyr	Gly	Asn	Ala	Cys	Thr	Trp	Gly	His	Ile	Ala	Lys
			85					90					95		
Asn	Gln	Gly	Tyr	Pro	Val	Asn	Lys	Thr	Pro	Ser	Ile	Gly	Ala	Ile	Ala
		100					105					110			
Trp	Phe	Asp	Lys	Asn	Ala	Tyr	Gln	Ser	Asn	Ala	Ala	Tyr	Gly	His	Val
	115					120					125				
Ala	Trp	Val	Ala	Asp	Ile	Arg	Gly	Asp	Thr	Val	Thr	Ile	Glu	Glu	Tyr
	130				135					140					
Asn	Tyr	Asn	Ala	Gly	Gln	Gly	Pro	Glu	Arg	Tyr	His	Lys	Arg	Gln	Ile
145				150				155					160		
Pro	Lys	Ser	Gln	Val	Ser	Gly	Tyr	Ile	His	Phe	Lys	Asp	Leu	Ser	Ser
			165				170					175			
Gln	Thr	Ser	His	Ser	Tyr	Pro	Arg	Gln	Leu	Lys	His	Ile	Ser	Gln	Ala
		180				185						190			
Ser	Phe	Asp	Pro	Ser	Gly	Thr	Tyr	His	Phe	Thr	Thr	Arg	Leu	Pro	Val
	195				200						205				
Lys	Gly	Gln	Thr	Ser	Ile	Asp	Ser	Pro	Asp	Leu	Ala	Tyr	Tyr	Glu	Ala
	210				215					220					
Gly	Gln	Ser	Val	Tyr	Tyr	Asp	Lys	Val	Val	Thr	Ala	Gly	Gly	Tyr	Thr
225				230				235					240		
Trp	Leu	Ser	Tyr	Leu	Ser	Phe	Ser	Gly	Asn	Arg	Arg	Tyr	Ile	Pro	Ile
			245				250					255			
Lys	Glu	Pro	Ala	Gln	Ser	Val	Val	Gln	Asn	Asp	Asn	Thr	Lys	Pro	Ser
		260				265						270			
Ile	Lys	Val	Gly	Asp	Thr	Val	Thr	Phe	Pro	Gly	Val	Phe	Arg	Val	Asp
	275				280						285				
Gln	Leu	Val	Asn	Asn	Leu	Ile	Val	Asn	Lys	Glu	Leu	Ala	Gly	Gly	Asp

290	295	300
Pro Thr Pro Leu Asn Trp	Ile Asp Pro Thr Pro	Leu Asp Glu Thr Asp
305	310	315
Asn Gln Gly Lys Val Leu	Gly Asp Gln Ile Leu	Arg Val Gly Glu Tyr
325	330	335
Phe Ile Val Thr Gly Ser Tyr Lys	Val Leu Lys Ile Asp	Gln Pro Ser
340	345	350
Asn Gly Ile Tyr Val Gln Ile	Gly Ser Arg Gly Thr	Trp Val Asn Ala
355	360	365
Asp Lys Ala Asn Lys Leu		
370		

<210> SEQ ID NO 599

<211> LENGTH: 1197

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 599

atgaaaaaaa	gaattttatc	agcagttctt	gtaagtgggtg	ttaccctcgg	agcagctaca	60
actgtaggag	cggaggattt	aagtactaag	attgctaagc	aagattctat	tatctcaa	120
ctgactacag	agcaaaaagc	tgacagaat	caagtttcag	cggtacaggc	tcaagtaagt	180
tcactacaat	ctgaacaaga	taaactgacc	gcaagaaata	cagaacttga	ggcgctttca	240
aagcgatttg	agcaagaaat	taaggctcta	acaagtcaaa	ttgttgctcg	taatgaaaaa	300
ttaaaaaatc	aagctcgtag	tgcttataaa	aacaatgaaa	cttctgggta	tattaatgca	360
cttttggaatt	ctaaatcaat	ttctgatggt	gtaaaccggt	tagtagcaat	taatagagct	420
gtctctgcta	acgctaaaatt	gtagaacia	caaaaagctg	ataaagtttc	ccttgaagaa	480
aagcaagctg	ctaaccaaaac	agctattaat	accattgccg	ctaatatggc	aatggctgaa	540
gaaaacaaaa	atacattacg	tactcaacia	gctaatttgg	tagctgcaac	tgcaaattta	600
gctctccaat	tagcatctgc	tactgaagat	aaagctaatt	tggtagctca	aaaagaagct	660
gcagaaaaag	ctgctgctga	agccttagca	caagaacagg	ctgctaaagt	taaggcacaa	720
gaacaggctg	cacaacaagc	agcatctggt	gaagcagcaa	aatctgctat	tactccagca	780
ccacaagcta	ctccggcagc	gcaaagtagt	aatgctattg	aaccagctgc	actcacggct	840
ccggcagctc	cttctgcagg	accacaaaca	tcatatgatt	cttctaatac	ttatccagtt	900
ggacaatgca	catggggagc	taaattcttta	gctccttggg	caggaaataa	ttggggaaat	960
gggtgggtcaat	gggcttatag	tgctcaagca	gctgggtatc	gtactgggtc	aacgccgatg	1020
gtagggtgcga	ttgccgtttg	gaacgatggg	ggttatggac	atgtcgccgt	tgtagttgag	1080
gttcaaaagtg	cctcaagtat	tcgtgtgatg	gagtctaact	acagtggtag	acagtacatt	1140
gctgaccacc	gtggctgggt	taatccaaca	ggtgttacat	ttatttatcc	acactaa	1197

<210> SEQ ID NO 600

<211> LENGTH: 398

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 600

Met	Lys	Lys	Arg	Ile	Leu	Ser	Ala	Val	Leu	Val	Ser	Gly	Val	Thr	Leu
1				5					10					15	
Gly	Ala	Ala	Thr	Thr	Val	Gly	Ala	Glu	Asp	Leu	Ser	Thr	Lys	Ile	Ala
			20					25					30		
Lys	Gln	Asp	Ser	Ile	Ile	Ser	Asn	Leu	Thr	Thr	Glu	Gln	Lys	Ala	Ala
		35				40					45				
Gln	Asn	Gln	Val	Ser	Ala	Leu	Gln	Ala	Gln	Val	Ser	Ser	Leu	Gln	Ser
	50					55				60					
Glu	Gln	Asp	Lys	Leu	Thr	Ala	Arg	Asn	Thr	Glu	Leu	Glu	Ala	Leu	Ser
65				70					75					80	
Lys	Arg	Phe	Glu	Gln	Glu	Ile	Lys	Ala	Leu	Thr	Ser	Gln	Ile	Val	Ala
				85				90					95		
Arg	Asn	Glu	Lys	Leu	Lys	Asn	Gln	Ala	Arg	Ser	Ala	Tyr	Lys	Asn	Asn
			100					105					110		

Glu	Thr	Ser	Gly	Tyr	Ile	Asn	Ala	Leu	Leu	Asn	Ser	Lys	Ser	Ile	Ser		
		115					120					125					
Asp	Val	Val	Asn	Arg	Leu	Val	Ala	Ile	Asn	Arg	Ala	Val	Ser	Ala	Asn		
		130					135					140					
Ala	Lys	Leu	Leu	Glu	Gln	Gln	Lys	Ala	Asp	Lys	Val	Ser	Leu	Glu	Glu		
					150					155					160		
Lys	Gln	Ala	Ala	Asn	Gln	Thr	Ala	Ile	Asn	Thr	Ile	Ala	Ala	Asn	Met		
				165					170						175		
Ala	Met	Ala	Glu	Glu	Asn	Gln	Asn	Thr	Leu	Arg	Thr	Gln	Gln	Ala	Asn		
			180					185					190				
Leu	Val	Ala	Ala	Thr	Ala	Asn	Leu	Ala	Leu	Gln	Leu	Ala	Ser	Ala	Thr		
		195					200					205					
Glu	Asp	Lys	Ala	Asn	Leu	Val	Ala	Gln	Lys	Glu	Ala	Ala	Glu	Lys	Ala		
		210				215					220						
Ala	Ala	Glu	Ala	Leu	Ala	Gln	Glu	Gln	Ala	Ala	Lys	Val	Lys	Ala	Gln		
				230						235					240		
Glu	Gln	Ala	Ala	Gln	Gln	Ala	Ala	Ser	Val	Glu	Ala	Ala	Lys	Ser	Ala		
				245					250						255		
Ile	Thr	Pro	Ala	Pro	Gln	Ala	Thr	Pro	Ala	Ala	Gln	Ser	Ser	Asn	Ala		
			260					265						270			
Ile	Glu	Pro	Ala	Ala	Leu	Thr	Ala	Pro	Ala	Ala	Pro	Ser	Ala	Gly	Pro		
		275					280					285					
Gln	Thr	Ser	Tyr	Asp	Ser	Ser	Asn	Thr	Tyr	Pro	Val	Gly	Gln	Cys	Thr		
		290				295					300						
Trp	Gly	Ala	Lys	Ser	Leu	Ala	Pro	Trp	Ala	Gly	Asn	Asn	Trp	Gly	Asn		
					310					315					320		
Gly	Gly	Gln	Trp	Ala	Tyr	Ser	Ala	Gln	Ala	Ala	Gly	Tyr	Arg	Thr	Gly		
				325					330						335		
Ser	Thr	Pro	Met	Val	Gly	Ala	Ile	Ala	Val	Trp	Asn	Asp	Gly	Gly	Tyr		
			340					345					350				
Gly	His	Val	Ala	Val	Val	Val	Glu	Val	Gln	Ser	Ala	Ser	Ser	Ile	Arg		
		355					360					365					
Val	Met	Glu	Ser	Asn	Tyr	Ser	Gly	Arg	Gln	Tyr	Ile	Ala	Asp	His	Arg		
		370				375					380						
Gly	Trp	Phe	Asn	Pro	Thr	Gly	Val	Thr	Phe	Ile	Tyr	Pro	His				
					390					395							

<210> SEQ ID NO 601

<211> LENGTH: 1287

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 601

atgagaaaat	tattagcggc	tatgttaatg	actttttttc	tgactccttt	accagtgatt	60
agtacagaaa	aaaaacttat	attttcaaaa	aatgctgttt	atcaattgaa	acaagatgtc	120
gttcaatcaa	cacaattcta	taatcaaata	ccctctaata	caaatactta	tcaagaaacg	180
tgtgcctata	aagacagtga	tttaactcta	ccagcaggaa	gattaggtgt	aaatcaacca	240
ttacttatta	aatcgcttgt	gcttaacaaa	gaatctttac	cggtttttga	gttagctgat	300
ggtacctatg	ttgaggctaa	tcgacaattg	atztatgacg	atattgtact	taatcaagta	360
gatatataga	gctatttttg	gacacaaaag	aaacttaggc	tttattcagc	cccttatggt	420
ttaggtagcg	aaacaattcc	ttcttctttt	ttatttgctc	aaaaagttca	tgccactcaa	480
atggcacaaa	caaaccatgg	aacttattat	cttattgatg	ataagggctg	ggcatcacia	540
gaagatctag	ttcaatttga	taaccgcatg	ttaaaagtcc	aggaaatgct	cttacaaaaa	600
tataataacc	caaattattc	aatttttgta	aagcaactca	acacacaaac	aagtgtctggt	660
attaatgctg	ataaaaaaat	gtatgctgca	agtatctcga	agttagcacc	actttatatt	720
gttcaaaaac	aattacaaaa	aaagaaatta	gcagagaata	aaactttgac	ttatactaaa	780
gatgttaatc	attttttatg	agactatgat	ccattgggaa	gtggtaaaat	tagtaaaata	840
gctgataata	aagattatcg	tgttgaagac	ctactgaaag	ctgtagcaca	acaatcggat	900

aatgtagcaa	ctaataat	tttt	aggttatt	at	ctatgtcatc	agtatgataa	agctttccgc	960
tcagagataa	aagctttatc	aggatatcgat	tgggatatgg	agcagcgctt	attaacttct			1020
cgttcagctg	caaatatgat	ggaagctatt	tatcatcaaa	aaggccaaat	tatttcttac			1080
ctttcaaata	cgaatttga	tcaacaacgt	atcacaaaaa	atattactgt	tccagttgca			1140
cataaaattg	gtgatgctta	tgattataaaa	catgacgttg	ctattgttta	cggtaatact			1200
ccatttat	tttt	tgtctat	tttt	tacaaataaa	tcaacctatg	aagatattac	ggctattgca	1260
gatgacgt	ttt	atgg	tatttt	aaaatga				1287

<210> SEQ ID NO 602

<211> LENGTH: 428

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 602

Met	Arg	Lys	Leu	Ala	Ala	Met	Leu	Met	Thr	Phe	Phe	Leu	Thr	Pro	
1			5					10				15			
Leu	Pro	Val	Ile	Ser	Thr	Glu	Lys	Lys	Leu	Ile	Phe	Ser	Lys	Asn	Ala
			20					25					30		
Val	Tyr	Gln	Leu	Lys	Gln	Asp	Val	Val	Gln	Ser	Thr	Gln	Phe	Tyr	Asn
		35					40					45			
Gln	Ile	Pro	Ser	Asn	Pro	Asn	Leu	Tyr	Gln	Glu	Thr	Cys	Ala	Tyr	Lys
		50				55					60				
Asp	Ser	Asp	Leu	Thr	Leu	Pro	Ala	Gly	Arg	Leu	Gly	Val	Asn	Gln	Pro
65					70				75					80	
Leu	Leu	Ile	Lys	Ser	Leu	Val	Leu	Asn	Lys	Glu	Ser	Leu	Pro	Val	Phe
			85					90					95		
Glu	Leu	Ala	Asp	Gly	Thr	Tyr	Val	Glu	Ala	Asn	Arg	Gln	Leu	Ile	Tyr
		100					105					110			
Asp	Asp	Ile	Val	Leu	Asn	Gln	Val	Asp	Ile	Asp	Ser	Tyr	Phe	Trp	Thr
		115				120						125			
Gln	Lys	Lys	Leu	Arg	Leu	Tyr	Ser	Ala	Pro	Tyr	Val	Leu	Gly	Thr	Gln
		130				135					140				
Thr	Ile	Pro	Ser	Ser	Phe	Leu	Phe	Ala	Gln	Lys	Val	His	Ala	Thr	Gln
145					150					155					160
Met	Ala	Gln	Thr	Asn	His	Gly	Thr	Tyr	Tyr	Leu	Ile	Asp	Asp	Lys	Gly
			165					170						175	
Trp	Ala	Ser	Gln	Glu	Asp	Leu	Val	Gln	Phe	Asp	Asn	Arg	Met	Leu	Lys
			180					185					190		
Val	Gln	Glu	Met	Leu	Leu	Gln	Lys	Tyr	Asn	Asn	Pro	Asn	Tyr	Ser	Ile
		195				200						205			
Phe	Val	Lys	Gln	Leu	Asn	Thr	Gln	Thr	Ser	Ala	Gly	Ile	Asn	Ala	Asp
		210				215					220				
Lys	Lys	Met	Tyr	Ala	Ala	Ser	Ile	Ser	Lys	Leu	Ala	Pro	Leu	Tyr	Ile
225					230					235					240
Val	Gln	Lys	Gln	Leu	Gln	Lys	Lys	Lys	Leu	Ala	Glu	Asn	Lys	Thr	Leu
			245					250						255	
Thr	Tyr	Thr	Lys	Asp	Val	Asn	His	Phe	Tyr	Gly	Asp	Tyr	Asp	Pro	Leu
			260					265					270		
Gly	Ser	Gly	Lys	Ile	Ser	Lys	Ile	Ala	Asp	Asn	Lys	Asp	Tyr	Arg	Val
		275				280						285			
Glu	Asp	Leu	Leu	Lys	Ala	Val	Ala	Gln	Gln	Ser	Asp	Asn	Val	Ala	Thr
		290				295					300				
Asn	Ile	Leu	Gly	Tyr	Tyr	Leu	Cys	His	Gln	Tyr	Asp	Lys	Ala	Phe	Arg
305					310					315					320
Ser	Glu	Ile	Lys	Ala	Leu	Ser	Gly	Ile	Asp	Trp	Asp	Met	Glu	Gln	Arg
			325					330					335		
Leu	Leu	Thr	Ser	Arg	Ser	Ala	Ala	Asn	Met	Met	Glu	Ala	Ile	Tyr	His
			340					345					350		

Gln	Lys	Gly	Gln	Ile	Ile	Ser	Tyr	Leu	Ser	Asn	Thr	Glu	Phe	Asp	Gln
		355					360					365			
Gln	Arg	Ile	Thr	Lys	Asn	Ile	Thr	Val	Pro	Val	Ala	His	Lys	Ile	Gly
	370					375					380				
Asp	Ala	Tyr	Asp	Tyr	Lys	His	Asp	Val	Ala	Ile	Val	Tyr	Gly	Asn	Thr
385					390					395					400
Pro	Phe	Ile	Leu	Ser	Ile	Phe	Thr	Asn	Lys	Ser	Thr	Tyr	Glu	Asp	Ile
			405						410					415	
Thr	Ala	Ile	Ala	Asp	Asp	Val	Tyr	Gly	Ile	Leu	Lys				
			420					425							

<210> SEQ ID NO 603

<211> LENGTH: 2577

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 603

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attatattta	tcatccttct	atcgatgggc	atttattata	atagtataaa	aacaattcta	120
gctagtgatg	cttttcatca	gtatgttatt	tttgcgagc	actttcgtaa	catcatgcac	180
ggttctgata	gtttttttta	tacctttaca	agcggactag	ggataaattt	ttatgcttta	240
atgtgttatt	atcttggcag	tttcttttct	ccattacttt	tcttttttaa	tttaacctct	300
atgccagatg	ctatctatct	gtttaccttg	ataaaatttg	ggttaatagg	attagctgca	360
tgctattctt	ttcatagatt	atatccaaaa	atcagtgcct	tcttgatgat	ttccatctca	420
gttttttata	gcttaaatgag	cttcttgaca	agtcaaattg	aactaaattc	ttgggttagat	480
gttttcatct	ttcttccact	tggtataact	ggattaaata	aacttatcac	agaaaaataa	540
accagaactt	attatctttc	gatatcatta	ttattcattc	aaaattacta	ctttggctac	600
atgattgctc	ttttttgtat	tctttacgcc	ttagtgtgtc	ttttacgtct	caatgatttt	660
aacaaaatgt	ttatcgcttt	tgtaggtgtt	acagctgtgt	caatatgtgc	tgctttaaca	720
agtgtcttag	taatacttcc	tacctatcta	gatttgtcaa	cttatggaga	gaatctatcc	780
ccgataaaac	agttagttac	gaacaatgct	tggttttttg	atatacctgc	taagctctca	840
ataggagtgt	acgatactac	caagttaaat	gctctgccta	tgatttacgt	aggattatct	900
cccctaattg	ttagtgttat	ttattttact	ttagaaagta	tccctttaaa	aataaaaatta	960
gccaatgcct	gcttggttaac	ttttattata	ataagttttt	acctacagcc	acttgatctt	1020
ttttggcagg	ggatgcactc	accaaataat	tttttgcata	gctacgcttg	gtctttttcc	1080
atagtatatc	tattactcgc	atgtgagact	ctctctcgac	taaaagaagt	gactcaaata	1140
aaagcagggt	ttgcttttat	tttctctatt	atactgacat	ctcttcctta	tagcttttct	1200
caacaatata	attttctacc	tttaactctt	tttttactta	gtgttttttt	attattaggt	1260
tatactatct	cactattttc	gtttagaaat	tctcaaattc	catctacttt	tatttctgct	1320
ttcatactta	tctttagcct	tcttgaatca	gggttaaaca	cctactacca	gcttcaagga	1380
attaataagg	agtggggatt	cccatcacga	cagatatata	atagtcaatt	aaaggatatt	1440
aacaaccttg	tcaactctgt	gtcaaaaaat	agtcaacctt	tttttagaat	ggaaaggcta	1500
cttcccaaaa	cagggaacga	tagcatgaaa	tttaattatt	acggcatttc	acaattttcc	1560
tctgtaagaa	atagactatc	tagttcttta	ttggatcgat	tggtatttca	gtctaaaggc	1620
acaaatttaa	accttagata	ccaaaacaat	actattatta	tggtacagtct	acttggtata	1680
aaatataatc	ttagcgaagg	acctccaaat	aaatttggat	ttacaaaact	aaaaactagc	1740
gggaataact	ctctttatca	aaatcactat	agtagccctt	tagctatatt	aacacgtaat	1800
gtttacaaag	atgtcaacct	aaatgtcaat	acccttgata	accaaaccac	attacttaac	1860
caactaagtg	ggaaatcttt	aacctatttt	aacttacagc	cagctcaact	tatttctggt	1920
gctaatacat	ttaacggaca	aatatctgca	caagcttctg	attatcaaaa	ctccgttacc	1980
cttaattatc	aaattaacat	ccctaaacat	agtcaactct	atgttagcat	acccaatatt	2040
atattttcaa	atcctgatgc	taaagagatg	cgtattcaga	cagataatca	taatttcata	2100
tatactacag	ataacgctta	ctcttttttt	gatttaggat	atttcgccga	tgccaaagtt	2160
gctacatttt	cgtttggttt	tccaaaaaat	aaacaaatta	gttttaagga	acctcatttt	2220
tatagtgtgt	ctattgaatc	ttaccttgaa	gcaattgaata	gcattaaaca	aaaaaatgtt	2280
catacttacy	ctaaaagtaa	tacggtaatc	actgattata	attcaaaaac	gaaaagttct	2340
cttattttta	cacttcctta	cgataaagg	tggtcagcac	aaaaagatgg	gaaaaatctt	2400
ccagtcaaaa	aagcacaagg	aggattttct	tcagttacta	ttcctaaagg	aaagggtacg	2460

gttatccctta cctttattcc taatgggtttt aaattagggt tatctctatc ttgtgtagga 2520
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<210> SEQ ID NO 604
 <211> LENGTH: 858
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 604

Met	Lys	Asn	Asn	Asn	Lys	Trp	Ile	Ile	Ala	Gly	Leu	Ala	Ser	Phe	Leu
1			5						10					15	
Phe	Pro	Leu	Ser	Ile	Ile	Phe	Ile	Ile	Leu	Leu	Ser	Met	Gly	Ile	Tyr
		20						25					30		
Tyr	Asn	Ser	Asp	Lys	Thr	Ile	Leu	Ala	Ser	Asp	Ala	Phe	His	Gln	Tyr
		35					40					45			
Val	Ile	Phe	Ala	Gln	Asn	Phe	Arg	Asn	Ile	Met	His	Gly	Ser	Asp	Ser
	50					55				60					
Phe	Phe	Tyr	Thr	Phe	Thr	Ser	Gly	Leu	Gly	Ile	Asn	Phe	Tyr	Ala	Leu
65					70					75					80
Met	Cys	Tyr	Tyr	Leu	Gly	Ser	Phe	Phe	Ser	Pro	Leu	Leu	Phe	Phe	Phe
				85					90					95	
Asn	Leu	Thr	Ser	Met	Pro	Asp	Ala	Ile	Tyr	Leu	Phe	Thr	Leu	Ile	Lys
			100					105					110		
Phe	Gly	Leu	Ile	Gly	Leu	Ala	Ala	Cys	Tyr	Ser	Phe	His	Arg	Leu	Tyr
	115					120						125			
Pro	Lys	Ile	Ser	Ala	Phe	Leu	Met	Ile	Ser	Ile	Ser	Val	Phe	Tyr	Ser
	130					135					140				
Leu	Met	Ser	Phe	Leu	Thr	Ser	Gln	Met	Glu	Leu	Asn	Ser	Trp	Leu	Asp
145					150					155					160
Val	Phe	Ile	Leu	Leu	Pro	Leu	Val	Ile	Leu	Gly	Leu	Asn	Lys	Leu	Ile
			165						170					175	
Thr	Glu	Asn	Lys	Thr	Arg	Thr	Tyr	Tyr	Leu	Ser	Ile	Ser	Leu	Leu	Phe
			180					185					190		
Ile	Gln	Asn	Tyr	Tyr	Phe	Gly	Tyr	Met	Ile	Ala	Leu	Phe	Cys	Ile	Leu
	195					200						205			
Tyr	Ala	Leu	Val	Cys	Leu	Leu	Arg	Leu	Asn	Asp	Phe	Asn	Lys	Met	Phe
	210					215					220				
Ile	Ala	Phe	Val	Arg	Phe	Thr	Ala	Val	Ser	Ile	Cys	Ala	Ala	Leu	Thr
225					230					235					240
Ser	Ala	Leu	Val	Ile	Leu	Pro	Thr	Tyr	Leu	Asp	Leu	Ser	Thr	Tyr	Gly
			245						250					255	
Glu	Asn	Leu	Ser	Pro	Ile	Lys	Gln	Leu	Val	Thr	Asn	Asn	Ala	Trp	Phe
		260						265					270		
Leu	Asp	Ile	Pro	Ala	Lys	Leu	Ser	Ile	Gly	Val	Tyr	Asp	Thr	Thr	Lys
	275						280				285				
Phe	Asn	Ala	Leu	Pro	Met	Ile	Tyr	Val	Gly	Leu	Phe	Pro	Leu	Met	Leu
	290					295					300				
Ser	Val	Ile	Tyr	Phe	Thr	Leu	Glu	Ser	Ile	Pro	Leu	Lys	Ile	Lys	Leu
305					310					315					320
Ala	Asn	Ala	Cys	Leu	Leu	Thr	Phe	Ile	Ile	Ile	Ser	Phe	Tyr	Leu	Gln
			325						330					335	
Pro	Leu	Asp	Leu	Phe	Trp	Gln	Gly	Met	His	Ser	Pro	Asn	Met	Phe	Leu
		340					345						350		
His	Arg	Tyr	Ala	Trp	Ser	Phe	Ser	Ile	Val	Ile	Leu	Leu	Ala	Cys	
	355					360					365				
Glu	Thr	Leu	Ser	Arg	Leu	Lys	Glu	Val	Thr	Gln	Ile	Lys	Ala	Gly	Phe
	370					375					380				
Ala	Phe	Ile	Phe	Leu	Ile	Ile	Leu	Thr	Ser	Leu	Pro	Tyr	Ser	Phe	Ser

385					390					395					400
Gln	Gln	Tyr	Asn	Phe	Leu	Pro	Leu	Thr	Leu	Phe	Leu	Leu	Ser	Val	Phe
				405					410					415	
Leu	Leu	Leu	Gly	Tyr	Thr	Ile	Ser	Leu	Phe	Ser	Phe	Arg	Asn	Ser	Gln
			420					425					430		
Ile	Pro	Ser	Thr	Phe	Ile	Ser	Ala	Phe	Ile	Leu	Ile	Phe	Ser	Leu	Leu
		435					440					445			
Glu	Ser	Gly	Leu	Asn	Thr	Tyr	Tyr	Gln	Leu	Gln	Gly	Ile	Asn	Lys	Glu
	450					455					460				
Trp	Gly	Phe	Pro	Ser	Arg	Gln	Ile	Tyr	Asn	Ser	Gln	Leu	Lys	Asp	Ile
465					470					475					480
Asn	Asn	Leu	Val	Asn	Ser	Val	Ser	Lys	Asn	Ser	Gln	Pro	Phe	Phe	Arg
				485					490					495	
Met	Glu	Arg	Leu	Leu	Pro	Gln	Thr	Gly	Asn	Asp	Ser	Met	Lys	Phe	Asn
			500					505					510		
Tyr	Tyr	Gly	Ile	Ser	Gln	Phe	Ser	Ser	Val	Arg	Asn	Arg	Leu	Ser	Ser
		515					520					525			
Ser	Leu	Leu	Asp	Arg	Leu	Gly	Phe	Gln	Ser	Lys	Gly	Thr	Asn	Leu	Asn
	530					535					540				
Leu	Arg	Tyr	Gln	Asn	Asn	Thr	Ile	Ile	Met	Asp	Ser	Leu	Leu	Gly	Ile
545					550					555					560
Lys	Tyr	Asn	Leu	Ser	Glu	Gly	Pro	Pro	Asn	Lys	Phe	Gly	Phe	Thr	Lys
				565					570					575	
Leu	Lys	Thr	Ser	Gly	Asn	Thr	Thr	Leu	Tyr	Gln	Asn	His	Tyr	Ser	Ser
			580					585					590		
Pro	Leu	Ala	Ile	Leu	Thr	Arg	Asn	Val	Tyr	Lys	Asp	Val	Asn	Leu	Asn
		595					600					605			
Val	Asn	Thr	Leu	Asp	Asn	Gln	Thr	Lys	Leu	Leu	Asn	Gln	Leu	Ser	Gly
	610					615					620				
Lys	Ser	Leu	Thr	Tyr	Phe	Asn	Leu	Gln	Pro	Ala	Gln	Leu	Ile	Ser	Gly
625					630					635					640
Ala	Asn	Gln	Phe	Asn	Gly	Gln	Ile	Ser	Ala	Gln	Ala	Ser	Asp	Tyr	Gln
				645					650					655	
Asn	Ser	Val	Thr	Leu	Asn	Tyr	Gln	Ile	Asn	Ile	Pro	Lys	His	Ser	Gln
			660					665					670		
Leu	Tyr	Val	Ser	Ile	Pro	Asn	Ile	Ile	Phe	Ser	Asn	Pro	Asp	Ala	Lys
		675					680					685			
Glu	Met	Arg	Ile	Gln	Thr	Asp	Asn	His	Asn	Phe	Ile	Tyr	Thr	Thr	Asp
	690					695				700					
Asn	Ala	Tyr	Ser	Phe	Phe	Asp	Leu	Gly	Tyr	Phe	Ala	Asp	Ala	Lys	Val
705					710					715					720
Ala	Thr	Phe	Ser	Phe	Val	Phe	Pro	Lys	Asn	Lys	Gln	Ile	Ser	Phe	Lys
				725					730					735	
Glu	Pro	His	Phe	Tyr	Ser	Leu	Ser	Ile	Glu	Ser	Tyr	Leu	Glu	Ala	Met
			740					745					750		
Asn	Ser	Ile	Lys	Gln	Lys	Asn	Val	His	Thr	Tyr	Ala	Lys	Ser	Asn	Thr
		755					760					765			
Val	Ile	Thr	Asp	Tyr	Asn	Ser	Lys	Thr	Lys	Gly	Ser	Leu	Ile	Phe	Thr
	770					775					780				
Leu	Pro	Tyr	Asp	Lys	Gly	Trp	Ser	Ala	Gln	Lys	Asp	Gly	Lys	Asn	Leu
785					790					795					800
Pro	Val	Lys	Lys	Ala	Gln	Gly	Gly	Phe	Leu	Ser	Val	Thr	Ile	Pro	Lys
				805					810					815	
Gly	Lys	Gly	Arg	Val	Ile	Leu	Thr	Phe	Ile	Pro	Asn	Gly	Phe	Lys	Leu
			820					825					830		
Gly	Leu	Ser	Leu	Ser	Cys	Val	Gly	Ile	Ile	Ala	Tyr	Met	Leu	Leu	Tyr
		835					840					845			

Lys Tyr Ile Asp Ile Lys Ser Lys Leu Leu
850 855

<210> SEQ ID NO 605
<211> LENGTH: 864
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 605

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ttattttcat tagctgtttg gttaattggt agacctgaga tgacactgca actttggctt      180
tttggaatat tgggtggttt tatctggtca attggtcaaa ctggtcaatt tcatgccatg      240
caatacatgg gagtctccgt tgccaatcct ttgtcaagtg gctctcaact tgttctggga      300
agtttgattg gtgtcctcgt ttttcatgaa tggacaagac ctatgcaatt tgtagtagga      360
agtctagcac tattacttct gattgttggt ttttactttt ctagtaaaca agatgatgct      420
aatgcacaag tcaatcacct tcataatttt tcaaaaggat ttagggcgct cacttattca      480
acaattgggtt acgtgatgta tgctgtatta tttaataaca tcatgaaatt tgaagttttg      540
tcagtcattt taccatggc agtaggtatg gttttaggag ctataacttt catgtcattt      600
aaaattttcca ttgaccagta tgtgattaaa aatagcgttg ttggattact ttggggcatt      660
gggaatatatt ttatgctttt agctgcatca aaagcaggac ttgctattgc ctttagtttc      720
tcacaattag gtgctatcat ttcgattgtc ggaggcattt tattcctagg cgaaaccaaa      780
accaaaaaag aaatgcgttg ggttgtcaca ggaattattt gttttatcgt aggtgctatt      840
ttattagggtg tgggtcaaattc ttaa

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<210> SEQ ID NO 606
<211> LENGTH: 287
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 606

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Met Glu Gly Ile Phe Tyr Ala Leu Ile Pro Met Phe Thr Trp Gly Ser
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Ile Gly Phe Val Ser Asn Lys Ile Gly Gly Lys Pro Ser Gln Thr
20     25     30
Leu Gly Met Thr Phe Gly Ala Leu Leu Phe Ser Leu Ala Val Trp Leu
35     40     45
Ile Val Arg Pro Glu Met Thr Leu Gln Leu Trp Leu Phe Gly Ile Leu
50     55     60
Gly Gly Phe Ile Trp Ser Ile Gly Gln Thr Gly Gln Phe His Ala Met
65     70     75     80
Gln Tyr Met Gly Val Ser Val Ala Asn Pro Leu Ser Ser Gly Ser Gln
85     90     95
Leu Val Leu Gly Ser Leu Ile Gly Val Leu Val Phe His Glu Trp Thr
100    105    110
Arg Pro Met Gln Phe Val Val Gly Ser Leu Ala Leu Leu Leu Ile
115    120    125
Val Gly Phe Tyr Phe Ser Ser Lys Gln Asp Asp Ala Asn Ala Gln Val
130    135    140
Asn His Leu His Asn Phe Ser Lys Gly Phe Arg Ala Leu Thr Tyr Ser
145    150    155    160
Thr Ile Gly Tyr Val Met Tyr Ala Val Leu Phe Asn Asn Ile Met Lys
165    170    175
Phe Glu Val Leu Ser Val Ile Leu Pro Met Ala Val Gly Met Val Leu
180    185    190
Gly Ala Ile Thr Phe Met Ser Phe Lys Ile Ser Ile Asp Gln Tyr Val
195    200    205
Ile Lys Asn Ser Val Val Gly Leu Leu Trp Gly Ile Gly Asn Ile Phe
210    215    220

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Met	Leu	Leu	Ala	Ala	Ser	Lys	Ala	Gly	Leu	Ala	Ile	Ala	Phe	Ser	Phe
225					230					235					240
Ser	Gln	Leu	Gly	Ala	Ile	Ile	Ser	Ile	Val	Gly	Gly	Ile	Leu	Phe	Leu
			245						250					255	
Gly	Glu	Thr	Lys	Thr	Lys	Lys	Glu	Met	Arg	Trp	Val	Val	Thr	Gly	Ile
			260					265					270		
Ile	Cys	Phe	Ile	Val	Gly	Ala	Ile	Leu	Leu	Gly	Val	Val	Lys	Ser	
		275					280						285		

<210> SEQ ID NO 607

<211> LENGTH: 915

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 607

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gctaccaaag	ctcttgccaa	agagatgttg	cccatcgttg	ataaaccaac	catccagttt	120
atcgtcgaag	aagcgctaaa	atctggcatc	gaggaaatcc	ttgtggtgac	cggaaaagct	180
aaacgctcta	tcgaggacca	ttttgattca	aactttgaat	tagaatacaa	cctccaagct	240
aaggggaaaa	atgaactggt	gaaattagtg	gatgaaacca	ctgccattaa	ccttcatttt	300
atccgtcaaa	gccacccaag	agggtggga	gatgctgtct	tacaagccaa	agcctttgtg	360
ggcaatgaac	cctttgtggt	catgcttgga	gatgacttaa	tggacattac	aaatgcatcc	420
gctaaacctc	tcaccaaaca	actcatggag	gactatgaca	agacgcatgc	atccactatc	480
gctgtgatga	aagttcctca	tgaagatgtg	tctagctatg	gggttatcgc	tcctcaaggc	540
aaggctgtca	agggccttta	cagtgtagac	acctttgttg	aaaaaccaca	accagaagat	600
gcgcctagtg	atttggttat	tattggtcgt	tacctcctaa	cccctgaaat	ttttggtatt	660
ttggaaagac	agacccctgg	agcaggtaac	gaagtgcac	tcacagatgc	tatcgatacc	720
ctcaataaaa	ctcagcgtgt	ctttgcacga	gaatttaaag	gcaatcggtta	cgatgttggg	780
gataaatttg	gattcatgaa	aacatctatc	gactatgcct	tagaacaccc	acaggtcaaa	840
gaggacttga	aaaattacat	tatcaaacta	ggaaaagctt	tggaaaaaag	taaagtacca	900
acacattcaa	agtaa					915

<210> SEQ ID NO 608

<211> LENGTH: 304

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 608

Met	Thr	Lys	Val	Arg	Lys	Ala	Ile	Ile	Pro	Ala	Ala	Gly	Leu	Gly	Thr
1				5					10					15	
Arg	Phe	Leu	Pro	Ala	Thr	Lys	Ala	Leu	Ala	Lys	Glu	Met	Leu	Pro	Ile
			20					25					30		
Val	Asp	Lys	Pro	Thr	Ile	Gln	Phe	Ile	Val	Glu	Glu	Ala	Leu	Lys	Ser
		35				40						45			
Gly	Ile	Glu	Glu	Ile	Leu	Val	Val	Thr	Gly	Lys	Ala	Lys	Arg	Ser	Ile
	50				55						60				
Glu	Asp	His	Phe	Asp	Ser	Asn	Phe	Glu	Leu	Glu	Tyr	Asn	Leu	Gln	Ala
65				70					75					80	
Lys	Gly	Lys	Asn	Glu	Leu	Leu	Lys	Leu	Val	Asp	Glu	Thr	Thr	Ala	Ile
			85					90						95	
Asn	Leu	His	Phe	Ile	Arg	Gln	Ser	His	Pro	Arg	Gly	Leu	Gly	Asp	Ala
			100					105					110		
Val	Leu	Gln	Ala	Lys	Ala	Phe	Val	Gly	Asn	Glu	Pro	Phe	Val	Val	Met
		115					120					125			
Leu	Gly	Asp	Asp	Leu	Met	Asp	Ile	Thr	Asn	Ala	Ser	Ala	Lys	Pro	Leu
	130				135						140				
Thr	Lys	Gln	Leu	Met	Glu	Asp	Tyr	Asp	Lys	Thr	His	Ala	Ser	Thr	Ile
145				150					155					160	
Ala	Val	Met	Lys	Val	Pro	His	Glu	Asp	Val	Ser	Ser	Tyr	Gly	Val	Ile

				165					170					175			
Ala	Pro	Gln	Gly	Lys	Ala	Val	Lys	Gly	Leu	Tyr	Ser	Val	Asp	Thr	Phe		
			180					185					190				
Val	Glu	Lys	Pro	Gln	Pro	Glu	Asp	Ala	Pro	Ser	Asp	Leu	Ala	Ile	Ile		
		195					200					205					
Gly	Arg	Tyr	Leu	Leu	Thr	Pro	Glu	Ile	Phe	Gly	Ile	Leu	Glu	Arg	Gln		
	210					215					220						
Thr	Pro	Gly	Ala	Gly	Asn	Glu	Val	Gln	Leu	Thr	Asp	Ala	Ile	Asp	Thr		
225					230					235				240			
Leu	Asn	Lys	Thr	Gln	Arg	Val	Phe	Ala	Arg	Glu	Phe	Lys	Gly	Asn	Arg		
			245					250					255				
Tyr	Asp	Val	Gly	Asp	Lys	Phe	Gly	Phe	Met	Lys	Thr	Ser	Ile	Asp	Tyr		
	260						265						270				
Ala	Leu	Glu	His	Pro	Gln	Val	Lys	Glu	Asp	Leu	Lys	Asn	Tyr	Ile	Ile		
	275					280						285					
Lys	Leu	Gly	Lys	Ala	Leu	Glu	Lys	Ser	Lys	Val	Pro	Thr	His	Ser	Lys		
	290					295					300						

<210> SEQ ID NO 609
 <211> LENGTH: 1338
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 609

ttgacattac	cccttattta	tattagaata	tcgagggtccc	tgtctttcaa	ggaaattaaa	60
aaagaaagag	gtgtaattgt	gcctatTTTT	aaaaaaaaactt	taattgtttt	atcctttatt	120
tttttgatat	ctatcttgat	ttatctaaat	atgtatctat	ttggaacatc	aactgtagga	180
atztatggag	taatattaat	aacctatcta	gttattaaac	ttggattatc	tttcctttat	240
gagccattta	aaggaaagcc	acatgactat	aaagttgctg	ctgtaattcc	ttcttataat	300
gaagatgccg	agtcattatt	agaaactcct	aaaagtgtgt	tagcacagac	ctatccgtta	360
tcagaaattt	atattgttga	tgatgggagt	tcaaacacag	atgcaataca	attaattgaa	420
gagtatgtaa	atagagaagt	ggatatttgt	cgaacggtta	tcgttcaccg	ttcccttgtc	480
aataaaggaa	aacgccatgc	tcaagcgtgg	gcatttgaaa	gatctgacgc	tgacgttttt	540
ttaaccgtag	attcagatac	ttatatctat	ccaaatgcct	tagaagaact	cctaaaaagc	600
ttcaatgatg	agacagttta	tgctgcaaca	ggacatttga	atgctagaaa	cagacaaaact	660
aatctattaa	cgcgacttac	agatatccgt	tacgataatg	cctttggggg	ggagcgtgct	720
gctcaatcat	taacaggtaa	tatttttagtt	tgctcaggac	cattgagtat	ttatcgacgt	780
gaagtgatta	ttcctaactt	agagcgctat	aaaaatcaaa	cattcctagg	tttacctggt	840
agcattgggg	atgatcgatg	tttaacaaat	tatgctattg	atttaggacg	cactgtctac	900
caatcaacag	ctagatgtga	tactgatgta	cctttccaat	taaaaagtta	tttaaagcaa	960
caaaatcgat	ggaataaatc	tttttttaga	gaatctatta	tttctgttaa	aaaaattcct	1020
tctaatacca	tcggtgcctt	atggactatt	ttcgaaatcg	ttatgtttat	gatgttgatt	1080
gtcgcaattg	ggaatctttt	gtttaatcaa	gctattcaat	tagaccttat	taaacttttt	1140
gcctttttat	ccatcatcct	tatcgttgct	ttatgtcgta	atgttcatta	tatgatcaaa	1200
catcctgcta	gttttttggt	atctcctctg	tatggaatat	tacacttggt	tgtcttacag	1260
cccctaaaac	tttattcttt	atgcaccatt	aaaaatacgg	aatggggaac	acgtaaaaag	1320
gtcactattt	ttaaataa					1338

<210> SEQ ID NO 610
 <211> LENGTH: 445
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 610

Met	Thr	Leu	Pro	Leu	Ile	Tyr	Ile	Arg	Ile	Ser	Arg	Ser	Leu	Ser	Phe
1			5					10					15		
Lys	Glu	Ile	Lys	Lys	Glu	Arg	Gly	Val	Ile	Val	Pro	Ile	Phe	Lys	Lys
			20				25				30				
Thr	Leu	Ile	Val	Leu	Ser	Phe	Ile	Phe	Leu	Ile	Ser	Ile	Leu	Ile	Tyr

	35					40					45				
Leu	Asn	Met	Tyr	Leu	Phe	Gly	Thr	Ser	Thr	Val	Gly	Ile	Tyr	Gly	Val
	50					55					60				
Ile	Leu	Ile	Thr	Tyr	Leu	Val	Ile	Lys	Leu	Gly	Leu	Ser	Phe	Leu	Tyr
65					70					75					80
Glu	Pro	Phe	Lys	Gly	Lys	Pro	His	Asp	Tyr	Lys	Val	Ala	Ala	Val	Ile
				85					90					95	
Pro	Ser	Tyr	Asn	Glu	Asp	Ala	Glu	Ser	Leu	Leu	Glu	Thr	Leu	Lys	Ser
			100					105					110		
Val	Leu	Ala	Gln	Thr	Tyr	Pro	Leu	Ser	Glu	Ile	Tyr	Ile	Val	Asp	Asp
		115					120					125			
Gly	Ser	Ser	Asn	Thr	Asp	Ala	Ile	Gln	Leu	Ile	Glu	Glu	Tyr	Val	Asn
	130					135					140				
Arg	Glu	Val	Asp	Ile	Cys	Arg	Asn	Val	Ile	Val	His	Arg	Ser	Leu	Val
145					150					155					160
Asn	Lys	Gly	Lys	Arg	His	Ala	Gln	Ala	Trp	Ala	Phe	Glu	Arg	Ser	Asp
			165						170					175	
Ala	Asp	Val	Phe	Leu	Thr	Val	Asp	Ser	Asp	Thr	Tyr	Ile	Tyr	Pro	Asn
		180						185					190		
Ala	Leu	Glu	Glu	Leu	Leu	Lys	Ser	Phe	Asn	Asp	Glu	Thr	Val	Tyr	Ala
	195						200					205			
Ala	Thr	Gly	His	Leu	Asn	Ala	Arg	Asn	Arg	Gln	Thr	Asn	Leu	Leu	Thr
	210					215					220				
Arg	Leu	Thr	Asp	Ile	Arg	Tyr	Asp	Asn	Ala	Phe	Gly	Val	Glu	Arg	Ala
225					230					235					240
Ala	Gln	Ser	Leu	Thr	Gly	Asn	Ile	Leu	Val	Cys	Ser	Gly	Pro	Leu	Ser
			245						250					255	
Ile	Tyr	Arg	Arg	Glu	Val	Ile	Ile	Pro	Asn	Leu	Glu	Arg	Tyr	Lys	Asn
		260						265					270		
Gln	Thr	Phe	Leu	Gly	Leu	Pro	Val	Ser	Ile	Gly	Asp	Asp	Arg	Cys	Leu
	275						280					285			
Thr	Asn	Tyr	Ala	Ile	Asp	Leu	Gly	Arg	Thr	Val	Tyr	Gln	Ser	Thr	Ala
	290					295					300				
Arg	Cys	Asp	Thr	Asp	Val	Pro	Phe	Gln	Leu	Lys	Ser	Tyr	Leu	Lys	Gln
305					310					315					320
Gln	Asn	Arg	Trp	Asn	Lys	Ser	Phe	Phe	Arg	Glu	Ser	Ile	Ile	Ser	Val
			325						330					335	
Lys	Lys	Ile	Leu	Ser	Asn	Pro	Ile	Val	Ala	Leu	Trp	Thr	Ile	Phe	Glu
		340						345					350		
Ile	Val	Met	Phe	Met	Met	Leu	Ile	Val	Ala	Ile	Gly	Asn	Leu	Leu	Phe
	355						360					365			
Asn	Gln	Ala	Ile	Gln	Leu	Asp	Leu	Ile	Lys	Leu	Phe	Ala	Phe	Leu	Ser
	370					375					380				
Ile	Ile	Phe	Ile	Val	Ala	Leu	Cys	Arg	Asn	Val	His	Tyr	Met	Ile	Lys
385					390					395					400
His	Pro	Ala	Ser	Phe	Leu	Leu	Ser	Pro	Leu	Tyr	Gly	Ile	Leu	His	Leu
			405						410					415	
Phe	Val	Leu	Gln	Pro	Leu	Lys	Leu	Tyr	Ser	Leu	Cys	Thr	Ile	Lys	Asn
		420						425					430		
Thr	Glu	Trp	Gly	Thr	Arg	Lys	Lys	Val	Thr	Ile	Phe	Lys			
	435						440					445			

<210> SEQ ID NO 611

<211> LENGTH: 543

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 611

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atgataaaaa aagaaaatat tcctaatacta ttaactcttg ttcgaatcgc aatgattcct      60
ttctttcttt ttattacttc ctcatactaat aagggtggggg ggcataatttt tgcagctgtg      120
atTTTTgcaa ttgccagttt taccgattat ctagatgggt atcttgcgcg taagtggcat      180
gtagccagta atTTTtgaaa gtttgccgat cctctagcag ataagatgct tgtcatgagt      240
gcctttatca tgttagttgg acttggctta gttcctgcgt ggggtgtcagc tgttattatt      300
tgccgagaat tggcagtaac tggctcttca ttactacttg ttgaaaccgg aggaaaggtc      360
cttgccagctg ctatgccggg aaaaatcaaaa acagcgacac aaatgttgctc tattattttta      420
ttactttgcc attggatatt cctaggaaac gtcttactct atattgctct ttttttcact      480
atttattctg gatatgatta ttttaaagga gcaagctttc tttttaagga tacgtttaaa      540
taa                                                                    543

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<210> SEQ ID NO 612
 <211> LENGTH: 180
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 612

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Met Ile Lys Lys Glu Asn Ile Pro Asn Leu Leu Thr Leu Val Arg Ile
1           5           10           15
Ala Met Ile Pro Phe Phe Leu Phe Ile Thr Ser Ser Ser Asn Lys Val
20          25          30
Gly Trp His Ile Phe Ala Ala Val Ile Phe Ala Ile Ala Ser Phe Thr
35          40          45
Asp Tyr Leu Asp Gly Tyr Leu Ala Arg Lys Trp His Val Ala Ser Asn
50          55          60
Phe Gly Lys Phe Ala Asp Pro Leu Ala Asp Lys Met Leu Val Met Ser
65          70          75          80
Ala Phe Ile Met Leu Val Gly Leu Gly Leu Val Pro Ala Trp Val Ser
85          90          95
Ala Val Ile Ile Cys Arg Glu Leu Ala Val Thr Gly Leu Arg Leu Leu
100         105         110
Leu Val Glu Thr Gly Gly Lys Val Leu Ala Ala Ala Met Pro Gly Lys
115         120         125
Ile Lys Thr Ala Thr Gln Met Leu Ser Ile Ile Leu Leu Leu Cys His
130         135         140
Trp Ile Phe Leu Gly Asn Val Leu Leu Tyr Ile Ala Leu Phe Phe Thr
145         150         155         160
Ile Tyr Ser Gly Tyr Asp Tyr Phe Lys Gly Ala Ser Phe Leu Phe Lys
165         170         175
Asp Thr Phe Lys
180

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<210> SEQ ID NO 613
 <211> LENGTH: 921
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 613

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ttgctctttt tttcactatt tattctggat atgattatTTt taaaggagca agctttcttt      60
ttaaggatac gtttaaataa catgtcagct attattgaac ttaaaaaagt tacattttaa      120
taccataaaag accaagaaaa accaacatta gatggcgtat cgtttcatgt gaaacaaggT      180
gagtggctgt ctatcattgg ccataatgga tctggtaaTt caacgactat tcggttaatt      240
gatggattat tggaaccaga atcagggTct attattgttg atggagatct actaaccata      300
actaatgttt gggaaattcg tcataaaatt ggtatggTct ttcaaaaccc tgataatcag      360
tttgttggag caactgttga agatgatgtt gcttttgggc ttgaaaataa aggtattgca      420
catgaagata taaaagagag ggTtaatcat gctttagagt tagtcggcat gcagaacttt      480
aaagaaaaaag aaccagcccg tttatctggT ggccaaaaac agcgcgtagc tattgcaggt      540
gcagttgcta tgaagcctaa aattattatt ttagatgaag ctactagtat gcttgaccct      600
aaaggacgat tagagttaaT caaaactata aaaaacatcc gtgacgacta ccagctgact      660

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gttattttcca ttactcatga cttagatgaa gttgctctta gtgatagagt tttagtgatg	720
aaagatgggtc aagtggaatc aacatcaaca ccagaacaat tatttgcaag aggggatgaa	780
ctactccaat taggtcttga tatccctttt acaacatctg ttgtacagat gcttcaagaa	840
gaaggttatc ctgttgacta tggatatctc acagaaaagg aattagaaaa tcagttatgt	900
caattaatct ccaaaatgta a	921

<210> SEQ ID NO 614
 <211> LENGTH: 306
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 614

Met	Leu	Phe	Phe	Ser	Leu	Phe	Ile	Leu	Asp	Met	Ile	Ile	Leu	Lys	Glu
1				5					10					15	
Gln	Ala	Phe	Phe	Leu	Arg	Ile	Arg	Leu	Asn	Asn	Met	Ser	Ala	Ile	Ile
			20					25					30		
Glu	Leu	Lys	Lys	Val	Thr	Phe	Asn	Tyr	His	Lys	Asp	Gln	Glu	Lys	Pro
		35					40					45			
Thr	Leu	Asp	Gly	Val	Ser	Phe	His	Val	Lys	Gln	Gly	Glu	Trp	Leu	Ser
	50					55					60				
Ile	Ile	Gly	His	Asn	Gly	Ser	Gly	Lys	Ser	Thr	Thr	Ile	Arg	Leu	Ile
65				70					75					80	
Asp	Gly	Leu	Leu	Glu	Pro	Glu	Ser	Gly	Ser	Ile	Ile	Val	Asp	Gly	Asp
			85					90					95		
Leu	Leu	Thr	Ile	Thr	Asn	Val	Trp	Glu	Ile	Arg	His	Lys	Ile	Gly	Met
		100						105					110		
Val	Phe	Gln	Asn	Pro	Asp	Asn	Gln	Phe	Val	Gly	Ala	Thr	Val	Glu	Asp
	115						120					125			
Asp	Val	Ala	Phe	Gly	Leu	Glu	Asn	Lys	Gly	Ile	Ala	His	Glu	Asp	Ile
	130					135					140				
Lys	Glu	Arg	Val	Asn	His	Ala	Leu	Glu	Leu	Val	Gly	Met	Gln	Asn	Phe
145				150						155				160	
Lys	Glu	Lys	Glu	Pro	Ala	Arg	Leu	Ser	Gly	Gly	Gln	Lys	Gln	Arg	Val
			165						170					175	
Ala	Ile	Ala	Gly	Ala	Val	Ala	Met	Lys	Pro	Lys	Ile	Ile	Ile	Leu	Asp
		180					185						190		
Glu	Ala	Thr	Ser	Met	Leu	Asp	Pro	Lys	Gly	Arg	Leu	Glu	Leu	Ile	Lys
	195					200						205			
Thr	Ile	Lys	Asn	Ile	Arg	Asp	Asp	Tyr	Gln	Leu	Thr	Val	Ile	Ser	Ile
	210					215					220				
Thr	His	Asp	Leu	Asp	Glu	Val	Ala	Leu	Ser	Asp	Arg	Val	Leu	Val	Met
225				230						235				240	
Lys	Asp	Gly	Gln	Val	Glu	Ser	Thr	Ser	Thr	Pro	Glu	Gln	Leu	Phe	Ala
			245						250				255		
Arg	Gly	Asp	Glu	Leu	Leu	Gln	Leu	Gly	Leu	Asp	Ile	Pro	Phe	Thr	Thr
		260						265					270		
Ser	Val	Val	Gln	Met	Leu	Gln	Glu	Glu	Gly	Tyr	Pro	Val	Asp	Tyr	Gly
	275					280					285				
Tyr	Leu	Thr	Glu	Lys	Glu	Leu	Glu	Asn	Gln	Leu	Cys	Gln	Leu	Ile	Ser
	290					295					300				
Lys	Met														
305															

<210> SEQ ID NO 615
 <211> LENGTH: 615
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 615

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ctaacaatat	tagccatcat	ttttgccttc	tcaagtaaaa	atgctgatac	taagtcttat	120
gctaagaagt	cagaaagtaa	aatggtaaca	atcgacaagg	ctccaaaaaa	taatcatgct	180
attactaaag	aagaaagcaa	agaaaaagca	aagagcattg	cttcggagcc	tattcccaca	240
gtagaaaact	ctgtagctcc	gacagtaaca	gaggaagtac	cggttgttca	gcaagaagtg	300
actcaaactg	ttcagcaggt	atcttcagta	gcctataatc	caaacaatgt	ggtagctttcc	360
aatggaaata	ctgctgggtat	tgtaggaagt	caagcggcgg	cacagatggc	agcagcaaca	420
ggtgtttccac	aatcaacttg	ggaacatata	attgcgcgtg	aatctaattg	aaatcctaac	480
gcagctaattg	cttctggggc	atcaggggtg	ttccagacaa	tgccagggtg	gggttctaca	540
gcaacgggtg	aagatcaagt	caatgcagcc	ttgaaagcct	atagtgcaca	aggtttatca	600
gcttgggggtt	actaa					615

<210> SEQ ID NO 616
 <211> LENGTH: 204
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 616

Met	Phe	Lys	Lys	Glu	Asn	Leu	Lys	Gln	Arg	Tyr	Phe	Asn	Phe	Gly	Leu
1				5					10					15	
Val	Ala	Leu	Ala	Leu	Thr	Ile	Leu	Ala	Ile	Ile	Phe	Ala	Phe	Ser	Ser
			20					25					30		
Lys	Asn	Ala	Asp	Thr	Lys	Ser	Tyr	Ala	Lys	Lys	Ser	Glu	Ser	Lys	Met
		35					40				45				
Val	Thr	Ile	Asp	Lys	Ala	Pro	Lys	Asn	Asn	His	Ala	Ile	Thr	Lys	Glu
	50					55				60					
Glu	Ser	Lys	Glu	Lys	Ala	Lys	Ser	Ile	Ala	Ser	Glu	Pro	Ile	Pro	Thr
65				70					75					80	
Val	Glu	Asn	Ser	Val	Ala	Pro	Thr	Val	Thr	Glu	Glu	Val	Pro	Val	Val
			85					90					95		
Gln	Gln	Glu	Val	Thr	Gln	Thr	Val	Gln	Gln	Val	Ser	Ser	Val	Ala	Tyr
			100					105					110		
Asn	Pro	Asn	Asn	Val	Val	Leu	Ser	Asn	Gly	Asn	Thr	Ala	Gly	Ile	Val
		115					120				125				
Gly	Ser	Gln	Ala	Ala	Ala	Gln	Met	Ala	Ala	Ala	Thr	Gly	Val	Pro	Gln
		130				135					140				
Ser	Thr	Trp	Glu	His	Ile	Ile	Ala	Arg	Glu	Ser	Asn	Gly	Asn	Pro	Asn
145				150					155					160	
Ala	Ala	Asn	Ala	Ser	Gly	Ala	Ser	Gly	Leu	Phe	Gln	Thr	Met	Pro	Gly
			165					170					175		
Trp	Gly	Ser	Thr	Ala	Thr	Val	Glu	Asp	Gln	Val	Asn	Ala	Ala	Leu	Lys
			180					185					190		
Ala	Tyr	Ser	Ala	Gln	Gly	Leu	Ser	Ala	Trp	Gly	Tyr				
		195					200								

<210> SEQ ID NO 617
 <211> LENGTH: 1977
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 617

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ctgctggcac	tttgtgtcag	tattatgcaa	tcaaaaatat	taatattatt	agctattttt	120
ctcgttttgc	tatttgttgt	tgctctttta	tggtatcaaa	aagaagctta	tcaattatca	180
gacttagctc	atattgagct	cttaaatgaa	caaacagaag	ataacctaaa	aacgctactt	240
gataatatgc	ctgttggagt	agttcaattt	gatcaagaga	ccaacgctgt	agaatgggat	300
aatccttatg	cagaattaat	ttttacaact	gaagagggtt	ttatacaaaa	cggtttgatt	360
cagcaaatga	ttacggaaaa	acgtcgtgaa	gatatttttc	aaacatttga	agtttctggt	420
aataaataca	cttcttatat	tgatgtatca	tcaggaattt	tttatttttt	tgatagcttt	480

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gtgggaaaca ggcaattagc tgatgctagt atgttaagac cggttgttgg cattatttcg 540
gttgataatt atgatgatat cactgatgat ttatcagatg cagatacctc aaaaattaat 600
tcatttgtag ctaacttcat tgatgagttt atggagtcaa aacggatttt ttaccgtcgt 660
gttaatatgg atcgctacta tttctttaca gactttaaaa cattaaatga tttgatggat 720
aataaatttt ctgtcttaga agagtttcgt aaagaagctc aagatgctca gcgcccttta 780
acactcagca taggaatttc ttttggtgaa gaaaatcata gccagattgg acaggtagct 840
cttgagaatc ttaatatggc gcttgttcgt ggtggtgatc agattgtcat tcgtgaaaat 900
gcggatcata cgaatccaat ttatttcggg ggagggctctg tttctacagt taaacgttca 960
agaacacgta cccgtgctat gatgacagct atttcagatc gaatcaagat ggtggacaat 1020
gtttttattg ttggacatag gaaacttgat atggatgcac taggttcagc tgttggtatg 1080
caatttttcg caggtaacat tattgaaaaat agttttgccg tttacaatcc agatgagatg 1140
agtccagata ttgaaagggc tattgagcga ttgcaggctg acggaaaagac tcgtctaate 1200
agtgtttctc aagcaatggg tttagtgtac ccaagatcac ttttagtaat ggttgaccat 1260
tctaagatat cttaacact ttctaaagaa ttttatgaac agtttcaaaa tgttattgta 1320
gttgatcatc acagaagaga tgatgatttt cctgataatg ctatcttaac ttttattgaa 1380
agtggagcaa gtagtgctgc ggagctcgtc actgagttaa ttcaatttca aaatgctaaa 1440
aaatgtttta ataagatcca agccagtgtt ttaatggcag gtattatgct tgatactaaa 1500
aatttttcta cgcgagtgc aagtcgtacc tttgatgtcg ctagtactt aagaagcaaa 1560
ggaagtgata gtgttgaaat tcaaaatata tccgcaacag attttgaaga atataagcaa 1620
ataaatgaaa ttattttaca aggagaacgt cttggtgaca gtatcattgt agctgcagga 1680
gaaaaaaatc atctttatag caatgttatt gctagtaaag ctgcagatac gatactgtca 1740
atggctcacg ttgaggctag ctttgtatta gttgaaacag cttctcataa gattgctatt 1800
tcagctagaa gtcgtagtaa aatcaatgtt caacgtgtga tggaaaaatt aggtggagga 1860
ggccacttta atcttgctgc ctgtcagtta acggatatca gtcttcccca agcgaagtac 1920
ttattattga aaactattaa tatgacaatg aaagaaacag gagaagtaga atcatga 1977

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<210> SEQ ID NO 618
<211> LENGTH: 658
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 618

```

```

Met Lys Lys Phe Arg Phe Glu Thr Ile His Leu Ile Met Met Gly Leu
1          5          10          15
Ile Leu Phe Gly Leu Leu Ala Leu Cys Val Ser Ile Met Gln Ser Lys
20          25          30
Ile Leu Ile Leu Leu Ala Ile Phe Leu Val Leu Leu Phe Val Val Ala
35          40          45
Leu Leu Trp Tyr Gln Lys Glu Ala Tyr Gln Leu Ser Asp Leu Ala His
50          55          60
Ile Glu Leu Leu Asn Glu Gln Thr Glu Asp Asn Leu Lys Thr Leu Leu
65          70          75          80
Asp Asn Met Pro Val Gly Val Val Gln Phe Asp Gln Glu Thr Asn Ala
85          90          95
Val Glu Trp Tyr Asn Pro Tyr Ala Glu Leu Ile Phe Thr Thr Glu Glu
100         105         110
Gly Phe Ile Gln Asn Gly Leu Ile Gln Gln Ile Ile Thr Glu Lys Arg
115         120         125
Arg Glu Asp Ile Ser Gln Thr Phe Glu Val Ser Gly Asn Lys Tyr Thr
130         135         140
Ser Tyr Ile Asp Val Ser Ser Gly Ile Phe Tyr Phe Phe Asp Ser Phe
145         150         155         160
Val Gly Asn Arg Gln Leu Ala Asp Ala Ser Met Leu Arg Pro Val Val
165         170         175
Gly Ile Ile Ser Val Asp Asn Tyr Asp Asp Ile Thr Asp Asp Leu Ser
180         185         190
Asp Ala Asp Thr Ser Lys Ile Asn Ser Phe Val Ala Asn Phe Ile Asp
195         200         205

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Glu	Phe	Met	Glu	Ser	Lys	Arg	Ile	Phe	Tyr	Arg	Arg	Val	Asn	Met	Asp
210						215					220				
Arg	Tyr	Tyr	Phe	Phe	Thr	Asp	Phe	Lys	Thr	Leu	Asn	Asp	Leu	Met	Asp
225					230					235					240
Asn	Lys	Phe	Ser	Val	Leu	Glu	Glu	Phe	Arg	Lys	Glu	Ala	Gln	Asp	Ala
				245					250					255	
Gln	Arg	Pro	Leu	Thr	Leu	Ser	Ile	Gly	Ile	Ser	Phe	Gly	Glu	Glu	Asn
			260					265					270		
His	Ser	Gln	Ile	Gly	Gln	Val	Ala	Leu	Glu	Asn	Leu	Asn	Ile	Ala	Leu
		275					280					285			
Val	Arg	Gly	Gly	Asp	Gln	Ile	Val	Ile	Arg	Glu	Asn	Ala	Asp	His	Thr
	290					295					300				
Asn	Pro	Ile	Tyr	Phe	Gly	Gly	Gly	Ser	Val	Ser	Thr	Val	Lys	Arg	Ser
305					310					315					320
Arg	Thr	Arg	Thr	Arg	Ala	Met	Met	Thr	Ala	Ile	Ser	Asp	Arg	Ile	Lys
				325					330					335	
Met	Val	Asp	Asn	Val	Phe	Ile	Val	Gly	His	Arg	Lys	Leu	Asp	Met	Asp
			340					345					350		
Ala	Leu	Gly	Ser	Ala	Val	Gly	Met	Gln	Phe	Phe	Ala	Gly	Asn	Ile	Ile
		355					360					365			
Glu	Asn	Ser	Phe	Ala	Val	Tyr	Asn	Pro	Asp	Glu	Met	Ser	Pro	Asp	Ile
	370					375					380				
Glu	Arg	Ala	Ile	Glu	Arg	Leu	Gln	Ala	Asp	Gly	Lys	Thr	Arg	Leu	Ile
385					390					395					400
Ser	Val	Ser	Gln	Ala	Met	Gly	Leu	Val	Thr	Pro	Arg	Ser	Leu	Leu	Val
				405					410					415	
Met	Val	Asp	His	Ser	Lys	Ile	Ser	Leu	Thr	Leu	Ser	Lys	Glu	Phe	Tyr
			420					425					430		
Glu	Gln	Phe	Gln	Asn	Val	Ile	Val	Val	Asp	His	His	Arg	Arg	Asp	Asp
		435					440					445			
Asp	Phe	Pro	Asp	Asn	Ala	Ile	Leu	Thr	Phe	Ile	Glu	Ser	Gly	Ala	Ser
	450					455					460				
Ser	Ala	Ala	Glu	Leu	Val	Thr	Glu	Leu	Ile	Gln	Phe	Gln	Asn	Ala	Lys
465					470					475					480
Lys	Cys	Leu	Asn	Lys	Ile	Gln	Ala	Ser	Val	Leu	Met	Ala	Gly	Ile	Met
				485					490					495	
Leu	Asp	Thr	Lys	Asn	Phe	Ser	Thr	Arg	Val	Thr	Ser	Arg	Thr	Phe	Asp
			500					505					510		
Val	Ala	Ser	Tyr	Leu	Arg	Ser	Lys	Gly	Ser	Asp	Ser	Val	Glu	Ile	Gln
		515					520					525			
Asn	Ile	Ser	Ala	Thr	Asp	Phe	Glu	Glu	Tyr	Lys	Gln	Ile	Asn	Glu	Ile
	530					535					540				
Ile	Leu	Gln	Gly	Glu	Arg	Leu	Gly	Asp	Ser	Ile	Ile	Val	Ala	Ala	Gly
545					550					555					560
Glu	Lys	Asn</													

<210> SEQ ID NO 619
 <211> LENGTH: 2304
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 619

```

ttgaacagta tgtccatttt aggagaaaaat atgttagaag aattgaaaac acttattaaa      60
aatccaaaat taatgattac aatgattggt gtggccctag tgctgcctt atataattta      120
tcctttctag gctcaatgtg ggatccttat ggtcgggtca atgaccttcc cattgctggt      180
gttaatcatg ataagcctgc aaagagagct gataagtcac tgacaattgg gaatgatatg      240
gtggacaaga tgtctaaaag taaagattta gagtatcatt ttgtctcagc taagcaagct      300
caagagggag ttaaagaagg tgattattat atggttatta ctttaccgga agatctttct      360
caacgggcag caaccttatt aaatcccga ccccaaaaat taactatccg ttaccaaacg      420
agtaaaggac atggaatggt cgctgctaag atgggggaaa cagcgatggc taagctgaaa      480
gagtctgttt cgcaaaacat tacgaagact tatacctcag cagtttttag cagtatgaca      540
gacctccaat caggattaaa agaagcctca gctggaagtc aagcacttgc ttcaggagcg      600
aagactgctc aggcggggag tcaaacactt tcgacgaact tagcagcctt aacgggtgct      660
agccaacagt ttcaacaagg tactggctga ttgacatcag gtttgactac ctatacagat      720
ggtgtcaacc aagtcaagaa tgggttagga acattatcaa cggacatccc caattatctg      780
aatggggttt ctagggtatc ccaggagct tctcagctta atcagggtct ttcacagttg      840
acacaagcaa caacactttc tgacgagaaa gctaagggaa ttcaatcctt aattgtagga      900
ctaccagtc taaatcaagg cattcagcaa ctaaatacag agctatcaac attgcaaccc      960
cctaacctta atgctgatga gttaggtaat agcttaggag ctatcgctca agctgccaaa     1020
caagtcattg ctgaagagac tgccgctcag aatgaagaat tatcggctct ccaagctact     1080
agcgtttacc aatcattaac tgctgaacaa caaggagagt tagctgcggc cctcagtcaa     1140
tctgataaaa gtcagaccgt atctgcagcc caaactatth taagtctctg tcaaactttg     1200
tcaacaagtt tacagtctct ctctcaagaa gatcagtcac aacagttgga gcaacttaag     1260
gaagctgttg cacagattgc taatcaatcc aatcaagctt tgccgggagc aagttctgct     1320
ttaactgaat tatcaacggg attagcaaaag gtaaatggta gcttaaatca acaagttcta     1380
ccaggaagta atcaattgac aacaggatta gcacaattaa acaggataaa tactgccatt     1440
ggttctgggg taataaaact ctcagaagggt gccaatgcct tgctatccaa gtccggagaa     1500
ttactagatg gtagccatca attatcagaa ggtgctacta aactagctga tggtagttct     1560
caattgagtc aggggtggtc tcaattaacg agcggattga ctgaattatc aacaggattg     1620
tcaaccttaa atggttcctt agccaaagcc tctcagcagt tatcgcttgt tctgtgact     1680
gataaaaaatg ctaaaagctgt cgcaaaacct cttgtgttaa atgagaaaga caaagatggg     1740
gttaagacga atgggatcgg gatggcacct tatatgattg ctgtttctct aatggttgtg     1800
gccctttcaa ccaacgtcat ttttgcta atctttatctg gtcgtccggg caaagataaa     1860
tggtgattgg ctaaaacaaa atttgttatt aatggtttta tttcgactat gggatccatt     1920
gttctctact tagctattca attattagggt tttgaagccc gttatgggat ggaaacctta     1980
ggatttatta tgctaagtgg ttggacgttt atggctcttg tcacagcttt ggtcggttgg     2040
gatgatcgat atggctcttt tgcttctttg gtcattgttat tgcttcaggt tggctcttca     2100
ggtggctctt accccattga gttaagtggg gcattcttcc aaaagttaca tcctttctta     2160
ccaatgactt atgtggtatc tggtttacga caaaccttt cattatcagg tcatattgga     2220
gtagaagtga aagtcttaac tggtttctta ctggcattta tggatttagc actactcatt     2280
tatcgthcca agaaaacagt cttaa                                     2304

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<210> SEQ ID NO 620
 <211> LENGTH: 767
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 620

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Met Asn Ser Met Ser Ile Leu Gly Glu Asn Met Leu Glu Glu Leu Lys
1              5              10              15
Thr Leu Ile Lys Asn Pro Lys Leu Met Ile Thr Met Ile Gly Val Ala
              20              25              30
Leu Val Pro Ala Leu Tyr Asn Leu Ser Phe Leu Gly Ser Met Trp Asp
              35              40              45

```

Pro	Tyr	Gly	Arg	Val	Asn	Asp	Leu	Pro	Ile	Ala	Val	Val	Asn	His	Asp	
50						55					60					
Lys	Pro	Ala	Lys	Arg	Ala	Asp	Lys	Ser	Leu	Thr	Ile	Gly	Asn	Asp	Met	
65					70					75					80	
Val	Asp	Lys	Met	Ser	Lys	Ser	Lys	Asp	Leu	Glu	Tyr	His	Phe	Val	Ser	
				85					90					95		
Ala	Lys	Gln	Ala	Gln	Glu	Gly	Leu	Lys	Glu	Gly	Asp	Tyr	Tyr	Met	Val	
			100					105					110			
Ile	Thr	Leu	Pro	Glu	Asp	Leu	Ser	Gln	Arg	Ala	Ala	Thr	Leu	Leu	Asn	
	115						120					125				
Pro	Glu	Pro	Gln	Lys	Leu	Thr	Ile	Arg	Tyr	Gln	Thr	Ser	Lys	Gly	His	
130						135					140					
Gly	Met	Val	Ala	Ala	Lys	Met	Gly	Glu	Thr	Ala	Met	Ala	Lys	Leu	Lys	
145					150					155					160	
Glu	Ser	Val	Ser	Gln	Asn	Ile	Thr	Lys	Thr	Tyr	Thr	Ser	Ala	Val	Phe	
				165				170						175		
Ser	Ser	Met	Thr	Asp	Leu	Gln	Ser	Gly	Leu	Lys	Glu	Ala	Ser	Ala	Gly	
			180					185					190			
Ser	Gln	Ala	Leu	Ala	Ser	Gly	Ala	Lys	Thr	Ala	Gln	Ala	Gly	Ser	Gln	
	195						200					205				
Thr	Leu	Ser	Thr	Asn	Leu	Ala	Ala	Leu	Thr	Gly	Ala	Ser	Gln	Gln	Phe	
	210					215					220					
Gln	Gln	Gly	Thr	Gly	Arg	Leu	Thr	Ser	Gly	Leu	Thr	Thr	Tyr	Thr	Asp	
225					230					235					240	
Gly	Val	Asn	Gln	Val	Lys	Asn	Gly	Leu	Gly	Thr	Leu	Ser	Thr	Asp	Ile	
				245					250					255		
Pro	Asn	Tyr	Leu	Asn	Gly	Val	Ser	Arg	Leu	Ser	Gln	Gly	Ala	Ser	Gln	
			260					265					270			
Leu	Asn	Gln	Gly	Leu	Ser	Gln	Leu	Thr	Gln	Ala	Thr	Thr	Leu	Ser	Asp	
	275						280					285				
Glu	Lys	Ala	Lys	Gly	Ile	Gln	Ser	Leu	Ile	Val	Gly	Leu	Pro	Val	Leu	
290						295					300					
Asn	Gln	Gly	Ile	Gln	Gln	Leu	Asn	Thr	Glu	Leu	Ser	Thr	Leu	Gln	Pro	
305					310					315					320	
Pro	Asn	Leu	Asn	Ala	Asp	Glu	Leu	Gly	Asn	Ser	Leu	Gly	Ala	Ile	Ala	
				325					330					335		
Gln	Ala	Ala	Lys	Gln	Val	Ile	Ala	Glu	Glu	Thr	Ala	Ala	Gln	Asn	Glu	
			340					345					350			
Glu	Leu	Ser	Ala	Leu	Gln	Ala	Thr	Ser	Val	Tyr	Gln	Ser	Leu	Thr	Ala	
	355						360					365				
Glu	Gln	Gln	Gly	Glu	Leu	Ala	Ala	Ala	Leu	Ser	Gln	Ser	Asp	Lys	Ser	
370						375					380					
Gln	Thr	Val	Ser	Ala	Ala	Gln	Thr	Ile	Leu	Ser	Ser	Val	Gln	Thr	Leu	
385					390					395					400	
Ser	Thr	Ser	Leu	Gln	Ser	Leu	Ser	Gln	Glu	Asp	Gln	Ser	Lys	Gln	Leu	
				405					410					415		
Glu	Gln	Leu	Lys	Glu	Ala	Val	Ala	Gln	Ile	Ala	Asn	Gln	Ser	Asn	Gln	
			420					425					430			
Ala	Leu	Pro	Gly	Ala	Ser	Ser	Ala	Leu	Thr	Glu	Leu	Ser	Thr	Gly	Leu	
	435						440					445				
Ala	Lys	Val	Asn	Gly	Ser	Leu	Asn	Gln	Gln	Val	Leu	Pro	Gly	Ser	Asn	
450						455					460					
Gln	Leu	Thr	Thr	Gly	Leu	Ala	Gln	Leu	Asn	Arg	Tyr	Asn	Thr	Ala	Ile	
465					470					475					480	
Gly	Ser	Gly	Val	Ile	Lys	Leu	Ser	Glu	Gly	Ala	Asn	Ala	Leu	Ser	Ser	
				485					490					495		
Lys	Ser	Gly	Glu	Leu	Leu	Asp	Gly	Ser	His	Gln	Leu	Ser	Glu	Gly	Ala	

			500					505					510				
Thr	Lys	Leu	Ala	Asp	Gly	Ser	Ser	Gln	Leu	Ser	Gln	Gly	Gly	His	Gln		
		515					520					525					
Leu	Thr	Ser	Gly	Leu	Thr	Glu	Leu	Ser	Thr	Gly	Leu	Ser	Thr	Leu	Asn		
	530					535					540						
Gly	Ser	Leu	Ala	Lys	Ala	Ser	Gln	Gln	Leu	Ser	Leu	Val	Ser	Val	Thr		
545				550					555						560		
Asp	Lys	Asn	Ala	Lys	Ala	Val	Ala	Lys	Pro	Leu	Val	Leu	Asn	Glu	Lys		
		565						570					575				
Asp	Lys	Asp	Gly	Val	Lys	Thr	Asn	Gly	Ile	Gly	Met	Ala	Pro	Tyr	Met		
	580						585						590				
Ile	Ala	Val	Ser	Leu	Met	Val	Val	Ala	Leu	Ser	Thr	Asn	Val	Ile	Phe		
	595						600					605					
Ala	Asn	Ser	Leu	Ser	Gly	Arg	Pro	Val	Lys	Asp	Lys	Trp	Asp	Trp	Ala		
	610					615					620						
Lys	Gln	Lys	Phe	Val	Ile	Asn	Gly	Phe	Ile	Ser	Thr	Met	Gly	Ser	Ile		
625				630					635						640		
Val	Leu	Tyr	Leu	Ala	Ile	Gln	Leu	Leu	Gly	Phe	Glu	Ala	Arg	Tyr	Gly		
		645					650						655				
Met	Glu	Thr	Leu	Gly	Phe	Ile	Met	Leu	Ser	Gly	Trp	Thr	Phe	Met	Ala		
	660						665					670					
Leu	Val	Thr	Ala	Leu	Val	Gly	Trp	Asp	Asp	Arg	Tyr	Gly	Ser	Phe	Ala		
	675					680					685						
Ser	Leu	Val	Met	Leu	Leu	Leu	Gln	Val	Gly	Ser	Ser	Gly	Gly	Ser	Tyr		
	690					695					700						
Pro	Ile	Glu	Leu	Ser	Gly	Ala	Phe	Phe	Gln	Lys	Leu	His	Pro	Phe	Leu		
705				710					715						720		
Pro	Met	Thr	Tyr	Val	Val	Ser	Gly	Leu	Arg	Gln	Thr	Ile	Ser	Leu	Ser		
		725					730						735				
Gly	His	Ile	Gly	Val	Glu	Val	Lys	Val	Leu	Thr	Gly	Phe	Leu	Leu	Ala		
	740						745					750					
Phe	Met	Val	Leu	Ala	Leu	Leu	Ile	Tyr	Arg	Pro	Lys	Lys	Thr	Val			
	755						760					765					

<210> SEQ ID NO 621

<211> LENGTH: 843

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 621

atggtttcat	ttattttcaag	agttttttaa	ggcatgatta	ttgcactagg	ttttatttta	60
cctggtgtat	ccggtggtgt	tctcgcagcc	atttttaggaa	tctatgagcg	aatgatttcc	120
tttttagctc	atatgaggga	taactttatt	gaaaatgtct	tatttttctt	accagtagga	180
attggtggta	tttttaggtat	tgctctcttt	tctttccccg	ttgagttttt	gcttaagcac	240
tatcaagtta	gcgtcttatg	gggatttgct	ggcgctattg	tcggcactat	tcctagtctg	300
attaaggagt	caaccaagca	gtctcaaaga	gacaaagctg	actggctatg	gctagtcctt	360
acctttgtta	tttcaggact	aggtctttac	ttcttaaagt	acttaatcgg	taccttacca	420
gctaactttt	taacctttat	tttagcaggt	gccttaattg	ctttaggagt	actggtcctt	480
ggactaagcc	cgtcaaactc	cttacttatc	ttaggactct	atggctcctat	gttaataggg	540
ttcaaactct	tggatttatt	agggactttc	ttacctattg	ctatcggagg	agtcctagcc	600
atcttggtct	tttctaaaag	tatggattat	gctttacagc	accatcattc	aaaagtttac	660
cactttatca	ttggtattgt	attatccagc	acgctattaa	ttcttattcc	aaatagtagt	720
agtcccgaat	ccatttccta	cagtcatgca	ggtatcttaa	cctggcttat	ggcctttgtg	780
ttatttgctc	ttggtatttg	gctcggactt	tggatgagtc	aattagaaga	aaaatacaaa	840
taa						843

<210> SEQ ID NO 622

<211> LENGTH: 280

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 622

```
Met Val Ser Phe Ile Ser Arg Val Phe Lys Gly Met Ile Ile Ala Leu
1      5      10      15
Gly Phe Ile Leu Pro Gly Val Ser Gly Gly Val Leu Ala Ala Ile Leu
20      25      30
Gly Ile Tyr Glu Arg Met Ile Ser Phe Leu Ala His Met Arg Asp Asn
35      40      45
Phe Ile Glu Asn Val Leu Phe Phe Leu Pro Val Gly Ile Gly Gly Ile
50      55      60
Leu Gly Ile Ala Leu Phe Ser Phe Pro Val Glu Phe Leu Leu Lys His
65      70      75      80
Tyr Gln Val Ser Val Leu Trp Gly Phe Ala Gly Ala Ile Val Gly Thr
85      90      95
Ile Pro Ser Leu Ile Lys Glu Ser Thr Lys Gln Ser Gln Arg Asp Lys
100     105     110
Ala Asp Trp Leu Trp Leu Val Leu Thr Phe Val Ile Ser Gly Leu Gly
115     120     125
Leu Tyr Phe Leu Asn Asp Leu Ile Gly Thr Leu Pro Ala Asn Phe Leu
130     135     140
Thr Phe Ile Leu Ala Gly Ala Leu Ile Ala Leu Gly Val Leu Val Pro
145     150     155     160
Gly Leu Ser Pro Ser Asn Leu Leu Leu Ile Leu Gly Leu Tyr Gly Pro
165     170     175
Met Leu Ile Gly Phe Lys Ser Leu Asp Leu Leu Gly Thr Phe Leu Pro
180     185     190
Ile Ala Ile Gly Gly Val Leu Ala Ile Leu Ala Phe Ser Lys Ser Met
195     200     205
Asp Tyr Ala Leu Gln His His His Ser Lys Val Tyr His Phe Ile Ile
210     215     220
Gly Ile Val Leu Ser Ser Thr Leu Leu Ile Leu Ile Pro Asn Ser Ser
225     230     235     240
Ser Pro Glu Ser Ile Ser Tyr Ser His Ala Gly Ile Leu Thr Trp Leu
245     250     255
Met Ala Phe Val Leu Phe Ala Leu Gly Ile Trp Leu Gly Leu Trp Met
260     265     270
Ser Gln Leu Glu Glu Lys Tyr Lys
275     280
```

<210> SEQ ID NO 623

<211> LENGTH: 942

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 623

```
atgattaaga aaacaaccta taagaaaaaa gttaaataatg tcattagtag aggggcccaag      60
aaagttggcc tactccacgc tctaagaagt atttcaagag aaaaatatgc agagaagatt      120
tcggcttctc tgctttatgg cattctctct agtattgctg tgaatttttt cttccagcct      180
gggcatgttt attcaagtgg agcaactggt ctagcacagg ttttttcagc tcttagtcat      240
cgtcttttag gctatgattt tcccatcgcc tttgcgtttt atttgattaa tattcctttg      300
cttatttttag cttggtataa aattgggcat caatttacca tttttacctt tatcacagtc      360
agcatgagtt ctttctttat tcaaatcatg cctcaagtga cgctgacgac tgatcctctt      420
atcaatgcta tttttggtgg tttggttatg ggaatgggaa ttggtacagg tctcaaatca      480
cgatatctcta gtggggggac tgatattgtc agtttgacct ttaggaaacg aacaggcaag      540
gatgtgggca gtctctcatt gatggttaat ggtgcaattt tagcctttgc agggatttta      600
tttggctggc agtacgccct ttattctatg gtctctatct ttgtatcaag tcgtgttacg      660
gatgccattt tcaccaagca aaagaaaatg caggcaacta ttgttaccag ccatccagag      720
```

cgtgtgattc	atatgatcca	taaacgtctg	catcgcggag	tgaccagtat	caacgacgca	780
gaagggactt	acaagcatga	acaaaaagca	gttttgatta	ccatttttgac	atgtgaagaa	840
tacccagaat	tcaaattggct	gatgttaaaa	acagacccac	aagcctttgt	ttcagtggct	900
gagaatgtta	gaattatcgg	tcgtttttgtg	gaagatgatt	aa		942

<210> SEQ ID NO 624
 <211> LENGTH: 313
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 624

Met	Ile	Lys	Lys	Thr	Tyr	Lys	Lys	Lys	Val	Lys	Tyr	Val	Ile	Ser
1			5					10					15	
Arg	Gly	Ala	Lys	Val	Gly	Leu	Leu	His	Ala	Leu	Arg	Ser	Ile	Ser
			20				25					30		
Arg	Glu	Lys	Tyr	Ala	Glu	Lys	Ile	Ser	Ala	Ser	Leu	Leu	Tyr	Gly
		35				40					45			Ile
Leu	Ser	Ser	Ile	Ala	Val	Asn	Phe	Phe	Phe	Gln	Pro	Gly	His	Val
	50					55				60				Tyr
Ser	Ser	Gly	Ala	Thr	Gly	Leu	Ala	Gln	Val	Phe	Ser	Ala	Leu	Ser
65				70					75					80
Arg	Leu	Leu	Gly	Tyr	Asp	Phe	Pro	Ile	Ala	Phe	Ala	Phe	Tyr	Leu
			85					90					95	Ile
Asn	Ile	Pro	Leu	Leu	Ile	Leu	Ala	Trp	Tyr	Lys	Ile	Gly	His	Gln
		100						105				110		Phe
Thr	Ile	Phe	Thr	Phe	Ile	Thr	Val	Ser	Met	Ser	Ser	Phe	Phe	Ile
	115					120						125		Gln
Ile	Met	Pro	Gln	Val	Thr	Leu	Thr	Thr	Asp	Pro	Leu	Ile	Asn	Ala
	130					135				140				Ile
Phe	Gly	Gly	Leu	Val	Met	Gly	Met	Gly	Ile	Gly	Thr	Gly	Leu	Lys
145				150					155					160
Arg	Ile	Ser	Ser	Gly	Gly	Thr	Asp	Ile	Val	Ser	Leu	Thr	Leu	Arg
			165					170					175	Lys
Arg	Thr	Gly	Lys	Asp	Val	Gly	Ser	Leu	Ser	Leu	Met	Val	Asn	Gly
		180					185					190		Ala
Ile	Leu	Ala	Phe	Ala	Gly	Ile	Leu	Phe	Gly	Trp	Gln	Tyr	Ala	Leu
	195					200					205			Tyr
Ser	Met	Val	Ser	Ile	Phe	Val	Ser	Ser	Arg	Val	Thr	Asp	Ala	Ile
	210					215				220				Phe
Thr	Lys	Gln	Lys	Lys	Met	Gln	Ala	Thr	Ile	Val	Thr	Ser	His	Pro
225				230					235					240
Arg	Val	Ile	His	Met	Ile	His	Lys	Arg	Leu	His	Arg	Gly	Val	Thr
			245					250					255	Ser
Ile	Asn	Asp	Ala	Glu	Gly	Thr	Tyr	Lys	His	Glu	Gln	Lys	Ala	Val
		260					265					270		Leu
Ile	Thr	Ile	Leu	Thr	Cys	Glu	Glu	Tyr	Pro	Glu	Phe	Lys	Trp	Leu
	275					280					285			Met
Leu	Lys	Thr	Asp	Pro	Gln	Ala	Phe	Val	Ser	Val	Ala	Glu	Asn	Val
	290				295						300			Arg
Ile	Ile	Gly	Arg	Phe	Val	Glu	Asp	Asp						
305				310										

<210> SEQ ID NO 625
 <211> LENGTH: 873
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 625

atggcacatc	acgataaatt	gactaaaacta	ctaaaactgt	ttttgattgc	cctaggtgta	60
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gccatttata ccttcggttt tgtaatttt aacatggcta atgctttggc tgaaggtggt 120
gtggcaggaa taaccttgat tttacacgcg cattttggga ttaatcctgc ttactcttct 180
ctcttattta atcttcact ttttatttta ggggcaaaga tttttgggaa gcgttctttg 240
gctctaacca tctatggaac agttctgatg tccgctttta tctggatgtg gcaaaaagtt 300
cctatcgaac ttggcttgga aaatgacatg atgttggtgg ctgtagtggc aggtctcttt 360
tcagggattg ggagtggcat tgtttttcgc tatggtgcaa ccacaggtgg aacggatatt 420
attggtcgca ttgcagaaga aaaatttgga gctaagctag gtcaaacttt gcttttggtg 480
gatgctcttg tattgacagc ttcgttgact tatgtggatt taaaacacat gctttacact 540
ttggtggcaa gctttgtttt tagccaaatg attagtgtgg ttcaaaatgg tggttacact 600
atccgtggaa tgattattat taccaagcat tcagaggctg ccgctcaagc tatcctaacc 660
gaaatcaatc gtggagtgc ttacttgaaa ggtcaaggag cttactctgg taatgattac 720
aatatcatgt atgtgacctt gaacccaact gaagttcggg aagtcaaacg tatttttagct 780
ggtttggatc cagatgcctt tatctccatt attgatgtgg acgaagttag tagctctgat 840
tttaaaattc gccgaagaaa ttatgataaa taa 873

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<210> SEQ ID NO 626

<211> LENGTH: 290

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 626

```

Met Ala His His Asp Lys Leu Thr Lys Leu Leu Lys Leu Phe Leu Ile
1          5          10          15
Ala Leu Gly Val Ala Ile Tyr Thr Phe Gly Phe Val Asn Phe Asn Met
20          25          30
Ala Asn Ala Leu Ala Glu Gly Gly Val Ala Gly Ile Thr Leu Ile Leu
35          40          45
His Ala His Phe Gly Ile Asn Pro Ala Tyr Ser Ser Leu Leu Phe Asn
50          55          60
Leu Pro Leu Phe Ile Leu Gly Ala Lys Ile Phe Gly Lys Arg Ser Leu
65          70          75          80
Ala Leu Thr Ile Tyr Gly Thr Val Leu Met Ser Ala Phe Ile Trp Met
85          90          95
Trp Gln Lys Val Pro Ile Glu Leu Gly Leu Glu Asn Asp Met Met Leu
100         105         110
Val Ala Val Val Ala Gly Leu Phe Ser Gly Ile Gly Ser Gly Ile Val
115         120         125
Phe Arg Tyr Gly Ala Thr Thr Gly Gly Thr Asp Ile Ile Gly Arg Ile
130         135         140
Ala Glu Glu Lys Phe Gly Ala Lys Leu Gly Gln Thr Leu Leu Leu Val
145         150         155         160
Asp Ala Leu Val Leu Thr Ala Ser Leu Thr Tyr Val Asp Leu Lys His
165         170         175
Met Leu Tyr Thr Leu Val Ala Ser Phe Val Phe Ser Gln Met Ile Ser
180         185         190
Val Val Gln Asn Gly Gly Tyr Thr Ile Arg Gly Met Ile Ile Ile Thr
195         200         205
Lys His Ser Glu Ala Ala Ala Gln Ala Ile Leu Thr Glu Ile Asn Arg
210         215         220
Gly Val Thr Tyr Leu Lys Gly Gln Gly Ala Tyr Ser Gly Asn Asp Tyr
225         230         235         240
Asn Ile Met Tyr Val Thr Leu Asn Pro Thr Glu Val Arg Glu Val Lys
245         250         255
Arg Ile Leu Ala Gly Leu Asp Pro Asp Ala Phe Ile Ser Ile Ile Asp
260         265         270
Val Asp Glu Val Ile Ser Ser Asp Phe Lys Ile Arg Arg Arg Asn Tyr
275         280         285
Asp Lys

```

<210> SEQ ID NO 627
 <211> LENGTH: 576
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 627

```

ttgatattta attttaagga gaatatagtg aaaaagaaat tagtttttagc taccttatgt      60
ctatcaatgg gtgctgtgag tgtagagcg gaaagtgatt ttgggaatgc taatgaaatc      120
gggctaggtt tttatggtag tgatgactat actaaccaac ctgctttaac aggagaccaa      180
gcgaaaatag gcttcagaaa cgattggaaa gatgctagag attttggagt aaaaccaata      240
aatctgggag atagtaaaat cgaagtaaaa acaaatccgg gagctcttgt aagagtttcc      300
ttgacaacgg gtgaaacaac caatagtata tgggagttaa caagtgtatc ttcctcaatg      360
agtaacggta tctacactaa cacttataaa ataaagccaa ctattgcaaa ttcctcagga      420
attgcaacgt tcgatttagc gaactcagga aaatacgaca aggaaaaaag tgaaattata      480
aagagtactg agagtaatgc aaagaaagggt gatacttact cagttactac aagtatagat      540
ggatggacaa taggttatgg agaatggact gtgtga                                576

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<210> SEQ ID NO 628
 <211> LENGTH: 191
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 628

```

Met Ile Phe Asn Phe Lys Glu Asn Ile Val Lys Lys Lys Leu Val Leu
1           5           10           15
Ala Thr Leu Cys Leu Ser Met Gly Ala Val Ser Val Arg Ala Glu Ser
20           25           30
Asp Phe Gly Asn Ala Asn Glu Ile Gly Leu Gly Phe Tyr Gly Ser Asp
35           40           45
Asp Tyr Thr Asn Gln Pro Ala Leu Thr Gly Asp Gln Ala Lys Ile Gly
50           55           60
Phe Arg Asn Asp Trp Lys Asp Ala Arg Asp Phe Gly Val Lys Pro Ile
65           70           75           80
Asn Leu Gly Asp Ser Lys Ile Glu Val Lys Thr Asn Pro Gly Ala Leu
85           90           95
Val Arg Val Ser Leu Thr Thr Gly Glu Thr Thr Asn Ser Ile Trp Glu
100          105          110
Leu Thr Ser Val Ser Ser Ser Met Ser Asn Gly Ile Tyr Thr Asn Thr
115          120          125
Tyr Lys Ile Lys Pro Thr Ile Ala Asn Ser Ser Gly Ile Ala Thr Phe
130          135          140
Asp Leu Ala Asn Ser Gly Lys Tyr Asp Lys Glu Lys Ser Glu Ile Ile
145          150          155          160
Lys Ser Thr Glu Ser Asn Ala Lys Lys Gly Asp Thr Tyr Ser Val Thr
165          170          175
Thr Ser Ile Asp Gly Trp Thr Ile Gly Tyr Gly Glu Trp Thr Val
180          185          190

```

<210> SEQ ID NO 629
 <211> LENGTH: 1221
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 629

```

atgcaagagt ttttaaacct tcctaagcag attcagctga ggcaactggg acgctttgtg      60
accattacct taggcagtag tatctttccc ttatggcca tgtattatac gacttacttt      120
gggtacgtttt ggacaggcct cttaatgatg attaccagtt tgatgggatt tgttggaact      180
ttatacgggtg ggcattctgtc agatgctctt ggtcgcaaaa aagtcattat gattgggtca      240

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gtaggaacaa cactaggctg gtttctgact atttttagcta atttgcctaa tgcggctatt 300
ccttggttaa cctttgcggg tattttattg gtagagattg cttctagttt ttatggctct 360
gcctatgaag ctatgttgat tgatttgact gatgagagta atcgtcgatt tgtttacacc 420
atcaattatt gggttatcaa tattgccgtc atgtttggtg cagggctatc tgggcttttt 480
tatgaccatc attttttagc cttgttagta gccttattac tcgtcaatgt actttgtttt 540
ggcgttgctt actactgttt tgatgaaact agaccagaaa cacacgcttt tgaccatggt 600
aaaggattac tggcgagttt tcagaactac cgtcagggtg ttcatgatcg tgcctttgtc 660
ttgtttacct taggtgccat cttttctggt agtatctgga tgcagatgga taactatgtg 720
ccagtcattt tgaaactgta ttttcagcca acggctgtat taggtttcca agtaactagt 780
tctaaaatgt tatcattaat ggttttaact aatacattgc tgattgtcct tttcatgaca 840
gtagtaaata aattaacgga aaaatggaaa ctattacctc agcttgtggt tgggtcctta 900
ctatttactc tagggatgct cttgtcattt acctttacgc agttctatgc tatctggta 960
tcagttgttt tgtaactttt tggggaaatg ataaatgttt ctgctagtca agtcctacgt 1020
gctgatatga tggatcattc ccaaatagga tcttatacag gttttgtgtc aatggcacia 1080
cccctagggtg ctattttggc tagtctacta gtatctgtca gccattttac aggtccttta 1140
ggcgtgcaat gcttatttgc agtcattgct ttgctaggga tttattttac gggtgtttct 1200
gcaaaaatga aaaagggtgta a 1221

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<210> SEQ ID NO 630

<211> LENGTH: 406

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 630

```

Met Gln Glu Phe Leu Asn Leu Pro Lys Gln Ile Gln Leu Arg Gln Leu
1          5          10          15
Val Arg Phe Val Thr Ile Thr Leu Gly Ser Ser Ile Phe Pro Phe Met
20        25        30
Ala Met Tyr Tyr Thr Thr Tyr Phe Gly Thr Phe Trp Thr Gly Leu Leu
35        40        45
Met Met Ile Thr Ser Leu Met Gly Phe Val Gly Thr Leu Tyr Gly Gly
50        55        60
His Leu Ser Asp Ala Leu Gly Arg Lys Lys Val Ile Met Ile Gly Ser
65        70        75        80
Val Gly Thr Thr Leu Gly Trp Phe Leu Thr Ile Leu Ala Asn Leu Pro
85        90        95
Asn Ala Ala Ile Pro Trp Leu Thr Phe Ala Gly Ile Leu Leu Val Glu
100       105       110
Ile Ala Ser Ser Phe Tyr Gly Pro Ala Tyr Glu Ala Met Leu Ile Asp
115       120       125
Leu Thr Asp Glu Ser Asn Arg Arg Phe Val Tyr Thr Ile Asn Tyr Trp
130       135       140
Phe Ile Asn Ile Ala Val Met Phe Gly Ala Gly Leu Ser Gly Leu Phe
145       150       155       160
Tyr Asp His His Phe Leu Ala Leu Leu Val Ala Leu Leu Leu Val Asn
165       170       175
Val Leu Cys Phe Gly Val Ala Tyr Tyr Cys Phe Asp Glu Thr Arg Pro
180       185       190
Glu Thr His Ala Phe Asp His Gly Lys Gly Leu Leu Ala Ser Phe Gln
195       200       205
Asn Tyr Arg Gln Val Phe His Asp Arg Ala Phe Val Leu Phe Thr Leu
210       215       220
Gly Ala Ile Phe Ser Gly Ser Ile Trp Met Gln Met Asp Asn Tyr Val
225       230       235       240
Pro Val His Leu Lys Leu Tyr Phe Gln Pro Thr Ala Val Leu Gly Phe
245       250       255
Gln Val Thr Ser Ser Lys Met Leu Ser Leu Met Val Leu Thr Asn Thr
260       265       270

```

Leu	Leu	Ile	Val	Leu	Phe	Met	Thr	Val	Val	Asn	Lys	Leu	Thr	Glu	Lys
		275					280				285				
Trp	Lys	Leu	Leu	Pro	Gln	Leu	Val	Val	Gly	Ser	Leu	Leu	Phe	Thr	Leu
	290					295					300				
Gly	Met	Leu	Leu	Ser	Phe	Thr	Phe	Thr	Gln	Phe	Tyr	Ala	Ile	Trp	Leu
305					310					315					320
Ser	Val	Val	Leu	Leu	Thr	Phe	Gly	Glu	Met	Ile	Asn	Val	Ser	Ala	Ser
					325					330				335	
Gln	Val	Leu	Arg	Ala	Asp	Met	Met	Asp	His	Ser	Gln	Ile	Gly	Ser	Tyr
			340					345					350		
Thr	Gly	Phe	Val	Ser	Met	Ala	Gln	Pro	Leu	Gly	Ala	Ile	Leu	Ala	Ser
		355					360						365		
Leu	Leu	Val	Ser	Val	Ser	His	Phe	Thr	Gly	Pro	Leu	Gly	Val	Gln	Cys
	370					375					380				
Leu	Phe	Ala	Val	Ile	Ala	Leu	Leu	Gly	Ile	Tyr	Phe	Thr	Val	Val	Ser
385					390					395					400
Ala	Lys	Met	Lys	Lys	Val										
					405										

<210> SEQ ID NO 631

<211> LENGTH: 2025

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 631

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atcaagggttg	tcacacactg	tgcaacgcgt	atgcgttttg	ttttgaatga	taataataag	120
gcaaatgtca	aagagattga	aaaaatctct	gtagttaaag	ggacatttac	caatgctggg	180
cagtttcagg	taatcattgg	taatgatgtt	ccagtttttt	ataatgactt	tacagctggt	240
tctagtattg	aaggggtgtc	taaagaagct	gccaaatcag	cagctaaaaa	taatcaaaat	300
gccttacaac	gggtgatgac	catgtttggc	gagattttca	cacctattat	tccggcgatt	360
attgttgggg	ggcttatttt	aggtttccgt	aatatttttg	agagtgtgcc	ttttgaattt	420
cttgggcagc	aggtcgaaaa	agggaaatta	gtttttgatg	cagctgggga	tcctgtttgg	480
aatacgattg	tgagggtatc	tcctttctgg	tcaggggtta	accatttctt	gtggttacca	540
ggggaagcta	ttttccactt	cttaccagtt	gggattactt	ggtctgtgac	gcgtaagatg	600
ggaaccactc	aaattttagg	gattgtcctt	ggtatctgtt	tggtgtcacc	acaattattg	660
aatgcctatg	cgggtggcagg	aacgcctgct	gctgagattg	ccaaaaactg	ggtttgggat	720
tttggtttct	ttaccattaa	tcgtattggg	tatcaggcac	aggttattcc	agccctttta	780
gctgggtctgt	cccttgctta	tcttgaaatt	ttctggcgta	aacggattcc	agaagtgggt	840
tcaatgattt	ttgtgccatt	cctttctttg	attccagctt	tgatttttagc	gcatacggtta	900
ttggggccaa	tcggttgac	tattggtaaa	gggatttcct	ttgttgtgtt	agctggattg	960
actggtcctg	ttaaatggct	attcggtgct	atcctttggtg	ccttgtatgc	tccgctagtt	1020
attactgggt	tacatcacat	gacaaatgcc	attgataccc	aattaattgc	tgatactgca	1080
actcgtacaa	ctgggtttgtg	gccaatgatt	gctctttcaa	atatcgctca	agggtcagcc	1140
gtttttgctt	actatttaat	gaatcgtcac	gaagaacgtg	aggctgaaat	atcgcttcct	1200
gcagcaattt	ctgcttacct	tggggtaact	gagcctgcct	tatttggggg	taatgttaaa	1260
tacgtttatc	cctttgtagc	cggaatgatt	ggctcaggta	ttgcgggtct	cttatcaaca	1320
acctttaatg	ttcaggcaaa	ttctattggg	gttgggtggt	taccagggtt	catggctatc	1380
aatgtgaagt	acatgattcc	attcttcac	tgtatggcag	tagccattgt	ggtgccgatg	1440
tttttaacct	tctttttccg	taaatcacat	atcatgacta	agacagaaga	tgaagctaaa	1500
ctacctgaga	cacccgtttc	ggatgctcct	gtagcaactg	ctccacataa	gactatgcaa	1560
ggaacagtta	tcactttaac	aagcccttta	acgggtgaag	ttaaagcgtt	gtctgaagct	1620
gttgatcctg	tctttgcaca	gggagttatg	ggccaagggtg	ctcttcttca	accgacagaa	1680
ggggtggttag	tagcgccttg	tgatgctgaa	gtatcggtct	tgttcccaac	taaacacgct	1740
atttgtttgg	tgacgactga	aggtttgga	ttattgatgc	atattggcat	ggatacgggt	1800
aacttagatg	gtcaaggatt	tgaagctttg	gtgaagcaag	gtgatcaggt	taaggctgga	1860
caaacattga	ttcaatttga	tatagcagca	atcttctgaag	ctggatacgc	actgaaacg	1920
cctcttggtg	tgactaatca	agatgttttt	acggtaactg	ttgaaggtag	tttaccgcgt	1980

cagattaagg ttaatgataa gtttagcagta gcggtgaaaa agtag

2025

<210> SEQ ID NO 632

<211> LENGTH: 674

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 632

Met	Gly	Lys	Phe	Glu	Gln	Asp	Ala	Lys	Ser	Leu	Leu	Thr	Ala	Ile	Gly
1				5					10					15	
Gly	Lys	Glu	Asn	Ile	Lys	Val	Val	Thr	His	Cys	Ala	Thr	Arg	Met	Arg
			20					25					30		
Phe	Val	Leu	Asn	Asp	Asn	Asn	Lys	Ala	Asn	Val	Lys	Glu	Ile	Glu	Lys
		35					40					45			
Ile	Ser	Val	Val	Lys	Gly	Thr	Phe	Thr	Asn	Ala	Gly	Gln	Phe	Gln	Val
	50					55					60				
Ile	Ile	Gly	Asn	Asp	Val	Pro	Val	Phe	Tyr	Asn	Asp	Phe	Thr	Ala	Val
65				70					75					80	
Ser	Ser	Ile	Glu	Gly	Val	Ser	Lys	Glu	Ala	Ala	Lys	Ser	Ala	Ala	Lys
			85					90					95		
Ser	Asn	Gln	Asn	Ala	Leu	Gln	Arg	Val	Met	Thr	Met	Leu	Ala	Glu	Ile
			100					105					110		
Phe	Thr	Pro	Ile	Ile	Pro	Ala	Ile	Ile	Val	Gly	Gly	Leu	Ile	Leu	Gly
		115				120						125			
Phe	Arg	Asn	Ile	Leu	Glu	Ser	Val	Pro	Phe	Glu	Phe	Leu	Gly	Gln	Gln
	130					135					140				
Val	Glu	Lys	Gly	Lys	Leu	Val	Phe	Asp	Ala	Ala	Gly	Asp	Pro	Val	Trp
145				150					155					160	
Asn	Thr	Ile	Val	Arg	Val	Ser	Pro	Phe	Trp	Ser	Gly	Val	Asn	His	Phe
			165					170					175		
Leu	Trp	Leu	Pro	Gly	Glu	Ala	Ile	Phe	His	Phe	Leu	Pro	Val	Gly	Ile
		180					185						190		
Thr	Trp	Ser	Val	Thr	Arg	Lys	Met	Gly	Thr	Thr	Gln	Ile	Leu	Gly	Ile
		195				200						205			
Val	Leu	Gly	Ile	Cys	Leu	Val	Ser	Pro	Gln	Leu	Leu	Asn	Ala	Tyr	Ala
	210					215					220				
Val	Ala	Gly	Thr	Pro	Ala	Ala	Glu	Ile	Ala	Lys	Asn	Trp	Val	Trp	Asp
225				230					235					240	
Phe	Gly	Phe	Phe	Thr	Ile	Asn	Arg	Ile	Gly	Tyr	Gln	Ala	Gln	Val	Ile
			245					250					255		
Pro	Ala	Leu	Leu	Ala	Gly	Leu	Ser	Leu	Ala	Tyr	Leu	Glu	Ile	Phe	Trp
		260				265						270			
Arg	Lys	Arg	Ile	Pro	Glu	Val	Val	Ser	Met	Ile	Phe	Val	Pro	Phe	Leu
		275				280						285			
Ser	Leu	Ile	Pro	Ala	Leu	Ile	Leu	Ala	His	Thr	Val	Leu	Gly	Pro	Ile
	290					295					300				
Gly	Trp	Thr	Ile	Gly	Lys	Gly	Ile	Ser	Phe	Val	Val	Leu	Ala	Gly	Leu
305				310					315					320	
Thr	Gly	Pro	Val	Lys	Trp	Leu	Phe	Gly	Ala	Ile	Phe	Gly	Ala	Leu	Tyr
			325					330					335		
Ala	Pro	Leu	Val	Ile	Thr	Gly	Leu	His	His	Met	Thr	Asn	Ala	Ile	Asp
		340					345						350		
Thr	Gln	Leu	Ile	Ala	Asp	Thr	Ala	Thr	Arg	Thr	Thr	Gly	Leu	Trp	Pro
	355					360						365			
Met	Ile	Ala	Leu	Ser	Asn	Ile	Ala	Gln	Gly	Ser	Ala	Val	Phe	Ala	Tyr
	370				375						380				
Tyr	Leu	Met	Asn	Arg	His	Glu	Glu	Arg	Glu	Ala	Glu	Ile	Ser	Leu	Pro
385					390					395					400

Ala	Ala	Ile	Ser	Ala	Tyr	Leu	Gly	Val	Thr	Glu	Pro	Ala	Leu	Phe	Gly		
				405					410					415			
Val	Asn	Val	Lys	Tyr	Val	Tyr	Pro	Phe	Val	Ala	Gly	Met	Ile	Gly	Ser		
			420					425					430				
Gly	Ile	Ala	Gly	Leu	Leu	Ser	Thr	Thr	Phe	Asn	Val	Gln	Ala	Asn	Ser		
		435					440					445					
Ile	Gly	Val	Gly	Gly	Leu	Pro	Gly	Phe	Met	Ala	Ile	Asn	Val	Lys	Tyr		
	450					455					460						
Met	Ile	Pro	Phe	Phe	Ile	Cys	Met	Ala	Val	Ala	Ile	Val	Val	Pro	Met		
465					470					475				480			
Phe	Leu	Thr	Phe	Phe	Arg	Lys	Ser	His	Ile	Met	Thr	Lys	Thr	Glu			
			485					490						495			
Asp	Glu	Ala	Lys	Leu	Pro	Glu	Thr	Pro	Val	Ser	Asp	Ala	Pro	Val	Ala		
			500					505					510				
Thr	Ala	Pro	His	Lys	Thr	Met	Gln	Gly	Thr	Val	Ile	Thr	Leu	Thr	Ser		
		515					520					525					
Pro	Leu	Thr	Gly	Glu	Val	Lys	Ala	Leu	Ser	Glu	Ala	Val	Asp	Pro	Val		
	530					535					540						
Phe	Ala	Gln	Gly	Val	Met	Gly	Gln	Gly	Ala	Leu	Leu	Gln	Pro	Thr	Glu		
545				550				555						560			
Gly	Val	Leu	Val	Ala	Pro	Cys	Asp	Ala	Glu	Val	Ser	Val	Leu	Phe	Pro		
			565					570					575				
Thr	Lys	His	Ala	Ile	Cys	Leu	Val	Thr	Thr	Glu	Gly	Leu	Glu	Leu	Leu		
			580					585					590				
Met	His	Ile	Gly	Met	Asp	Thr	Val	Asn	Leu	Asp	Gly	Gln	Gly	Phe	Glu		
	595					600					605						
Ala	Leu	Val	Lys	Gln	Gly	Asp	Gln	Val	Lys	Ala	Gly	Gln	Thr	Leu	Ile		
	610				615						620						
Gln	Phe	Asp	Ile	Ala	Ala	Ile	Ser	Glu	Ala	Gly	Tyr	Ala	Thr	Glu	Thr		
625				630				635						640			
Pro	Leu	Val	Val	Thr	Asn	Gln	Asp	Val	Phe	Thr	Val	Thr	Val	Glu	Gly		
			645					650						655			
Ser	Leu	Pro	Arg	Gln	Ile	Lys	Val	Asn	Asp	Lys	Leu	Ala	Val	Ala	Val		
			660					665					670				
Lys	Lys																

<210> SEQ ID NO 633

<211> LENGTH: 2337

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 633

atgagatttc	tagaactttt	acaaaagaaa	ttttttccta	aagcatatca	ggaaaaacaa	60
ttcttaatgc	atcaaaaaac	gcgtttaacg	ccacaacaca	atcaaaagca	gtattcgcca	120
aatgccaatc	atttggactc	atcagctacc	aaaaactcag	aacaagaccc	tgcaacagct	180
ctgcaacgca	gtagagccta	cgaaggaagc	cctaaaagtc	ggcccgttg	gttgcaaaag	240
ctggaagctg	ttttgccgtc	tcttcaacgt	ccaattcggc	gtttttggcg	ccgctatcac	300
atcggaaaac	tgctaattgat	tctgattgga	actcttgtct	tactcttagg	atcatacttg	360
ttttacttat	caaaaaacagc	taaagtatct	gatttacaag	atgccttgaa	ggctacaacg	420
gttattttatg	atcacaaaag	agagtatgca	ggcagtttat	ctgggtcaaaa	agggagttat	480
gttgagctca	acgctatttc	agatgatctt	gagaatgctg	ttattgccac	tgaggatagg	540
actttttaca	gtaatagcgg	tattaatctt	aaacgcttct	tattggcggg	agttacggcg	600
ggccgctttg	gaggtggctc	aacgattaca	cagcaactgg	ctaaaaatgc	ttatctctca	660
caagatcaga	caattaaacg	aaaggcccga	gagttttttt	tggcggttaga	gttgaccaaa	720
aaatacagta	aaaaagatat	tcttactatg	taccttaaca	actcctactt	tggaaatgga	780
gtttggggag	ttgaagatgc	cagtcaaaaa	tattttggaa	ccacagctgc	taacttaaca	840
ctggatgaag	ctgccacatt	agcaggtatg	ctcaaaggac	ctgaaatata	taacccttac	900
cattctctaa	aaaatgctac	tcaccgtaga	gatactgttt	taggagcgat	ggttgatgcc	960

aaaaagatta	cccaaacaaa	agctcagcaa	gctagagcag	tagggctaaa	aaatcgctta	1020
gctgatactt	atggttggtaa	gacagatgac	tacaaatacc	catcctactt	tgatgctggt	1080
attagtgaag	caatagcaac	ttatggtctt	tcagaaaaag	acattgttaa	taatggatac	1140
aaagtttaca	ctgagctaga	tcaaaattac	caaactggca	tgcaagacgac	ttttaacaac	1200
gatgaactat	ttcctgtttc	agcttatgac	ggtagctctg	ctcaagcagc	tagtgttgct	1260
ttagatccta	aaacaggagg	tgttagaggt	ctgattggtc	gtgtgaatag	tagtgaaaat	1320
ccgactttca	gaagttttta	ctatgcgact	caagcaaaaac	gtagtcccg	atcaacaatc	1380
aaaccactcg	tggttttacgc	gccagccggt	gcttcaggat	ggtcaattga	aaaagaacta	1440
ccaaataccg	ttcaagattt	cgatggctat	cagccacata	attatggaaa	ttatgaatca	1500
gaagatgttc	ctatgtatca	agcattagca	aactcttata	atattccagc	agtttctaca	1560
ttgaacgata	tcggaatcga	taaagccttt	acctatggta	aaacatttgg	gttagatatg	1620
agctctgcca	aaaaagagtt	gggggtagct	ttaggtggca	gcgtgacaac	caatccattg	1680
gagatggctc	aggcatatgc	tgccctttgcc	aataatggag	taatccatcc	tgcgacttg	1740
attaaccgga	ttgaaaatgc	caggggtgaa	gtgcttaaaa	cctttactga	taaggctaaa	1800
cgtgttgtca	gccagtctgt	tgcaagataag	atgacagcca	tgatgctagg	taccttttca	1860
aatggaacag	cagtcaatgc	taacgtatat	ggctatacac	tagctggtaa	aacagggacg	1920
acagaaacca	acttcaatcc	cgacttagca	ggcgatcagt	gggttattgg	ttatacgcca	1980
gatgttggtta	ttagtcaatg	ggtaggattt	aatcagaccg	atgaaaatca	ttatctaacg	2040
gattcaagtg	caggcacggc	ctcagctatt	tttagcactc	aggcatctta	cattttgcct	2100
tataccaagg	gcagccaatt	tcatgtagat	aatgcctacg	ctcaaaatgg	tatttcagct	2160
gtttatggag	tcaatgaaac	aggtaatcaa	tcaggagtgtg	atactcaatc	tattattgat	2220
ggtttaagaa	aatcagcaca	agaagcttcg	caatcactat	caaaagcagt	cgatcagtca	2280
gggttacggtg	ataaagccca	atctatttgg	aaagagattg	ttgactattt	tagatag	2337

<210> SEQ ID NO 634

<211> LENGTH: 778

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 634

Met	Arg	Phe	Leu	Glu	Leu	Leu	Gln	Lys	Lys	Phe	Phe	Pro	Lys	Ala	Tyr
1			5						10					15	
Gln	Glu	Lys	Gln	Phe	Leu	Met	His	Gln	Lys	Thr	Arg	Leu	Thr	Pro	Gln
			20					25					30		
His	Asn	Gln	Lys	Gln	Tyr	Ser	Pro	Asn	Ala	Asn	His	Leu	Asp	Ser	Ser
			35				40					45			
Ala	Thr	Lys	Asn	Ser	Glu	Gln	Asp	Pro	Ala	Thr	Ala	Leu	Gln	Arg	Ser
	50					55				60					
Arg	Ala	Tyr	Glu	Gly	Ser	Pro	Lys	Ser	Arg	Pro	Ala	Trp	Leu	Gln	Lys
65				70					75					80	
Leu	Glu	Ala	Val	Leu	Pro	Ser	Pro	Gln	Arg	Pro	Ile	Arg	Arg	Phe	Trp
			85					90					95		
Arg	Arg	Tyr	His	Ile	Gly	Lys	Leu	Leu	Met	Ile	Leu	Ile	Gly	Thr	Leu
			100				105						110		
Val	Leu	Leu	Leu	Gly	Ser	Tyr	Leu	Phe	Tyr	Leu	Ser	Lys	Thr	Ala	Lys
	115						120					125			
Val	Ser	Asp	Leu	Gln	Asp	Ala	Leu	Lys	Ala	Thr	Thr	Val	Ile	Tyr	Asp
	130					135					140				
His	Lys	Gly	Glu	Tyr	Ala	Gly	Ser	Leu	Ser	Gly	Gln	Lys	Gly	Ser	Tyr
145				150					155					160	
Val	Glu	Leu	Asn	Ala	Ile	Ser	Asp	Asp	Leu	Glu	Asn	Ala	Val	Ile	Ala
			165					170					175		
Thr	Glu	Asp	Arg	Thr	Phe	Tyr	Ser	Asn	Ser	Gly	Ile	Asn	Leu	Lys	Arg
		180					185					190			
Phe	Leu	Leu	Ala	Val	Val	Thr	Ala	Gly	Arg	Phe	Gly	Gly	Gly	Ser	Thr
	195					200					205				
Ile	Thr	Gln	Gln	Leu	Ala	Lys	Asn	Ala	Tyr	Leu	Ser	Gln	Asp	Gln	Thr
	210					215					220				

Ile	Lys	Arg	Lys	Ala	Arg	Glu	Phe	Phe	Leu	Ala	Leu	Glu	Leu	Thr	Lys	225	230	235	240
Lys	Tyr	Ser	Lys	Lys	Asp	Ile	Leu	Thr	Met	Tyr	Leu	Asn	Asn	Ser	Tyr	245	250	255	
Phe	Gly	Asn	Gly	Val	Trp	Gly	Val	Glu	Asp	Ala	Ser	Gln	Lys	Tyr	Phe	260	265	270	
Gly	Thr	Thr	Ala	Ala	Asn	Leu	Thr	Leu	Asp	Glu	Ala	Ala	Thr	Leu	Ala	275	280	285	
Gly	Met	Leu	Lys	Gly	Pro	Glu	Ile	Tyr	Asn	Pro	Tyr	His	Ser	Leu	Lys	290	295	300	
Asn	Ala	Thr	His	Arg	Arg	Asp	Thr	Val	Leu	Gly	Ala	Met	Val	Asp	Ala	305	310	315	320
Lys	Lys	Ile	Thr	Gln	Thr	Lys	Ala	Gln	Gln	Ala	Arg	Ala	Val	Gly	Leu	325	330	335	
Lys	Asn	Arg	Leu	Ala	Asp	Thr	Tyr	Val	Gly	Lys	Thr	Asp	Asp	Tyr	Lys	340	345	350	
Tyr	Pro	Ser	Tyr	Phe	Asp	Ala	Val	Ile	Ser	Glu	Ala	Ile	Ala	Thr	Tyr	355	360	365	
Gly	Leu	Ser	Glu	Lys	Asp	Ile	Val	Asn	Asn	Gly	Tyr	Lys	Val	Tyr	Thr	370	375	380	
Glu	Leu	Asp	Gln	Asn	Tyr	Gln	Thr	Gly	Met	Gln	Thr	Thr	Phe	Asn	Asn	385	390	395	400
Asp	Glu	Leu	Phe	Pro	Val	Ser	Ala	Tyr	Asp	Gly	Ser	Ser	Ala	Gln	Ala	405	410	415	
Ala	Ser	Val	Ala	Leu	Asp	Pro	Lys	Thr	Gly	Gly	Val	Arg	Gly	Leu	Ile	420	425	430	
Gly	Arg	Val	Asn	Ser	Ser	Glu	Asn	Pro	Thr	Phe	Arg	Ser	Phe	Asn	Tyr	435	440	445	
Ala	Thr	Gln	Ala	Lys	Arg	Ser	Pro	Ala	Ser	Thr	Ile	Lys	Pro	Leu	Val	450	455	460	
Val	Tyr	Ala	Pro	Ala	Val	Ala	Ser	Gly	Trp	Ser	Ile	Glu	Lys	Glu	Leu	465	470	475	480
Pro	Asn	Thr	Val	Gln	Asp	Phe	Asp	Gly	Tyr	Gln	Pro	His	Asn	Tyr	Gly	485	490	495	
Asn	Tyr	Glu	Ser	Glu	Asp	Val	Pro	Met	Tyr	Gln	Ala	Leu	Ala	Asn	Ser	500	505	510	
Tyr	Asn	Ile	Pro	Ala	Val	Ser	Thr	Leu	Asn	Asp	Ile	Gly	Ile	Asp	Lys	515	520	525	
Ala	Phe	Thr	Tyr	Gly	Lys	Thr	Phe	Gly	Leu	Asp	Met	Ser	Ser	Ala	Lys	530	535	540	
Lys	Glu	Leu	Gly	Val	Ala	Leu	Gly	Gly	Ser	Val	Thr	Thr	Asn	Pro	Leu	545	550	555	560
Glu	Met	Ala	Gln	Ala	Tyr	Ala	Ala	Phe	Ala	Asn	Asn	Gly	Val	Ile	His	565	570	575	
Pro	Ala	His	Leu	Ile	Asn	Arg	Ile	Glu	Asn	Ala	Arg	Gly	Glu	Val	Leu	580	585	590	
Lys	Thr	Phe	Thr	Asp	Lys	Ala	Lys	Arg	Val	Val	Ser	Gln	Ser	Val	Ala	595	600	605	
Asp	Lys	Met	Thr	Ala	Met	Met	Leu	Gly	Thr	Phe	Ser	Asn	Gly	Thr	Ala	610	615	620	
Val	Asn	Ala	Asn	Val	Tyr	Gly	Tyr	Thr	Leu	Ala	Gly	Lys	Thr	Gly	Thr	625	630	635	640
Thr	Glu	Thr	Asn	Phe	Asn	Pro	Asp	Leu	Ala	Gly	Asp	Gln	Trp	Val	Ile	645	650	655	
Gly	Tyr	Thr	Pro	Asp	Val	Val	Ile	Ser	Gln	Trp	Val	Gly	Phe	Asn	Gln	660	665	670	
Thr	Asp	Glu	Asn	His	Tyr	Leu	Thr	Asp	Ser	Ser	Ala	Gly	Thr	Ala	Ser				

	675		680		685										
Ala	Ile	Phe	Ser	Thr	Gln	Ala	Ser	Tyr	Ile	Leu	Pro	Tyr	Thr	Lys	Gly
	690					695					700				
Ser	Gln	Phe	His	Val	Asp	Asn	Ala	Tyr	Ala	Gln	Asn	Gly	Ile	Ser	Ala
705					710					715					720
Val	Tyr	Gly	Val	Asn	Glu	Thr	Gly	Asn	Gln	Ser	Gly	Val	Asp	Thr	Gln
				725					730					735	
Ser	Ile	Ile	Asp	Gly	Leu	Arg	Lys	Ser	Ala	Gln	Glu	Ala	Ser	Gln	Ser
			740					745					750		
Leu	Ser	Lys	Ala	Val	Asp	Gln	Ser	Gly	Leu	Arg	Asp	Lys	Ala	Gln	Ser
		755				760						765			
Ile	Trp	Lys	Glu	Ile	Val	Asp	Tyr	Phe	Arg						
	770					775									

<210> SEQ ID NO 635
 <211> LENGTH: 330
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 635

atgactaaaa	aggagattga	catgattaaa	attggattgt	tttgtgcagc	aggattttca	60
accggtatgt	tgggtgaacaa	catgaaagta	gctgctgaaa	aaaaaggcat	tgattgtcag	120
attgaagcct	atgctcaagg	gaaattagcg	gactatgcac	cattacttga	tgtggcactt	180
ttaggcccac	aggttgccta	tactctggat	aaatcagaag	ctattttgtaa	agacaatgat	240
atccctattg	cagttatccc	aatggctgat	tatggaatgt	tagacggcaa	caagggtgctt	300
gatttagccc	ttagccttgt	taaagaatag				330

<210> SEQ ID NO 636
 <211> LENGTH: 109
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 636

Met	Thr	Lys	Lys	Glu	Ile	Asp	Met	Ile	Lys	Ile	Gly	Leu	Phe	Cys	Ala
1			5						10					15	
Ala	Gly	Phe	Ser	Thr	Gly	Met	Leu	Val	Asn	Asn	Met	Lys	Val	Ala	Ala
			20				25						30		
Glu	Lys	Lys	Gly	Ile	Asp	Cys	Gln	Ile	Glu	Ala	Tyr	Ala	Gln	Gly	Lys
		35				40					45				
Leu	Ala	Asp	Tyr	Ala	Pro	Leu	Leu	Asp	Val	Ala	Leu	Leu	Gly	Pro	Gln
	50					55				60					
Val	Ala	Tyr	Thr	Leu	Asp	Lys	Ser	Glu	Ala	Ile	Cys	Lys	Asp	Asn	Asp
65				70					75					80	
Ile	Pro	Ile	Ala	Val	Ile	Pro	Met	Ala	Asp	Tyr	Gly	Met	Leu	Asp	Gly
			85				90						95		
Asn	Lys	Val	Leu	Asp	Leu	Ala	Leu	Ser	Leu	Val	Lys	Glu			
			100				105								

<210> SEQ ID NO 637
 <211> LENGTH: 1305
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 637

atggcaaaaa	tgaatatgca	aaacatcatc	aagccaatca	tgacatttgt	gaatatgcgc	60
ggcatcattg	ccttaaaaga	cggtatgtta	gccattttac	ctttgaccgt	tgtggggagt	120
cttttcctga	ttgctgggca	gattcctttc	caaggggtta	atgatgccat	tgtagtgtg	180
tttggtgctg	actggacaga	accctttatg	caggtttacc	atggaacatt	tgctattatg	240
gggttgattt	cctgttttgc	aattggctat	tccttatgcta	aaaactcagg	tgttgaacct	300
ctcccttcag	gggttctatc	cttgctcagcc	ttctttatct	tattgagatc	atcttatgtt	360

ccagcagaag	gtgaagctat	tggagatgct	atcagtaagg	tttggtttgg	tggtcaaggg	420
attattggtg	ctattgtgat	tggtttaacg	gtcggagctg	tttacacaac	atztatccgt	480
cgtcatatcg	tcattaaaat	gccagatcaa	gtgccacaag	ccatcgccaa	acagtttgaa	540
gccatgattc	cagcctttgt	gatctttacc	ttgtcaatgc	ttgtgtatat	tattgccaag	600
tcagtaacag	gtggtggcac	ctttattgaa	atgatttatg	atgtcattca	ggtaccgctg	660
caaggggttaa	cgggttctct	ttatggcgca	ctaggtattg	ccttctttat	ttcctttctt	720
tggtgggttg	gcgtgcatgg	gcaatctgtg	gtcaatggaa	ttgtcactgc	tcttctctta	780
tcaaacttag	atgccaataa	ggccttgatg	gcagcagggtg	agttatccct	agacaagggg	840
gcccatattg	taacccaaca	attttttagac	tctttcttga	ttctatcagg	ttctggcatt	900
acctttgggt	tagtggtagc	tatgatcttt	gcggtctaaat	ccaaacaata	caaggcttta	960
ggcaagggtg	cagccttccc	agccctcttt	aatgttaatg	aaccagtcgt	ctttgggttt	1020
ccaattgtga	tgaatccagt	catgttcttg	ccatttatct	tggttccggg	cttggcagct	1080
ctcacagttt	atggcgccat	tgctattggt	ttcatgcagc	cctttgcagg	agtgaccctt	1140
ccgtgggtcaa	caccagccat	tatctcaggg	ttcatgggtg	gtggctggca	aggagctatt	1200
gtgcaaattc	ttatactcat	catgtcaacg	ttggtgtact	tccattctt	taaaatccaa	1260
gataatatgg	cttatcaaaa	tgaacaagct	agtgaagagt	catga		1305

<210> SEQ ID NO 638

<211> LENGTH: 434

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 638

Met	Ala	Lys	Met	Asn	Met	Gln	Asn	Ile	Ile	Lys	Pro	Ile	Met	Thr	Phe
1				5				10					15		
Val	Asn	Met	Arg	Gly	Ile	Ile	Ala	Leu	Lys	Asp	Gly	Met	Leu	Ala	Ile
			20					25					30		
Leu	Pro	Leu	Thr	Val	Val	Gly	Ser	Leu	Phe	Leu	Ile	Ala	Gly	Gln	Ile
			35				40					45			
Pro	Phe	Gln	Gly	Val	Asn	Asp	Ala	Ile	Ala	Ser	Val	Phe	Gly	Ala	Asp
	50					55					60				
Trp	Thr	Glu	Pro	Phe	Met	Gln	Val	Tyr	His	Gly	Thr	Phe	Ala	Ile	Met
65					70					75				80	
Gly	Leu	Ile	Ser	Cys	Phe	Ala	Ile	Gly	Tyr	Ser	Tyr	Ala	Lys	Asn	Ser
				85				90						95	
Gly	Val	Glu	Pro	Leu	Pro	Ser	Gly	Val	Leu	Ser	Leu	Ser	Ala	Phe	Phe
			100					105					110		
Ile	Leu	Leu	Arg	Ser	Ser	Tyr	Val	Pro	Ala	Glu	Gly	Glu	Ala	Ile	Gly
			115				120					125			
Asp	Ala	Ile	Ser	Lys	Val	Trp	Phe	Gly	Gly	Gln	Gly	Ile	Ile	Gly	Ala
	130					135					140				
Ile	Val	Ile	Gly	Leu	Thr	Val	Gly	Ala	Val	Tyr	Thr	Thr	Phe	Ile	Arg
145					150					155				160	
Arg	His	Ile	Val	Ile	Lys	Met	Pro	Asp	Gln	Val	Pro	Gln	Ala	Ile	Ala
				165				170						175	
Lys	Gln	Phe	Glu	Ala	Met	Ile	Pro	Ala	Phe	Val	Ile	Phe	Thr	Leu	Ser
			180				185						190		
Met	Leu	Val	Tyr	Ile	Ile	Ala	Lys	Ser	Val	Thr	Gly	Gly	Gly	Thr	Phe
	195					200						205			
Ile	Glu	Met	Ile	Tyr	Asp	Val	Ile	Gln	Val	Pro	Leu	Gln	Gly	Leu	Thr
	210				215					220					
Gly	Ser	Leu	Tyr	Gly	Ala	Leu	Gly	Ile	Ala	Phe	Phe	Ile	Ser	Phe	Leu
225					230					235					240
Trp	Trp	Phe	Gly	Val	His	Gly	Gln	Ser	Val	Val	Asn	Gly	Ile	Val	Thr
				245				250						255	
Ala	Leu	Leu	Leu	Ser	Asn	Leu	Asp	Ala	Asn	Lys	Ala	Leu	Met	Ala	Ala
			260				265						270		
Gly	Glu	Leu	Ser	Leu	Asp	Lys	Gly	Ala	His	Ile	Val	Thr	Gln	Gln	Phe

	275					280					285						
Leu	Asp	Ser	Phe	Leu	Ile	Leu	Ser	Gly	Ser	Gly	Ile	Thr	Phe	Gly	Leu		
	290					295					300						
Val	Val	Ala	Met	Ile	Phe	Ala	Ala	Lys	Ser	Lys	Gln	Tyr	Lys	Ala	Leu		
305					310					315					320		
Gly	Lys	Val	Ala	Ala	Phe	Pro	Ala	Leu	Phe	Asn	Val	Asn	Glu	Pro	Val		
			325						330					335			
Val	Phe	Gly	Phe	Pro	Ile	Val	Met	Asn	Pro	Val	Met	Phe	Leu	Pro	Phe		
			340					345					350				
Ile	Leu	Val	Pro	Val	Leu	Ala	Ala	Leu	Thr	Val	Tyr	Gly	Ala	Ile	Ala		
	355					360					365						
Ile	Gly	Phe	Met	Gln	Pro	Phe	Ala	Gly	Val	Thr	Leu	Pro	Trp	Ser	Thr		
370					375						380						
Pro	Ala	Ile	Ile	Ser	Gly	Phe	Met	Val	Gly	Gly	Trp	Gln	Gly	Ala	Ile		
385				390					395						400		
Val	Gln	Ile	Leu	Ile	Leu	Ile	Met	Ser	Thr	Leu	Val	Tyr	Phe	Pro	Phe		
			405					410					415				
Phe	Lys	Ile	Gln	Asp	Asn	Met	Ala	Tyr	Gln	Asn	Glu	Gln	Ala	Ser	Glu		
			420					425					430				
Glu	Ser																

<210> SEQ ID NO 639

<211> LENGTH: 846

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 639

gtgagcgaaa	ttagaaaaga	ggacaagcat	atgaatctac	ttggatcaag	acggggttttt	60
tctaaaaaat	gtcggctagt	aaaattttca	atggtagctc	ttgtatcagc	cacaatggct	120
gtaacaacag	tcacacttga	aaatactgca	ctggcacgac	aaacacaggt	ctcaaagtat	180
gttgttctaa	atgatggcgc	aagcaagtac	ctaaacgaag	cattagcttg	gacattcaat	240
gacagtccca	actattacaa	aaccttaggt	actagtcaga	tcaactccagc	actctttcct	300
aaagcaggag	atattctcta	tagcaaatta	gatgagttag	gaaggacgcg	tactgctaga	360
ggtacattga	cttatgccaa	tgttgaaggt	agctacgggtg	ttagacaatc	tttcggtaaa	420
aatcaaaaacc	ccgcaggctg	gactggaaac	cctaatacatg	tcaaatataa	aattgaatgg	480
ttaaattggc	tatcttatgt	cggagatttc	tggaatagaa	gtcatctcat	tcagatagt	540
ctcgggtggc	atgcactcag	agtcaatgcc	gttacaggga	cacgtaccca	aaatgtagga	600
ggtcgtgacc	aaaaaaggcgg	catgcgctat	accgaacaaa	gagctcaaga	atgggttagaa	660
gcaaatcgtg	atggctatct	ttattatgaa	gctgctccaa	tctataacgc	agacgagttg	720
attccaagag	ctgctgtggt	atcaatgcaa	tcttctgata	ataccatcaa	cgagaaagta	780
ttagttttaca	acacagctaa	tggctacacc	attaactacc	ataacggtac	acctactcag	840
aaataa						846

<210> SEQ ID NO 640

<211> LENGTH: 281

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 640

Met	Ser	Glu	Ile	Arg	Lys	Glu	Asp	Lys	His	Met	Asn	Leu	Leu	Gly	Ser
1			5						10					15	
Arg	Arg	Val	Phe	Ser	Lys	Lys	Cys	Arg	Leu	Val	Lys	Phe	Ser	Met	Val
		20						25				30			
Ala	Leu	Val	Ser	Ala	Thr	Met	Ala	Val	Thr	Thr	Val	Thr	Leu	Glu	Asn
		35				40					45				
Thr	Ala	Leu	Ala	Arg	Gln	Thr	Gln	Val	Ser	Asn	Asp	Val	Val	Leu	Asn
	50				55					60					
Asp	Gly	Ala	Ser	Lys	Tyr	Leu	Asn	Glu	Ala	Leu	Ala	Trp	Thr	Phe	Asn
65					70				75						80

Asp	Ser	Pro	Asn	Tyr	Tyr	Lys	Thr	Leu	Gly	Thr	Ser	Gln	Ile	Thr	Pro	
				85					90					95		
Ala	Leu	Phe	Pro	Lys	Ala	Gly	Asp	Ile	Leu	Tyr	Ser	Lys	Leu	Asp	Glu	
			100					105					110			
Leu	Gly	Arg	Thr	Arg	Thr	Ala	Arg	Gly	Thr	Leu	Thr	Tyr	Ala	Asn	Val	
		115					120					125				
Glu	Gly	Ser	Tyr	Gly	Val	Arg	Gln	Ser	Phe	Gly	Lys	Asn	Gln	Asn	Pro	
	130					135					140					
Ala	Gly	Trp	Thr	Gly	Asn	Pro	Asn	His	Val	Lys	Tyr	Lys	Ile	Glu	Trp	
145					150					155					160	
Leu	Asn	Gly	Leu	Ser	Tyr	Val	Gly	Asp	Phe	Trp	Asn	Arg	Ser	His	Leu	
			165						170					175		
Ile	Ala	Asp	Ser	Leu	Gly	Gly	Asp	Ala	Leu	Arg	Val	Asn	Ala	Val	Thr	
		180						185					190			
Gly	Thr	Arg	Thr	Gln	Asn	Val	Gly	Gly	Arg	Asp	Gln	Lys	Gly	Gly	Met	
	195						200					205				
Arg	Tyr	Thr	Glu	Gln	Arg	Ala	Gln	Glu	Trp	Leu	Glu	Ala	Asn	Arg	Asp	
	210					215					220					
Gly	Tyr	Leu	Tyr	Tyr	Glu	Ala	Ala	Pro	Ile	Tyr	Asn	Ala	Asp	Glu	Leu	
225				230						235					240	
Ile	Pro	Arg	Ala	Val	Val	Val	Ser	Met	Gln	Ser	Ser	Asp	Asn	Thr	Ile	
			245						250				255			
Asn	Glu	Lys	Val	Leu	Val	Tyr	Asn	Thr	Ala	Asn	Gly	Tyr	Thr	Ile	Asn	
		260						265					270			
Tyr	His	Asn	Gly	Thr	Pro	Thr	Gln	Lys								
		275					280									

<210> SEQ ID NO 641

<211> LENGTH: 1197

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 641

atgaataaaa	agaaattagg	tgctcagatta	ttaagtcttt	tagcattagg	tggatttggt	60
cttgctaacc	cagtatttgc	cgatcaaaac	tttgctcgta	acgaaaaaga	agcaaaagat	120
agcgctatca	catttatcca	aaaatcagca	gctatcaaag	cagggtgcacg	aagcgcagaa	180
gatattaagc	ttgacaaaagt	taacttaggt	ggagaacttt	ctggctctaa	tatgtatggt	240
tacaatat	ctactggagg	atttggtatc	gtttcaggag	ataaacgttc	tccagaaatt	300
ctaggatact	ctaccagcgg	atcatttgac	gctaacggta	aagaaaacat	tgcttccttc	360
atggaaagtt	atgtcgaaca	aatcaaagaa	aacaaaaaat	tagacactac	ttatgctggt	420
accgctgaga	ttaaacaacc	agttgttaaa	tctctccttg	attcaaaagg	cattcattac	480
aatcaaggta	acccttaca	cctattgaca	cctgttattg	aaaaagtaaa	accaggtgaa	540
caatcttttg	taggtcaaca	tgacagctaca	ggatgtgttg	ctactgcaac	tgctcaaatt	600
atgaaatatc	ataattaccc	taacaaaggg	ttgaaagact	acacttacac	actaagctca	660
aataacccat	atttcaacca	tcctaagaac	ttgtttgcag	ctatctctac	tagacaatac	720
aactggaaca	acatcttacc	tacttatagc	ggaagagaat	ctaacgttca	aaaaatggcg	780
atttcagaat	tgatggctga	tgttggtatt	tcagtagaca	tggattatgg	tccatctagt	840
ggttctgcag	gtagctctcg	tgttcaaaga	gccttgaaag	aaaactttgg	ctacaaccaa	900
tctgttcacc	aaatcaaccg	tggcgacttt	agcaaacaag	attgggaagc	acaaattgac	960
aaagaattat	ctcaaaacca	accagtatac	taccaagggt	tcggtaaagt	aggcggacat	1020
gcctttgtta	tcgatggtgc	tgacggacgt	aacttctacc	atgttaactg	gggttgggggt	1080
ggagtctctg	acggcttctt	ccgtcttgac	gcactaaacc	cttcagctct	tggtactggt	1140
ggcggcgcag	gcggcttcaa	cggttaccaa	agtgcgtgtg	taggcatcaa	accttag	1197

<210> SEQ ID NO 642

<211> LENGTH: 398

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

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<400> SEQUENCE: 642
Met Asn Lys Lys Lys Leu Gly Val Arg Leu Leu Ser Leu Leu Ala Leu
1          5          10          15
Gly Gly Phe Val Leu Ala Asn Pro Val Phe Ala Asp Gln Asn Phe Ala
20          25          30
Arg Asn Glu Lys Glu Ala Lys Asp Ser Ala Ile Thr Phe Ile Gln Lys
35          40          45
Ser Ala Ala Ile Lys Ala Gly Ala Arg Ser Ala Glu Asp Ile Lys Leu
50          55          60
Asp Lys Val Asn Leu Gly Gly Glu Leu Ser Gly Ser Asn Met Tyr Val
65          70          75          80
Tyr Asn Ile Ser Thr Gly Gly Phe Val Ile Val Ser Gly Asp Lys Arg
85          90          95
Ser Pro Glu Ile Leu Gly Tyr Ser Thr Ser Gly Ser Phe Asp Ala Asn
100         105         110
Gly Lys Glu Asn Ile Ala Ser Phe Met Glu Ser Tyr Val Glu Gln Ile
115         120         125
Lys Glu Asn Lys Lys Leu Asp Thr Thr Tyr Ala Gly Thr Ala Glu Ile
130         135         140
Lys Gln Pro Val Val Lys Ser Leu Leu Asp Ser Lys Gly Ile His Tyr
145         150         155         160
Asn Gln Gly Asn Pro Tyr Asn Leu Leu Thr Pro Val Ile Glu Lys Val
165         170         175
Lys Pro Gly Glu Gln Ser Phe Val Gly Gln His Ala Ala Thr Gly Cys
180         185         190
Val Ala Thr Ala Thr Ala Gln Ile Met Lys Tyr His Asn Tyr Pro Asn
195         200         205
Lys Gly Leu Lys Asp Tyr Thr Tyr Thr Leu Ser Ser Asn Asn Pro Tyr
210         215         220
Phe Asn His Pro Lys Asn Leu Phe Ala Ala Ile Ser Thr Arg Gln Tyr
225         230         235         240
Asn Trp Asn Asn Ile Leu Pro Thr Tyr Ser Gly Arg Glu Ser Asn Val
245         250         255
Gln Lys Met Ala Ile Ser Glu Leu Met Ala Asp Val Gly Ile Ser Val
260         265         270
Asp Met Asp Tyr Gly Pro Ser Ser Gly Ser Ala Gly Ser Ser Arg Val
275         280         285
Gln Arg Ala Leu Lys Glu Asn Phe Gly Tyr Asn Gln Ser Val His Gln
290         295         300
Ile Asn Arg Gly Asp Phe Ser Lys Gln Asp Trp Glu Ala Gln Ile Asp
305         310         315         320
Lys Glu Leu Ser Gln Asn Gln Pro Val Tyr Tyr Gln Gly Val Gly Lys
325         330         335
Val Gly Gly His Ala Phe Val Ile Asp Gly Ala Asp Gly Arg Asn Phe
340         345         350
Tyr His Val Asn Trp Gly Trp Gly Gly Val Ser Asp Gly Phe Phe Arg
355         360         365
Leu Asp Ala Leu Asn Pro Ser Ala Leu Gly Thr Gly Gly Gly Ala Gly
370         375         380
Gly Phe Asn Gly Tyr Gln Ser Ala Val Val Gly Ile Lys Pro
385         390         395

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<210> SEQ ID NO 643
<211> LENGTH: 1389
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 643

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gtgagactaa tcaaaaaaac ctttttggtc atcaatggct taattattgt agtgggttacc      60
tctattttgt tagtgcttta ttttgcaatg ccaattttatt acaccaaagt caaagacaaa      120
gaagttaagt gtgaatttga ccaaacaagc aagcaaatca aaggcaaaac ggtaaccgag      180
attagagata tcctaacaaa aaaaatcaac aaagataata tttggtacag cttagtagac      240
agtgataacc aactgctcta tccttccttg cagctcctag acggcgctcag tgaaagcaaa      300
gacagtcaaa atgttaatat cgtcaccacc tttgacaact cttatttctaa tgtaagggtg      360
atgagtcaaa aagtaaccct acgcatgga aaaaaaatga cattgcttgg gcaatcttca      420
cttcaacccg taacagatgc tagcaaatg ctccttgacc tctaccgctc actattgatt      480
ttttcagtga ccgtagggag tattgtcgcc tacttatata gtaggacttc tagccggcgt      540
atccttagca tgtcacaaac cgccaaaaaa atgggtcaacc tagaaccaaa cttaacgtgt      600
accattcacg gcaaagatga aatagcaatg ttggctagtg atattaaccg tttgtatgcg      660
agtctttcaa cgagcatcaa atccttgcaa aaagagtatg aaaaagcttc tgattcagaa      720
agagagaaat ctgagttttt acgcatgaca tcgcacgagc taaagacacc aatcactagt      780
gttatcgga tgaattgatgg aatgctctat aatgttggtg actttgcaga tcgtgacaaa      840
tatttgcgaa agtgccgaga cgtccttgaa gggcaagccc aactggttca atccatttta      900
tctttatcta agattgaaac cctagcttct caaaatcaag aactgttttc actaaaaagc      960
agcctagaag aagaaatgga agtctttctc gtcttatcag aactaaaaca cctcaaagtg     1020
actatcaatc tcgaagaaca attcgtcaaa gccaaataaag tatacttact aaaggcgatt     1080
aaaaatatta ttgacaatgc ctttcactat accaaatcag gcggccaagt gatgattcaa     1140
ctaaaagaca accaactagt gattaaaaat gaagcagaga cattattgac acaacagcag     1200
atgaaacagt tattccaacc gttttatcga ccagattata gtcgtaacag gaaagacggt     1260
ggtacaggat tggggctggt tatcaccac cagattcttg atcagcatca tctggcttat     1320
cgctttgttg ttcttgatca aagatggatg gtatttacga ttgattttcc atcccatcat     1380
gacgattga                                     1389

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<210> SEQ ID NO 644
<211> LENGTH: 462
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 644

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Met Arg Leu Ile Lys Lys Thr Phe Leu Val Ile Asn Gly Leu Ile Ile
1          5          10          15
Val Val Val Thr Ser Ile Leu Leu Val Leu Tyr Phe Ala Met Pro Ile
20          25          30
Tyr Tyr Thr Lys Val Lys Asp Lys Glu Val Lys Cys Glu Phe Asp Gln
35          40          45
Thr Ser Lys Gln Ile Lys Gly Lys Thr Val Thr Glu Ile Arg Asp Ile
50          55          60
Leu Thr Lys Lys Ile Asn Lys Asp Asn Ile Trp Tyr Ser Leu Val Asp
65          70          75          80
Ser Asp Asn Gln Leu Leu Tyr Pro Ser Leu Gln Leu Leu Asp Gly Val
85          90          95
Ser Glu Ser Lys Asp Ser Gln Asn Val Asn Ile Val Thr Thr Phe Asp
100         105         110
Asn Ser Tyr Ser Asn Val Lys Val Met Ser Gln Lys Val Thr Leu Arg
115         120         125
Asp Gly Lys Lys Met Thr Leu Leu Gly Gln Ser Ser Leu Gln Pro Val
130         135         140
Thr Asp Ala Ser Lys Val Leu Leu Asp Leu Tyr Pro Ser Leu Leu Ile
145         150         155         160
Phe Ser Val Thr Val Gly Ser Ile Val Ala Tyr Leu Tyr Ser Arg Thr
165         170         175
Ser Ser Arg Arg Ile Leu Ser Met Ser Gln Thr Ala Lys Lys Met Val
180         185         190
Asn Leu Glu Pro Asn Leu Thr Cys Thr Ile His Gly Lys Asp Glu Ile
195         200         205
Ala Met Leu Ala Ser Asp Ile Asn Arg Leu Tyr Ala Ser Leu Ser Thr

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210		215		220
Ser Ile Lys Ser Leu Gln Lys Glu Tyr Glu Lys Ala Ser Asp Ser Glu				
225		230		240
Arg Glu Lys Ser Glu Phe Leu Arg Met Thr Ser His Glu Leu Lys Thr				
	245		250	255
Pro Ile Thr Ser Val Ile Gly Met Ile Asp Gly Met Leu Tyr Asn Val				
	260		265	270
Gly Asp Phe Ala Asp Arg Asp Lys Tyr Leu Arg Lys Cys Arg Asp Val				
	275		280	285
Leu Glu Gly Gln Ala Gln Leu Val Gln Ser Ile Leu Ser Leu Ser Lys				
	290		295	300
Ile Glu Thr Leu Ala Ser Gln Asn Gln Glu Leu Phe Ser Leu Lys Ser				
305		310		320
Ser Leu Glu Glu Glu Met Glu Val Phe Leu Val Leu Ser Glu Leu Lys				
	325		330	335
His Leu Lys Val Thr Ile Asn Leu Glu Glu Gln Phe Val Lys Ala Asn				
	340		345	350
Lys Val Tyr Leu Leu Lys Ala Ile Lys Asn Ile Ile Asp Asn Ala Phe				
	355		360	365
His Tyr Thr Lys Ser Gly Gly Gln Val Met Ile Gln Leu Lys Asp Asn				
	370		375	380
Gln Leu Val Ile Lys Asn Glu Ala Glu Thr Leu Leu Thr Gln Gln Gln				
385		390		400
Met Lys Gln Leu Phe Gln Pro Phe Tyr Arg Pro Asp Tyr Ser Arg Asn				
	405		410	415
Arg Lys Asp Gly Gly Thr Gly Leu Gly Leu Phe Ile Thr His Gln Ile				
	420		425	430
Leu Asp Gln His His Leu Ala Tyr Arg Phe Val Val Leu Asp Gln Arg				
	435		440	445
Trp Met Val Phe Thr Ile Asp Phe Pro Ser His His Asp Asp				
	450		455	460

<210> SEQ ID NO 645

<211> LENGTH: 1626

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 645

atgaagaaaa	ggaaattggt	agcagtaaca	ctattaagta	ccatactctt	aaacagtgca	60
gtgccattag	ttgttgctga	tacctccttg	cgtaatagca	catcatccac	tgatcagcct	120
actacagcag	atactgatac	ggatgacgag	agtgaacac	caaaaaaaga	caaaaaaagc	180
aaggaaacag	cgtcgcagca	cgacacccaa	aaagaccata	agccatcaca	cactcaccca	240
acccccctt	caaatgatac	taagcagacc	gatcaggcat	catctgaagc	tactgacaaa	300
ccaaataaag	acaaaaacga	caccaagcaa	ccagacagca	gtgatcaatc	caccccatct	360
cccaaagacc	agtcgtctca	aaaagagtca	caaaacaaag	acggccgacc	taccccatca	420
cctgatcagc	aaaaagatca	gacacctgat	aaaacaccag	aaaaatcagc	tgataaaacc	480
cctgaaaaaag	gaccagaaaa	agcaactgat	aaaacaccag	agccaaatcg	tgacgctcca	540
aaacccatcc	aacctccttt	agcagctgct	cctgtcttta	taccttggag	agaaagtgc	600
aaagacctga	gcaagctaaa	accaagcagt	cgctcatcag	cggcttacgt	gagacactgg	660
acaggtgact	ctgcctacac	tcacaacctg	ttgtcacgcc	gttatgggat	tactgctgaa	720
cagctagatg	gttttttgaa	cagtctaggt	attcactatg	ataaagaacg	cttaaacgga	780
aagcgtttat	tagaatggga	aaaactaaca	ggactagacg	ttcgagctat	cgtagctatt	840
gcaatggcag	aaagctcact	aggtactcag	ggagttgcta	aagaaaaagg	agccaatatg	900
tttggttatg	gcgcccttga	cttcaaccca	aacaatgcc	aaaaatacag	cgatgaggtt	960
gctattcgtc	acatggtaga	agacaccatc	attgccaa	aaaaccaa	ctttgaaaga	1020
caagacctca	aagcaaaaaa	atggtcacta	ggccagttgg	ataccttgat	tgatggtggg	1080
gtttacttta	cagatacaag	tggcagtg	caaagacgag	cagatatcat	gaccaaacta	1140
gaccaatgga	tagatgatca	tggaagcaca	cctgagattc	cagaacatct	caagataact	1200

tccgggacac aatttagcga agtgcccgtg ggttataaaa gaagtcagcc acaaaacggt	1260
ttgacctaca agtcagagac ctacagcttt ggccaatgca cttggtacgc ctataatcgt	1320
gtcaaagagc taggttatca agtcgacagg tacatgggta acggtggcga ctggcagcgc	1380
aagccagggt ttgtgaccac ccataaacct aaagtgggct atgtcgtctc atttgacca	1440
ggccaagcag gagcagatgc aacctatggg cactgtgctg ttgtagagca aatcaaagaa	1500
gatgggttcta tcttaatttc agagtcaaat gttatgggac taggcaccat ttcctatcgg	1560
acgttcacag ctgagcaggc tagtttggtg acctatgtcg taggggacaa actccaaga	1620
ccataa	1626

<210> SEQ ID NO 646
 <211> LENGTH: 541
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 646

Met	Lys	Lys	Arg	Lys	Leu	Leu	Ala	Val	Thr	Leu	Leu	Ser	Thr	Ile	Leu	
1				5					10					15		
Leu	Asn	Ser	Ala	Val	Pro	Leu	Val	Val	Ala	Asp	Thr	Ser	Leu	Arg	Asn	
			20					25					30			
Ser	Thr	Ser	Ser	Thr	Asp	Gln	Pro	Thr	Thr	Ala	Asp	Thr	Asp	Thr	Asp	
		35				40						45				
Asp	Glu	Ser	Glu	Thr	Pro	Lys	Lys	Asp	Lys	Lys	Ser	Lys	Glu	Thr	Ala	
	50					55					60					
Ser	Gln	His	Asp	Thr	Gln	Lys	Asp	His	Lys	Pro	Ser	His	Thr	His	Pro	
65					70					75					80	
Thr	Pro	Pro	Ser	Asn	Asp	Thr	Lys	Gln	Thr	Asp	Gln	Ala	Ser	Ser	Glu	
				85					90					95		
Ala	Thr	Asp	Lys	Pro	Asn	Lys	Asp	Lys	Asn	Asp	Thr	Lys	Gln	Pro	Asp	
			100					105					110			
Ser	Ser	Asp	Gln	Ser	Thr	Pro	Ser	Pro	Lys	Asp	Gln	Ser	Ser	Gln	Lys	
		115					120					125				
Glu	Ser	Gln	Asn	Lys	Asp	Gly	Arg	Pro	Thr	Pro	Ser	Pro	Asp	Gln	Gln	
	130					135					140					
Lys	Asp	Gln	Thr	Pro	Asp	Lys	Thr	Pro	Glu	Lys	Ser	Ala	Asp	Lys	Thr	
145					150					155					160	
Pro	Glu	Lys	Gly	Pro	Glu	Lys	Ala	Thr	Asp	Lys	Thr	Pro	Glu	Pro	Asn	
			165						170					175		
Arg	Asp	Ala	Pro	Lys	Pro	Ile	Gln	Pro	Pro	Leu	Ala	Ala	Ala	Pro	Val	
		180						185					190			
Phe	Ile	Pro	Trp	Arg	Glu	Ser	Asp	Lys	Asp	Leu	Ser	Lys	Leu	Lys	Pro	
	195						200					205				
Ser	Ser	Arg	Ser	Ser	Ala	Ala	Tyr	Val	Arg	His	Trp	Thr	Gly	Asp	Ser	
	210				215						220					
Ala	Tyr	Thr	His	Asn	Leu	Leu	Ser	Arg	Arg	Tyr	Gly	Ile	Thr	Ala	Glu	
225				230						235					240	
Gln	Leu	Asp	Gly	Phe	Leu	Asn	Ser	Leu	Gly	Ile	His	Tyr	Asp	Lys	Glu	
			245						250					255		
Arg	Leu	Asn	Gly	Lys	Arg	Leu	Leu	Glu	Trp	Glu	Lys	Leu	Thr	Gly	Leu	
		260						265					270			
Asp	Val	Arg	Ala	Ile	Val	Ala	Ile	Ala	Met	Ala	Glu	Ser	Ser	Leu	Gly	
	275						280					285				
Thr	Gln	Gly	Val	Ala	Lys	Glu	Lys	Gly	Ala	Asn	Met	Phe	Gly	Tyr	Gly	
	290				295						300					
Ala	Phe	Asp	Phe	Asn	Pro	Asn	Asn	Ala	Lys	Lys	Tyr	Ser	Asp	Glu	Val	
305				310						315					320	
Ala	Ile	Arg	His	Met	Val	Glu	Asp	Thr	Ile	Ile	Ala	Asn	Lys	Asn	Gln	
			325						330				335			
Thr	Phe	Glu	Arg	Gln	Asp	Leu	Lys	Ala	Lys	Lys	Trp	Ser	Leu	Gly	Gln	

Glu	Thr	Tyr	Thr	Ser	Arg	Asn	Phe	Asp	Trp	Ser	Gly	Asp	Asp	Trp	Ser		
		35					40					45					
Gly	Asp	Asp	Trp	Pro	Glu	Asp	Asp	Trp	Ser	Gly	Asp	Gly	Leu	Ser	Lys		
	50					55				60							
Tyr	Asp	Arg	Ser	Gly	Val	Gly	Leu	Ser	Gln	Tyr	Gly	Trp	Ser	Lys	Tyr		
65				70					75					80			
Gly	Trp	Ser	Ser	Asp	Lys	Glu	Glu	Trp	Pro	Glu	Asp	Trp	Pro	Glu	Asp		
			85					90					95				
Asp	Trp	Ser	Ser	Asp	Lys	Lys	Asp	Glu	Thr	Glu	Asp	Lys	Thr	Arg	Pro		
		100						105					110				
Pro	Tyr	Gly	Glu	Ala	Leu	Gly	Thr	Gly	Tyr	Glu	Lys	Arg	Asp	Asp	Trp		
	115					120						125					
Gly	Gly	Pro	Gly	Thr	Val	Ala	Thr	Asp	Pro	Tyr	Thr	Pro	Pro	Tyr	Gly		
	130				135						140						
Gly	Ala	Leu	Gly	Thr	Gly	Tyr	Glu	Lys	Arg	Asp	Asp	Trp	Gly	Gly	Pro		
145				150					155						160		
Gly	Thr	Val	Ala	Thr	Asp	Pro	Tyr	Thr	Pro	Pro	Tyr	Gly	Gly	Ala	Leu		
		165						170						175			
Gly	Thr	Gly	Tyr	Glu	Lys	Arg	Asp	Asp	Trp	Arg	Gly	Pro	Gly	His	Ile		
	180						185				190						
Pro	Lys	Pro	Glu	Asn	Glu	Gln	Ser	Pro	Asn	Pro	Leu	His	Ile	Pro	Glu		
	195					200			205								
Pro	Pro	Gln	Ile	Glu	Trp	Pro	Gln	Trp	Asn	Gly	Phe	Asp	Gly	Leu	Ser		
	210					215				220							
Phe	Gly	Pro	Ser	Asp	Trp	Gly	Gln	Ser	Glu	Asp	Thr	Pro	Pro	Ser	Glu		
225				230					235						240		
Pro	Arg	Val	Pro	Glu	Lys	Pro	Gln	His	Thr	Pro	Gln	Lys	Asn	Pro	Gln		
		245						250					255				
Glu	Ser	Asp	Phe	Asp	Arg	Gly	Phe	Ser	Ala	Gly	Leu	Lys	Ala	Lys	Asn		
	260					265							270				
Ser	Gly	Arg	Gly	Ile	Asp	Phe	Glu	Gly	Phe	Gln	Tyr	Gly	Gly	Trp	Ser		
	275					280					285						
Asp	Glu	Tyr	Lys	Lys	Gly	Tyr	Met	Gln	Ala	Phe	Gly	Thr	Pro	Tyr	Thr		
	290				295						300						
Pro	Ser	Ala	Thr														
305																	

<210> SEQ ID NO 649

<211> LENGTH: 822

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 649

atgatattga	aacgtcgaac	gatgggtttta	tggcaactgg	gtatcgccat	ttctctcatt	60
cttagtattc	tagccttaaa	cctttatttc	tataggacgc	ctttggaaac	caatgcagct	120
ttacgcaacc	tcgctccttc	cttaaaccat	ctttttggga	cagatgggtt	aggtagggat	180
atgtttgtca	gaacgattaa	agggctttat	ttctctttac	aagtcggctt	attaggcgcc	240
cttatgggag	tctttcttgc	gaccgttttt	ggagtgcctg	caggtctagg	aaatagcctt	300
attgataaaa	taatagcctg	gttggttgat	ttgtttattg	gtatgcctca	tttgattttt	360
atgattctca	tttcttttgt	tgttgggaaa	ggggctcaag	gggttatcat	tgcaacagct	420
gttaccatt	ggccctctct	agcaaggctt	atccgcaatg	aagtctatga	tctaaagaat	480
aaagcctttg	tccagctctc	taaaagcatg	ggaaaaacgc	cttattatat	tgtgaggcat	540
catatcctgc	ctttgattgc	ttctcaaatt	ttcattgggt	ttatcctctt	atttcgcac	600
gtcatcttgc	atgaagcatc	catgactttc	ttaggatttg	gcctttctgc	cgaacaacct	660
tcggttggtg	tcattttgtc	agaggcagct	aagcatatct	ctcttggcaa	ttggtggttg	720
gtgatttttc	caggccttta	tcttattttg	gttgtcaatg	cctttgatac	tatcggagaa	780
tctttaaaga	aactctttta	ccctcaaacy	gatcattttt	ag		822

<210> SEQ ID NO 650
 <211> LENGTH: 273
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 650

```

Met Ile Leu Lys Arg Arg Thr Met Val Leu Trp Gln Leu Gly Ile Ala
1      5      10      15
Ile Ser Leu Ile Leu Ser Ile Leu Ala Leu Asn Leu Tyr Phe Tyr Arg
      20      25      30
Thr Pro Leu Glu Thr Asn Ala Ala Leu Arg Asn Leu Ala Pro Ser Leu
      35      40      45
Asn His Leu Phe Gly Thr Asp Gly Leu Gly Arg Asp Met Phe Val Arg
      50      55      60
Thr Ile Lys Gly Leu Tyr Phe Ser Leu Gln Val Gly Leu Leu Gly Ala
65      70      75      80
Leu Met Gly Val Phe Leu Ala Thr Val Phe Gly Val Leu Ala Gly Leu
      85      90      95
Gly Asn Ser Leu Ile Asp Lys Ile Ile Ala Trp Leu Val Asp Leu Phe
      100     105     110
Ile Gly Met Pro His Leu Ile Phe Met Ile Leu Ile Ser Phe Val Val
      115     120     125
Gly Lys Gly Ala Gln Gly Val Ile Ile Ala Thr Ala Val Thr His Trp
      130     135     140
Pro Ser Leu Ala Arg Leu Ile Arg Asn Glu Val Tyr Asp Leu Lys Asn
145     150     155     160
Lys Ala Phe Val Gln Leu Ser Lys Ser Met Gly Lys Thr Pro Tyr Tyr
      165     170     175
Ile Val Arg His His Ile Leu Pro Leu Ile Ala Ser Gln Ile Phe Ile
      180     185     190
Gly Phe Ile Leu Leu Phe Pro His Val Ile Leu His Glu Ala Ser Met
      195     200     205
Thr Phe Leu Gly Phe Gly Leu Ser Ala Glu Gln Pro Ser Val Gly Ile
      210     215     220
Ile Leu Ser Glu Ala Ala Lys His Ile Ser Leu Gly Asn Trp Trp Leu
225     230     235     240
Val Ile Phe Pro Gly Leu Tyr Leu Ile Leu Val Val Asn Ala Phe Asp
      245     250     255
Thr Ile Gly Glu Ser Leu Lys Lys Leu Phe Tyr Pro Gln Thr Asp His
      260     265     270
Phe

```

<210> SEQ ID NO 651
 <211> LENGTH: 978
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 651

```

gtgaaacgta ctaccattat tatcatctgg aaaatcatca gatgtgtcac gcttattttt      60
ggggatatctg ttttgacctt cgttttggtt aaacaatctc cagtagatcc agtcatggca      120
agtgtcaatt atgacacatc actaaccctt gctcagtaca aagcgattgc tcaccactat      180
ggcttggata agccagctct agtccaatat tttatttggg tgaaaaatgt gatacaggga      240
gatttaggga cctcgctcgt ttatcggcaa cctggttagtg atattattag atcacgggca      300
ggtgcttctt tcatacttat gggactctct tggatcttat cgggtcttat tggatttatt      360
ttaggaacgt tatccgcttt ccatcaaggg aaattacttg accgagttgt caggtggttt      420
tcataccttc agatatcagt accaacgttt tggattggac tcattttttt attaatcttt      480
tctgtccagc tgggggtggtt cccgattggt atttcttccc cgataggcac tttgagtcaa      540
gatattacgt tagctgatcg agttaagcac cttatgtttac ctgttttcac gctaagtatt      600
ctaggcattg ccaatgtcac ccttcatacg agaactaaaa tgatgtcggg gcttttctagt      660

```

gaatatgtct	tatttgccag	agcgcgtggg	gaaacacagt	ggcaaatttt	taaacatcat	720
tgcccttagaa	atgctatcgt	accagctatt	acactgcatt	tttcctattt	tggaagaattg	780
tttggaggat	ctgttcttgc	tgagcaagtt	ttctcatatc	ctggccttagg	gtctaccctc	840
actgaagcag	gacttaaaag	tgatacacccg	ctccttctag	ctattgtgat	gatagggaca	900
ttatttgttt	ttgcgggcaa	tcttattgcg	gatattttta	atagcatcat	caatccacag	960
ttaaggagaa	aagtatga					978

<210> SEQ ID NO 652
 <211> LENGTH: 325
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 652

Met	Lys	Arg	Thr	Thr	Ile	Ile	Ile	Ile	Trp	Lys	Ile	Ile	Arg	Cys	Val
1				5					10					15	
Thr	Leu	Ile	Phe	Gly	Val	Ser	Val	Leu	Thr	Phe	Val	Leu	Leu	Lys	Gln
			20					25					30		
Ser	Pro	Val	Asp	Pro	Val	Met	Ala	Ser	Val	Asn	Tyr	Asp	Thr	Ser	Leu
		35					40					45			
Thr	Pro	Ala	Gln	Tyr	Lys	Ala	Ile	Ala	His	His	Tyr	Gly	Leu	Asp	Lys
		50				55					60				
Pro	Ala	Leu	Val	Gln	Tyr	Phe	Ile	Trp	Leu	Lys	Asn	Val	Ile	Gln	Gly
65					70					75				80	
Asp	Leu	Gly	Thr	Ser	Leu	Val	Tyr	Arg	Gln	Pro	Val	Ser	Asp	Ile	Ile
				85					90					95	
Arg	Ser	Arg	Ala	Gly	Ala	Ser	Phe	Ile	Leu	Met	Gly	Leu	Ser	Trp	Ile
			100					105					110		
Leu	Ser	Gly	Leu	Ile	Gly	Phe	Ile	Leu	Gly	Thr	Leu	Ser	Ala	Phe	His
		115					120					125			
Gln	Gly	Lys	Leu	Leu	Asp	Arg	Val	Val	Arg	Trp	Phe	Ser	Tyr	Leu	Gln
		130				135					140				
Ile	Ser	Val	Pro	Thr	Phe	Trp	Ile	Gly	Leu	Ile	Phe	Leu	Leu	Ile	Phe
145					150					155					160
Ser	Val	Gln	Leu	Gly	Trp	Phe	Pro	Ile	Gly	Ile	Ser	Ser	Pro	Ile	Gly
				165					170					175	
Thr	Leu	Ser	Gln	Asp	Ile	Thr	Leu	Ala	Asp	Arg	Val	Lys	His	Leu	Met
			180					185					190		
Leu	Pro	Val	Phe	Thr	Leu	Ser	Ile	Leu	Gly	Ile	Ala	Asn	Val	Thr	Leu
		195					200					205			
His	Thr	Arg	Thr	Lys	Met	Met	Ser	Val	Leu	Ser	Ser	Glu	Tyr	Val	Leu
		210				215					220				
Phe	Ala	Arg	Ala	Arg	Gly	Glu	Thr	Gln	Trp	Gln	Ile	Phe	Lys	His	His
225					230					235					240
Cys	Leu	Arg	Asn	Ala	Ile	Val	Pro	Ala	Ile	Thr	Leu	His	Phe	Ser	Tyr
				245					250					255	
Phe	Gly	Glu	Leu	Phe	Gly	Gly	Ser	Val	Leu	Ala	Glu	Gln	Val	Phe	Ser
			260					265					270		
Tyr	Pro	Gly	Leu	Gly	Ser	Thr	Leu	Thr	Glu	Ala	Gly	Leu	Lys	Ser	Asp
		275					280					285			
Thr	Pro	Leu	Leu	Leu	Ala	Ile	Val	Met	Ile	Gly	Thr	Leu	Phe	Val	Phe
		290				295					300				
Ala	Gly	Asn	Leu	Ile	Ala	Asp	Ile	Leu	Asn	Ser	Ile	Ile	Asn	Pro	Gln
305					310					315					320
Leu	Arg	Arg	Lys	Val											
				325											

<210> SEQ ID NO 653
 <211> LENGTH: 2187

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 653

```
atgaaaacat cattcaagca actgttttcgt ttcgaatttt ggcaaaaatt tgggaaatgt      60
cttatgggtcg ttattgctgt catgccagcg gctgggtttaa tgatcagtat cggaaactct      120
attccaatga ttaaccacga ctacagcattt ttggcatctc taggcaacat tatcgctcaa      180
attggttggg ctgttattgt taaccttcac ttgctatttg ccttggccat tgggtgtagt      240
tgggctaaag aaagagctgg agggggccttt gcctcagggc ttgcttttgt cttgatcaat      300
cggataacag gtgcttttta tggcgtgtct agtactatgc tagctgatcc agaagcaaaa      360
atcacaagcc tccttggcac tcaaatgatc gttaaagatt atttcaccag tgtcttgga      420
tctccagctt taaacacagg ggtttttgtt gggattattg cagggttcgt aggagcaacg      480
gcctataaca aatactataa ttaccgtaaa cttcctgaag ttttgacctt ctttaatggg      540
aagcgttttg taccatttgt cgttatttta cgttctattt ttgtagccct tattttgggt      600
gttggtttggc cgggtgatcca gtctgggatt aacagttttg ggatgtggat tgcctcttca      660
caagattcag ctccaatcct agccccattc ctatatgta ccttggaaag tctctgttg      720
ccatttgggtc ttcaccacat gttgacgatc ccaatgaact atacagctct tgggtggaact      780
tatgagggtca tgacagggtgc agcagcgggg acaaaaagtat ttggtcaaga ccctttgtgg      840
cttgcttggg taactgacct tgttcacctt aaaggatcag acgcttcagc ctatagtcac      900
ttaatggata gtgtgactcc agctcgtttc aaagtaggac aaatgattgg agctaccgga      960
acattgatgg gggttgcctt agccatgtac cgtaatgtgg atgccgataa aaaacacaca     1020
tacaaaatga tgttcatctc agcagcggca gcggtccttt tgacaggggt aactgagcca     1080
cttgagtacc tatttatgtt tgcagcaatg ccactttaca tcgtctatgc cttgttcaa      1140
ggagcttcat ttgccatggc agacctgtg aatctccgtg ttcactcatt tggaaatata     1200
gagctactaa cccgcacccc tatggctctt aaagcaggcc taggcatgga tgtgattaac     1260
tttggttggg tttctgtcct ctttgagtt atcatgtact ttattgcaga tatgatgatc     1320
aagaaaatgc atctcgcaac agctggccgt ttaggcaact acgatgccga tatactgggt     1380
gaccgtaaca ctcaaaacag acctacccaa gtagcagata gcaactctca agtcgtgcaa     1440
atcgттаатс tccttgggtg ggcaggcaat attgatgatg ttgatgcttg tatgacgcgc     1500
ttacgagtga cgggtcaaga ccccgctaag gttggtgctg aggacgattg gaaaaaagct     1560
ggcgctatag gcttgatcca aaaaggcaac ggcgttcaag cggctctatg ccctaaagca     1620
gatattttga aatcagatat tcaagatttg ctggactcag gtgctcttat tccagaagtc     1680
aatatgtcac agctcactag caaaccgact cccgcaaaag attttaaaca cgtgacagaa     1740
gatgtgctat cagtggcaga cgggatgggt ctcccaatca caggtgtaaa agaccagggt     1800
tttgcggtcta agatgatggg agatgggttt gcggttgaac caaccatgg taatatctat     1860
gcaccgtag ctggccttgt gaccagtgtc ttccgacca agcatgcctt tggtttactg     1920
acagataatg gtcttgaagt gctgggtcac gtgggacttg ataccgtcgc cttaaatggg     1980
gtgccttttt cagtcaaaag ctcaagaagg caacgggttc atgcagggtg cctattagtc     2040
gtagcagatc ttgctgctat taaatcagca gagcgtgaaa caatcattgt tgttgctttt     2100
accaacacaa cagagatcca agatgtgacc ttgacatctt taggagctca gcctgctaag     2160
actaaagtag ctaccgtaga actttaa                                     2187
```

<210> SEQ ID NO 654

<211> LENGTH: 728

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 654

```
Met Lys Thr Ser Phe Lys Gln Leu Phe Arg Phe Glu Phe Trp Gln Lys
1          5          10          15
Phe Gly Lys Cys Leu Met Val Val Ile Ala Val Met Pro Ala Ala Gly
          20          25          30
Leu Met Ile Ser Ile Gly Asn Ser Ile Pro Met Ile Asn His Asp Ser
          35          40          45
Ala Phe Leu Ala Ser Leu Gly Asn Ile Ile Ala Gln Ile Gly Trp Ala
          50          55          60
Val Ile Val Asn Leu His Leu Leu Phe Ala Leu Ala Ile Gly Gly Ser
65          70          75          80
Trp Ala Lys Glu Arg Ala Gly Gly Ala Phe Ala Ser Gly Leu Ala Phe
```

				85					90				95				
Val	Leu	Ile	Asn	Arg	Ile	Thr	Gly	Ala	Phe	Tyr	Gly	Val	Ser	Ser	Thr		
			100					105					110				
Met	Leu	Ala	Asp	Pro	Glu	Ala	Lys	Ile	Thr	Ser	Leu	Leu	Gly	Thr	Gln		
		115					120					125					
Met	Ile	Val	Lys	Asp	Tyr	Phe	Thr	Ser	Val	Leu	Glu	Ser	Pro	Ala	Leu		
	130					135					140						
Asn	Thr	Gly	Val	Phe	Val	Gly	Ile	Ile	Ala	Gly	Phe	Val	Gly	Ala	Thr		
145					150					155					160		
Ala	Tyr	Asn	Lys	Tyr	Tyr	Asn	Tyr	Arg	Lys	Leu	Pro	Glu	Val	Leu	Thr		
			165						170					175			
Phe	Phe	Asn	Gly	Lys	Arg	Phe	Val	Pro	Phe	Val	Val	Ile	Leu	Arg	Ser		
		180						185					190				
Ile	Phe	Val	Ala	Leu	Ile	Leu	Val	Val	Val	Trp	Pro	Val	Ile	Gln	Ser		
	195						200					205					
Gly	Ile	Asn	Ser	Phe	Gly	Met	Trp	Ile	Ala	Ser	Ser	Gln	Asp	Ser	Ala		
210					215						220						
Pro	Ile	Leu	Ala	Pro	Phe	Leu	Tyr	Gly	Thr	Leu	Glu	Arg	Leu	Leu	Leu		
225				230						235					240		
Pro	Phe	Gly	Leu	His	His	Met	Leu	Thr	Ile	Pro	Met	Asn	Tyr	Thr	Ala		
			245					250					255				
Leu	Gly	Gly	Thr	Tyr	Glu	Val	Met	Thr	Gly	Ala	Ala	Ala	Gly	Thr	Lys		
		260						265				270					
Val	Phe	Gly	Gln	Asp	Pro	Leu	Trp	Leu	Ala	Trp	Val	Thr	Asp	Leu	Val		
	275						280					285					
His	Leu	Lys	Gly	Ser	Asp	Ala	Ser	Ala	Tyr	Ser	His	Leu	Met	Asp	Ser		
290					295					300							
Val	Thr	Pro	Ala	Arg	Phe	Lys	Val	Gly	Gln	Met	Ile	Gly	Ala	Thr	Gly		
305				310					315						320		
Thr	Leu	Met	Gly	Val	Ala	Leu	Ala	Met	Tyr	Arg	Asn	Val	Asp	Ala	Asp		
			325					330					335				
Lys	Lys	His	Thr	Tyr	Lys	Met	Met	Phe	Ile	Ser	Ala	Ala	Ala	Ala	Val		
		340						345				350					
Phe	Leu	Thr	Gly	Val	Thr	Glu	Pro	Leu	Glu	Tyr	Leu	Phe	Met	Phe	Ala		
	355					360					365						
Ala	Met	Pro	Leu	Tyr	Ile	Val	Tyr	Ala	Leu	Val	Gln	Gly	Ala	Ser	Phe		
370					375						380						
Ala	Met	Ala	Asp	Leu	Val	Asn	Leu	Arg	Val	His	Ser	Phe	Gly	Asn	Ile		
385				390					395						400		
Glu	Leu	Leu	Thr	Arg	Thr	Pro	Met	Ala	Leu	Lys	Ala	Gly	Leu	Gly	Met		
			405					410					415				
Asp	Val	Ile	Asn	Phe	Val	Trp	Val	Ser	Val	Leu	Phe	Ala	Val	Ile	Met		
		420					425					430					
Tyr	Phe	Ile	Ala	Asp	Met	Met	Ile	Lys	Lys	Met	His	Leu	Ala	Thr	Ala		
	435					440					445						
Gly	Arg	Leu	Gly	Asn	Tyr	Asp	Ala	Asp	Ile	Leu	Gly	Asp	Arg	Asn	Thr		
450					455					460							
Gln	Thr	Arg	Pro	Thr	Gln	Val	Ala	Asp	Ser	Asn	Ser	Gln	Val	Val	Gln		
465				470					475						480		
Ile	Val	Asn	Leu	Leu	Gly	Gly	Ala	Gly	Asn	Ile	Asp	Asp	Val	Asp	Ala		
			485					490					495				
Cys	Met	Thr	Arg	Leu	Arg	Val	Thr	Val	Lys	Asp	Pro	Ala	Lys	Val	Gly		
		500					505					510					
Ala	Glu	Asp	Asp	Trp	Lys	Lys	Ala	Gly	Ala	Ile	Gly	Leu	Ile	Gln	Lys		
	515					520					525						
Gly	Asn	Gly	Val	Gln	Ala	Val	Tyr	Gly	Pro	Lys	Ala	Asp	Ile	Leu	Lys		
530						535					540						

Ser	Asp	Ile	Gln	Asp	Leu	Leu	Asp	Ser	Gly	Ala	Leu	Ile	Pro	Glu	Val
545					550				555					560	
Asn	Met	Ser	Gln	Leu	Thr	Ser	Lys	Pro	Thr	Pro	Ala	Lys	Asp	Phe	Lys
			565						570					575	
His	Val	Thr	Glu	Asp	Val	Leu	Ser	Val	Ala	Asp	Gly	Met	Val	Leu	Pro
			580					585					590		
Ile	Thr	Gly	Val	Lys	Asp	Gln	Val	Phe	Ala	Ala	Lys	Met	Met	Gly	Asp
		595				600						605			
Gly	Phe	Ala	Val	Glu	Pro	Thr	His	Gly	Asn	Ile	Tyr	Ala	Pro	Val	Ala
	610					615					620				
Gly	Leu	Val	Thr	Ser	Val	Phe	Pro	Thr	Lys	His	Ala	Phe	Gly	Leu	Leu
625					630					635				640	
Thr	Asp	Asn	Gly	Leu	Glu	Val	Leu	Val	His	Val	Gly	Leu	Asp	Thr	Val
			645						650					655	
Ala	Leu	Asn	Gly	Val	Pro	Phe	Ser	Val	Lys	Val	Ser	Glu	Gly	Gln	Arg
			660					665					670		
Val	His	Ala	Gly	Asp	Leu	Leu	Val	Val	Ala	Asp	Leu	Ala	Ala	Ile	Lys
		675					680					685			
Ser	Ala	Glu	Arg	Glu	Thr	Ile	Ile	Val	Val	Ala	Phe	Thr	Asn	Thr	Thr
	690					695					700				
Glu	Ile	Gln	Asp	Val	Thr	Leu	Thr	Ser	Leu	Gly	Ala	Gln	Pro	Ala	Lys
705					710					715				720	
Thr	Lys	Val	Ala	Thr	Val	Glu	Leu								
					725										

<210> SEQ ID NO 655

<211> LENGTH: 417

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 655

ttgttttctt	tgcgttttgt	aacggctagg	acaccagctg	ttgtcatcac	tgctactgct	60
gctgctgtaa	agaatggggt	ggcttgctca	ccagttgctg	gtagacgtct	gtgggtgttg	120
gctacaggtg	tcttagccat	attgccattg	cggcgttctg	gcgtttgggt	agcttccttg	180
tcagcaggtt	tttctgcagc	tggagttacc	tctttgctct	tttctggagc	tttttcgcct	240
ggttggcctg	cttcgccttc	tgggctcttt	tctggagctt	tttcgcctgg	ttggcctgct	300
tcaccttggtg	ggcctgctgg	gccttgctca	cctggtttgc	ctgcctcacc	ttgtgggcct	360
gctgggcctt	gggcgcccgt	ttcacctttt	tcaccttggtg	ggcctactgg	acctga	417

<210> SEQ ID NO 656

<211> LENGTH: 138

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 656

Met	Phe	Ser	Leu	Arg	Phe	Val	Thr	Ala	Arg	Thr	Pro	Ala	Val	Val	Ile
1				5					10					15	
Thr	Ala	Thr	Ala	Ala	Ala	Val	Lys	Asn	Gly	Leu	Ala	Cys	Ser	Pro	Val
			20					25					30		
Ala	Gly	Arg	Arg	Leu	Trp	Leu	Leu	Ala	Thr	Gly	Val	Leu	Ala	Ile	Leu
		35				40						45			
Pro	Leu	Arg	Arg	Ser	Gly	Val	Trp	Leu	Ala	Ser	Leu	Ser	Ala	Gly	Phe
	50				55						60				
Ser	Ala	Ala	Gly	Val	Thr	Ser	Leu	Leu	Phe	Ser	Gly	Ala	Phe	Ser	Pro
65					70					75				80	
Gly	Trp	Pro	Ala	Ser	Pro	Ser	Gly	Leu	Phe	Ser	Gly	Ala	Phe	Ser	Pro
				85					90					95	
Gly	Trp	Pro	Ala	Ser	Pro	Cys	Gly	Pro	Ala	Gly	Pro	Cys	Ser	Pro	Gly
			100					105					110		

Leu Pro Ala Ser Pro Cys Gly Pro Ala Gly Pro Trp Ala Pro Val Ser
 115 120 125
 Pro Phe Ser Pro Cys Gly Pro Thr Gly Pro
 130 135

<210> SEQ ID NO 657
 <211> LENGTH: 1323
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 657

```

atgaaaaatt acttatctat tggagtgatt gcactgctgt ttgcattaac atttggaaca      60
gtcaagtcgg tccaagctat tgctgggtat ggatggctac cagaccgtcc acctatcaat      120
aacagccagt tagttggttag tatggccggt atcgttgaag gtaccgataa aaaagttttt      180
ataaattttt ttgaaatcga tctaacaatca caacctgctc acggaggaaa gacagagcag      240
ggcttaagtc caaaatcaaaa accattttgct acagataatg gcgcaatgcc acataaactt      300
gaaaaagctg acttattaaa agctattcaa aaacagctga tcgctaactg tcacagtaac      360
gacggctact ttgaggtcat tgattttgca agcgatgcaa ccattactga tcgaaacggc      420
aaggtctact ttgctgacaa agatggttcg gtaaccttgc cgaccaacc tgtccaagaa      480
tttttggttaa agggacatgt gcgctgtaga ccatataaag aaaaaccagt acaaaatcaa      540
gcaaaatctg ttgatgtaga atatactgta cagtttactc ctttaaaccg tgatgacgat      600
ttcagaccag ggctcaaaga tactaagcta ttgaaaacac tagctatcgg tgacaccatc      660
acatctcaag aattactagc tcaagcacia agcattttaa acaaaaccca cccaggctat      720
acgatttatg aacgtgactc ctcaatcgtc actcatgaca atgacatttt ccgtacgatt      780
ttaccaatgg atcaagagtt tacttaccat gtcaaaaatc gggaacaagc ttatgagatc      840
aatcctaaaa caggtattaa agaaaaaacg aacaacactg atctggtctc tgagaaatat      900
tacgtcctta aacaagggga aaagccgtat gatccctttg atcgcagtca cttgaaactg      960
ttcaccatca aatacgttga tgtcaacacc aacgaattgc taaaaagcga gcagctctta     1020
acagctagcg aacgtaactt agacttcaga gatttatacg atcctcgtga taaggctaaa     1080
ctactctaca acaatctcga tgcttttgat atcatggact ataccttaac tggaaaagta     1140
gaggataatc acgataagaa taatcgtgtc gttacagttt atatgggcaa gcgccctaaa     1200
ggggcaaagg gtagctatca tttagcttat gataaagatc tctataaccg agaagaacga     1260
aaagcttaca gctacctgcg tgatacaggg acacctatac ctgataaacc taaagacaaa     1320
taa
  
```

<210> SEQ ID NO 658
 <211> LENGTH: 440
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 658

```

Met Lys Asn Tyr Leu Ser Ile Gly Val Ile Ala Leu Leu Phe Ala Leu
 1           5           10          15
Thr Phe Gly Thr Val Lys Ser Val Gln Ala Ile Ala Gly Tyr Gly Trp
          20          25          30
Leu Pro Asp Arg Pro Pro Ile Asn Asn Ser Gln Leu Val Val Ser Met
          35          40          45
Ala Gly Ile Val Glu Gly Thr Asp Lys Lys Val Phe Ile Asn Phe Phe
          50          55          60
Glu Ile Asp Leu Thr Ser Gln Pro Ala His Gly Gly Lys Thr Glu Gln
          65          70          75          80
Gly Leu Ser Pro Lys Ser Lys Pro Phe Ala Thr Asp Asn Gly Ala Met
          85          90          95
Pro His Lys Leu Glu Lys Ala Asp Leu Leu Lys Ala Ile Gln Lys Gln
          100         105         110
Leu Ile Ala Asn Val His Ser Asn Asp Gly Tyr Phe Glu Val Ile Asp
          115         120         125
Phe Ala Ser Asp Ala Thr Ile Thr Asp Arg Asn Gly Lys Val Tyr Phe
          130         135         140
  
```


tcacatcagc	gcttaaaaac	ggtggctgtg	aaaccacaaa	agcatgcaaa	gacatacacg	840
ataggagtta	aggcgagtct	gaaaacagga	tttaaggata	agctcttagg	cggtctagaa	900
ttagcttgga	gtagggcggt	tactattttg	aatgctttga	aaggattgat	cactggcttt	960
agtctcaata	aattaggtgg	acctgttgcc	atgtatgaca	tgtccaatca	ggctgctcaa	1020
aacggcttag	agtcagtctt	atctcttatg	gcaatgcttt	cgatcaattt	agggatcttt	1080
aacctgattc	cgattcctgc	acttgatggg	ggaaaaatct	tgatgaatat	cattgaagcc	1140
attcgtcgca	agcctatcaa	gcaagaaaca	gaggcctata	tcaccctagc	tggggttgct	1200
atcatggtcg	tattgatgat	tgctgtgaca	tggaatgata	tcatgcgcgt	ctttttctaa	1260

<210> SEQ ID NO 660
 <211> LENGTH: 419
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 660

Met	Leu	Gly	Ile	Ile	Thr	Phe	Ile	Ile	Ile	Phe	Gly	Ile	Leu	Val	Ile	
1			5					10					15			
Val	His	Glu	Phe	Gly	His	Phe	Tyr	Phe	Ala	Lys	Lys	Ser	Gly	Ile	Leu	
			20					25					30			
Val	Arg	Glu	Phe	Ala	Ile	Gly	Met	Gly	Pro	Lys	Ile	Phe	Ser	His	Val	
			35				40					45				
Asp	Gln	Gly	Gly	Thr	Leu	Tyr	Thr	Leu	Arg	Met	Leu	Pro	Leu	Gly	Gly	
			50				55				60					
Tyr	Val	Arg	Met	Ala	Gly	Trp	Gly	Asp	Asp	Lys	Thr	Glu	Ile	Lys	Thr	
65					70					75					80	
Gly	Thr	Pro	Ala	Ser	Leu	Thr	Leu	Asn	Glu	Gln	Gly	Phe	Val	Lys	Arg	
				85				90						95		
Ile	Asn	Leu	Ser	Gln	Ser	Lys	Leu	Asp	Pro	Thr	Ser	Leu	Pro	Met	His	
			100					105						110		
Val	Thr	Gly	Tyr	Asp	Leu	Glu	Asp	Gln	Leu	Ser	Ile	Thr	Gly	Leu	Val	
			115					120					125			
Leu	Glu	Glu	Thr	Lys	Thr	Tyr	Lys	Val	Ala	His	Asp	Ala	Thr	Ile	Val	
			130				135					140				
Glu	Glu	Asp	Gly	Thr	Glu	Ile	Arg	Ile	Ala	Pro	Leu	Asp	Val	Gln	Tyr	
145					150					155					160	
Gln	Asn	Ala	Ser	Ile	Gly	Gly	Arg	Leu	Ile	Thr	Asn	Phe	Ala	Gly	Pro	
			165					170						175		
Met	Asn	Asn	Phe	Ile	Leu	Gly	Ile	Val	Val	Phe	Ile	Leu	Leu	Val	Phe	
			180					185						190		
Leu	Gln	Gly	Gly	Met	Pro	Asp	Phe	Ser	Ser	Asn	His	Val	Arg	Val	Gln	
			195				200					205				
Glu	Asn	Gly	Ala	Ala	Ala	Lys	Ala	Gly	Leu	Arg	Asp	Asn	Asp	Gln	Ile	
			210				215					220				
Val	Ala	Ile	Asn	Gly	Tyr	Lys	Val	Thr	Ser	Trp	Asn	Asp	Leu	Thr	Glu	
225					230					235					240	
Ala	Val	Asp	Leu	Ala	Thr	Arg	Asp	Leu	Gly	Pro	Ser	Gln	Thr	Ile	Lys	
				245					250					255		
Val	Thr	Tyr	Lys	Ser	His	Gln	Arg	Leu	Lys	Thr	Val	Ala	Val	Lys	Pro	
			260					265						270		
Gln	Lys	His	Ala	Lys	Thr	Tyr	Thr	Ile	Gly	Val	Lys	Ala	Ser	Leu	Lys	
			275				280					285				
Thr	Gly	Phe	Lys	Asp	Lys	Leu	Leu	Gly	Gly	Leu	Glu	Leu	Ala	Trp	Ser	
			290				295				300					
Arg	Ala	Phe	Thr	Ile	Leu	Asn	Ala	Leu	Lys	Gly	Leu	Ile	Thr	Gly	Phe	
305					310					315					320	
Ser	Leu	Asn	Lys	Leu	Gly	Gly	Pro	Val	Ala	Met	Tyr	Asp	Met	Ser	Asn	
				325					330					335		
Gln	Ala	Ala	Gln	Asn	Gly	Leu	Glu	Ser	Val	Leu	Ser	Leu	Met	Ala	Met	

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 662

```
Met Ser Pro Ile Ala Val Lys Asn Asp Met Arg Gln Leu Asp Ser Ile
1          5          10          15
Tyr Leu Glu Asn Glu Asn Ala Ser Phe Tyr Thr Asp Ile Ile Gly Gly
20          25          30
Asp Asp Met Leu Ser His Glu Leu Ile Arg Asn Tyr Gln Leu Phe Ser
35          40          45
Lys Tyr Lys Gly His Ser Leu Glu Ala Phe Glu Ser Ile Leu Lys Ala
50          55          60
Ser Lys Arg His Ile Leu Ala Asp Ile Ala Lys Ile Asn Asp Thr Leu
65          70          75          80
Ser Leu Tyr Gln Leu Pro Leu Ile Ala Leu Asp Arg Gln Leu Val Tyr
85          90          95
Pro Pro Asp Leu Thr Glu Lys Asp Leu Leu Asn Arg Met Leu Pro Thr
100         105         110
Leu Asp Asp Tyr Leu Phe Gln Asp Glu Arg Leu Asp Met Ile Ile Ile
115         120         125
Tyr Ile Met Met Ala Lys Glu Phe Ile Ser Ile Asn His Leu Glu Ser
130         135         140
Leu Leu Arg Leu Ser Arg Asn Ser Val Ile Ala Asp Leu Asn Leu Val
145         150         155         160
Arg Asp Arg Val Gln Ala Phe Gln Val Thr Leu Ala Tyr Asn Arg Gln
165         170         175
Asp Gly Tyr Phe Phe Glu Gly Glu Pro Leu Ala Leu Arg Arg Leu Leu
180         185         190
Glu Ser Ala Val Ser Ser Leu Leu Gln Val Thr Ser Gly Pro Trp Val
195         200         205
Phe Ser Tyr Leu Leu His Glu Leu Gly Leu Pro Asp Gln Lys Lys Val
210         215         220
Met Ala Ala Thr Leu Glu Glu Leu Ser Arg Glu Asn His Leu Thr Phe
225         230         235         240
Ile Ser Glu Lys Leu Arg Asp Leu Ile Tyr Phe Phe Cys Leu Leu Ala
245         250         255
His Arg Pro Phe Ser Arg Asn Val Arg Ala Glu Ala Val Asp Thr Phe
260         265         270
Pro Leu Ala Ser Pro Ala Val Glu Thr Met Val Asp Gln Leu Leu Val
275         280         285
Asn Phe Pro Ser Leu Thr Glu Glu Lys Tyr Leu Val Gln Ser Arg Leu
290         295         300
Leu Gly Cys Ile Gln Gly Asp Leu Glu Leu Val Phe Gln Gln Pro Ile
305         310         315         320
Tyr Asp Ile Met Glu Glu Ile Ile Asn Ser Val Ala Val Asn Thr Gly
325         330         335
Leu Ser Ile Thr Asp Thr Pro Glu Leu Arg Gln Asn Leu Tyr Ser His
340         345         350
Leu Leu Pro Ala Tyr Tyr Arg Leu Tyr Tyr Asp Ile Asn Leu Thr Asn
355         360         365
Pro Leu Lys Glu Gln Ile Lys Gln Asp Tyr Glu Ser Leu Phe Tyr Leu
370         375         380
Val Lys Arg Ser Leu Ser Pro Leu Glu Lys Gln Leu Gly Lys Ser Val
385         390         395         400
Asn Glu Asp Glu Val Ala Tyr Phe Thr Ile His Phe Gly Arg Trp Leu
405         410         415
Gln Ala Pro Lys Lys Arg Pro Ser Asn Gln Leu Val Ala Leu Ser Val
420         425         430
Cys Pro Asn Gly Ile Ser Ser Ser Leu Met Leu Glu Ala Thr Leu Lys
```


<211> LENGTH: 265

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 664

```
Met Thr Thr Met Gln Lys Thr Ile Ser Leu Leu Ser Leu Ala Leu Leu
1           5           10           15
Ile Gly Leu Leu Gly Thr Ser Gly Lys Ala Ile Ser Val Tyr Ala Gln
20           25           30
Asp Gln His Thr Asp Asn Val Ile Ala Glu Ser Thr Ile Ser Gln Val
35           40           45
Ser Val Glu Ala Ser Met Arg Gly Thr Glu Pro Tyr Ile Asp Ala Thr
50           55           60
Val Thr Thr Asp Gln Pro Val Arg Gln Pro Thr Gln Ala Thr Ile Thr
65           70           75           80
Leu Lys Asp Ala Ser Asp Asn Thr Ile Asn Ser Trp Val Tyr Thr Met
85           90           95
Ala Ala Gln Gln Arg Arg Phe Thr Ala Trp Phe Asp Leu Thr Gly Gln
100          105          110
Lys Ser Gly Asp Tyr His Val Thr Val Thr Val His Thr Gln Glu Lys
115          120          125
Ala Val Thr Gly Gln Ser Gly Thr Val His Phe Asp Gln Asn Lys Ala
130          135          140
Arg Lys Thr Pro Thr Asn Met Gln Gln Lys Asp Thr Ser Lys Ala Met
145          150          155          160
Thr Asn Ser Val Asp Val Asp Thr Lys Ala Gln Thr Asn Gln Ser Ala
165          170          175
Asn Gln Glu Ile Asp Ser Thr Ser Asn Pro Phe Arg Ser Ala Thr Asn
180          185          190
His Arg Ser Thr Ser Leu Lys Arg Ser Thr Lys Asn Glu Lys Leu Thr
195          200          205
Pro Thr Ala Ser Asn Ser Gln Lys Asn Gly Ser Asn Lys Thr Lys Met
210          215          220
Leu Val Asp Lys Glu Glu Val Lys Pro Thr Ser Lys Arg Gly Phe Pro
225          230          235          240
Trp Val Leu Leu Gly Leu Val Val Ser Leu Ala Ala Gly Leu Phe Ile
245          250          255
Ala Ile Gln Lys Val Ser Arg Arg Lys
260          265
```

<210> SEQ ID NO 665

<211> LENGTH: 1908

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 665

```
atgatttggt caattacaaa atctaacatt aaaaaaaatt tttcgttata tcgtatctat      60
tttctagcta cgattggttt attaagtatt tttatagctt ttctaaattt tatctcagat      120
aaaatcatta cagaaaaaat tggggatagt ggtcaagctc tagttatcgc taatgggtca      180
ttgatttttt tgattgtatt tttggtggta ttcttaattt acttcaataa tttctttgta      240
aaaaaacgta gtcaagagct tggagtccta gcaatactag ggttttcaaa aagagaatta      300
acaaaattac taactttaga aaatcttggt attctagttc tgagttactt ggtaagttta      360
ttgctgggac cgactttata ttttttagct gtactggcaa ttactcatct attgaattta      420
acaatggaag ttcagtgggt tattacagtt aatgagatta tagagtcctt aggaatatta      480
gtcgtagttt ttctgattaa tgtcatcaca aatggactta tcattagtaa acagtcctttg      540
attgaatttg ttaatttctc aagaaaggct gagaaaaaaa ttaagataag aaaagtcaga      600
gctattattg ctatcactgc attgctattg tcatatatatt tatgtttggc gacagtgttt      660
tcatccacac gaaatatgct attaagcata gggatggtac cggtttctct attgataatt      720
gtcttagttg ttttaggaac agtgttcacc atcagatatg gattggcttt tgtagtttcg      780
```

ttgttaaaag	aaaataaaaa	aaggttatac	cgctcctctgt	ctaatatcat	ctatcccaaa	840
tttaactatc	gtattgcaac	aaaaaataaa	ttattaacag	tcttgggagg	tcttttaaca	900
gtaaccgttt	cagttgccgg	aatgatggta	atgctctatg	cttatttctt	taatgggata	960
gagagggtga	ctccatctgc	catagaatat	aatgttgaat	cagaaaacgg	tcaagtcaat	1020
gttacaacta	ttttagagaa	cgaccaagtg	agcttggttg	atgtcggcct	gttgcgattg	1080
aatactatcc	cagagggtgac	tatcacagac	tctggggcaa	caatacctta	ttttgatata	1140
attaactaca	gtgactacaa	agagttaatg	aaagctcaag	gcagaacaaa	ttctattgaa	1200
ggtagtaagt	cactcccat	gttaataaat	tattatccaa	cagaaattag	ccttggaana	1260
acctttaact	taggaaatgc	atatgatgtt	actgtaaaac	aagtatcaac	gaataatgtt	1320
tttagttttt	ctacaagtgt	cacgaccctg	gttggttctg	ataaattata	tgctaaactt	1380
agttctcggt	ttccagagaa	agaaatgaca	attaggactt	ttaatggaac	ttcgattagg	1440
tcaagtgaag	cattttacaa	tcagtttagt	atgggttcctg	atgttatcag	tagttatagt	1500
aaggaacaca	cagtaaagac	tgctaataat	gcgacttata	tctttataac	tttcctatcc	1560
atactcttta	ttattgttac	aggtagtatt	ctgtacttta	caagcctcat	cgaatcatg	1620
gaaaataaag	aagaatatgg	ctatctaagt	aagctagggt	atagtataaa	aatgattcat	1680
cggattcttc	gatatgaaac	aggataactt	ttccttattc	ctgtattcat	tgggattgta	1740
aatggtggta	tggtgcttat	ttactataaa	tatttattca	tggatacatt	ggtagcaggc	1800
aatatcataa	tggtatcttt	attgctttgt	ctgcttttct	tcttgataat	atatggcaca	1860
ttttatgtat	tgacattgcg	gttagtgaca	tccataatca	aaaattaa		1908

<210> SEQ ID NO 666
 <211> LENGTH: 635
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 666

Met	Ile	Trp	Ser	Ile	Thr	Lys	Ser	Asn	Ile	Lys	Lys	Asn	Phe	Ser	Leu
1				5					10					15	
Tyr	Arg	Ile	Tyr	Phe	Leu	Ala	Thr	Ile	Gly	Leu	Leu	Ser	Ile	Phe	Ile
			20					25					30		
Ala	Phe	Leu	Asn	Phe	Ile	Ser	Asp	Lys	Ile	Ile	Thr	Glu	Lys	Ile	Gly
		35					40					45			
Asp	Ser	Gly	Gln	Ala	Leu	Val	Ile	Ala	Asn	Gly	Ser	Leu	Ile	Phe	Leu
	50					55					60				
Ile	Val	Phe	Leu	Val	Val	Phe	Leu	Ile	Tyr	Phe	Asn	Asn	Phe	Phe	Val
65					70					75					80
Lys	Lys	Arg	Ser	Gln	Glu	Leu	Gly	Val	Leu	Ala	Ile	Leu	Gly	Phe	Ser
				85					90					95	
Lys	Arg	Glu	Leu	Thr	Lys	Leu	Leu	Thr	Leu	Glu	Asn	Leu	Val	Ile	Leu
			100					105					110		
Val	Leu	Ser	Tyr	Leu	Val	Ser	Leu	Leu	Leu	Gly	Pro	Thr	Leu	Tyr	Phe
	115					120					125				
Leu	Ala	Val	Leu	Ala	Ile	Thr	His	Leu	Leu	Asn	Leu	Thr	Met	Glu	Val
	130				135					140					
Gln	Trp	Phe	Ile	Thr	Val	Asn	Glu	Ile	Ile	Glu	Ser	Leu	Gly	Ile	Leu
145					150					155					160
Val	Val	Val	Phe	Leu	Ile	Asn	Val	Ile	Thr	Asn	Gly	Leu	Ile	Ile	Ser
				165					170					175	
Lys	Gln	Ser	Leu	Ile	Glu	Phe	Val	Asn	Phe	Ser	Arg	Lys	Ala	Glu	Lys
			180					185					190		
Lys	Ile	Lys	Ile	Arg	Lys	Val	Arg	Ala	Ile	Ile	Ala	Ile	Thr	Ala	Leu
	195					200					205				
Leu	Leu	Ser	Tyr	Ile	Leu	Cys	Leu	Ala	Thr	Val	Phe	Ser	Ser	Thr	Arg
	210					215					220				
Asn	Met	Leu	Leu	Ser	Ile	Gly	Met	Val	Pro	Val	Ser	Leu	Leu	Ile	Ile
225					230					235					240
Val	Leu	Val	Val	Leu	Gly	Thr	Val	Phe	Thr	Ile	Arg	Tyr	Gly	Leu	Ala
				245					250					255	

tcagggttttt	taatcgattt	agtggcagga	taccctcagt	ggatgtttca	tagtttgatt	240
gctcacagtg	tccaagggtg	ttttgcggga	tggagagggc	gcaagcggtg	gcttggtggt	300
gtgatagggt	cttttatcat	gatttttttg	tacttttttag	gctctcttat	gcttggttat	360
ggccttttcg	gatcttttag	cggatatttg	ggaaacgtca	tgcaaaatac	attagggtct	420
ttgttggtt	ttattatctt	taaggccata	ttaaggcaaa	aaaagagata	a	471

<210> SEQ ID NO 668
 <211> LENGTH: 156
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 668

Met	Gln	Asn	Ser	Lys	Ile	Arg	Gln	Met	Ser	Leu	Thr	Gly	Ile	Leu	Thr
1				5					10					15	
Ala	Leu	Val	Val	Val	Leu	Gly	Arg	Phe	Val	Met	Leu	Pro	Thr	Pro	Thr
			20					25					30		
Gly	Phe	Leu	Thr	Leu	Leu	Asp	Ala	Gly	Ile	Tyr	Ala	Val	Ser	Phe	Ser
	35						40					45			
Phe	Gly	Ser	Ala	Gln	Gly	Ala	Ile	Val	Gly	Gly	Leu	Ser	Gly	Phe	Leu
	50					55					60				
Ile	Asp	Leu	Val	Ala	Gly	Tyr	Pro	Gln	Trp	Met	Phe	His	Ser	Leu	Ile
65					70					75				80	
Ala	His	Ser	Val	Gln	Gly	Tyr	Phe	Ala	Gly	Trp	Arg	Gly	Arg	Lys	Arg
				85					90					95	
Trp	Leu	Gly	Val	Val	Ile	Gly	Ser	Phe	Ile	Met	Ile	Phe	Trp	Tyr	Phe
			100					105					110		
Leu	Gly	Ser	Leu	Met	Leu	Gly	Tyr	Gly	Leu	Ser	Gly	Ser	Leu	Ala	Gly
		115					120					125			
Ile	Trp	Gly	Asn	Val	Met	Gln	Asn	Thr	Leu	Gly	Leu	Phe	Val	Gly	Phe
	130					135					140				
Ile	Ile	Phe	Lys	Ala	Ile	Leu	Arg	Gln	Lys	Lys	Arg				
145					150					155					

<210> SEQ ID NO 669
 <211> LENGTH: 654
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 669

atggggaag	aaataaaagt	gaaatgcttt	ttgcgtagat	cagcttttgg	attagttgcg	60
gtgtcagcat	cagtattagt	cggttcaaca	gtatctgctg	ttgactcacc	tatcgaacag	120
cctcgaatta	ttccaaatgg	cggaacctta	actaatcttc	ttggcaatgc	tccagaaaaa	180
ctggcattac	gtaatgaaga	aagagccatt	gatgaattaa	aaaaacaagc	tattgaggat	240
aaagaagcta	cgacagctat	agaagcagca	agttcagatg	ccttagaagc	attagcggat	300
caaacagacg	ctttacaatc	agaagaagct	gcggttggtta	aagcggataa	cgctgctagt	360
gacgccttag	aagcattggc	ggatcaaaca	gacgctttac	aatcagaaga	agctgaagta	420
gttcaatcag	ataacgctgc	tagtgacgcc	tgggaaaaag	cagcaactcc	aatcgcttta	480
gatgttaaga	aaactaaaga	tacaaaacct	gtagttaaaa	aagaagaaag	acaaaacgtt	540
aatacccttc	ctacaactgg	tgaagagtct	aaccctattct	ttacagctgc	tgcgcttgca	600
ataatggtaa	gtacagggtgt	gttagttgta	agttcaaagt	gcaaagaaaa	ttag	654

<210> SEQ ID NO 670
 <211> LENGTH: 217
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 670

Met	Gly	Lys	Glu	Ile	Lys	Val	Lys	Cys	Phe	Leu	Arg	Arg	Ser	Ala	Phe
1				5					10					15	
Gly	Leu	Val	Ala	Val	Ser	Ala	Ser	Val	Leu	Val	Gly	Ser	Thr	Val	Ser

tcaacaggtg aaacagctaa cccattcttc acagcggcag cccttactgt tatggcaaca 1620
gctggagtag cagcagttgt aaaacgcaaa gaagaaaact aa 1662

<210> SEQ ID NO 672
<211> LENGTH: 553
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 672

Met	Pro	Pro	Pro	Pro	Gln	Leu	Arg	Gln	Pro	Asn	Cys	Ser	Asn	Ser	Lys
1				5					10					15	
Thr	Asp	Ser	Ser	Leu	Ile	Ala	Phe	Arg	Ser	Lys	Arg	Trp	Gln	Lys	Leu
			20					25					30		
Lys	Lys	Leu	Val	Phe	Thr	Phe	Trp	Leu	Leu	Leu	Phe	Thr	Ile	Glu	Leu
			35				40					45			
Leu	Glu	Leu	Asn	Pro	Glu	Asn	Glu	Gly	Phe	Phe	Leu	Lys	Asn	Asp	Ser
	50					55					60				
Ile	Arg	Ser	Ile	Lys	Met	Ala	Lys	Asn	Asn	Thr	Asn	Arg	His	Tyr	Ser
65					70					75					80
Leu	Arg	Lys	Leu	Lys	Thr	Gly	Thr	Ala	Ser	Val	Ala	Val	Ala	Leu	Thr
				85					90					95	
Val	Leu	Gly	Ala	Gly	Phe	Ala	Asn	Gln	Thr	Glu	Val	Lys	Ala	Asn	Gly
			100					105					110		
Asp	Gly	Asn	Pro	Arg	Glu	Val	Ile	Glu	Asp	Leu	Ala	Ala	Asn	Asn	Pro
		115					120					125			
Ala	Ile	Gln	Asn	Ile	Arg	Leu	Arg	Tyr	Glu	Asn	Lys	Asp	Leu	Lys	Ala
	130					135					140				
Arg	Leu	Glu	Asn	Ala	Met	Glu	Val	Ala	Gly	Arg	Asp	Phe	Lys	Arg	Ala
145					150					155					160
Glu	Glu	Leu	Glu	Lys	Ala	Lys	Gln	Ala	Leu	Glu	Asp	Gln	Arg	Lys	Asp
				165					170					175	
Leu	Glu	Thr	Lys	Leu	Lys	Glu	Leu	Gln	Gln	Asp	Tyr	Asp	Leu	Ala	Lys
			180					185					190		
Glu	Ser	Thr	Ser	Trp	Asp	Arg	Gln	Arg	Leu	Glu	Lys	Glu	Leu	Glu	Glu
		195					200					205			
Lys	Lys	Glu	Ala	Leu	Glu	Leu	Ala	Ile	Asp	Gln	Ala	Ser	Arg	Asp	Tyr
	210					215					220				
His	Arg	Ala	Thr	Ala	Leu	Glu	Lys	Glu	Leu	Glu	Glu	Lys	Lys	Lys	Ala
225					230					235					240
Leu	Glu	Leu	Ala	Ile	Asp	Gln	Ala	Ser	Gln	Asp	Tyr	Asn	Arg	Ala	Asn
				245					250					255	
Val	Leu	Glu	Lys	Glu	Leu	Glu	Thr	Ile	Thr	Arg	Glu	Gln	Glu	Ile	Asn
			260					265					270		
Arg	Asn	Leu	Leu	Gly	Asn	Ala	Lys	Leu	Glu	Leu	Asp	Gln	Leu	Ser	Ser
		275					280					285			
Glu	Lys	Glu	Gln	Leu	Thr	Ile	Glu	Lys	Ala	Lys	Leu	Glu	Glu	Glu	Lys
	290					295					300				
Gln	Ile	Ser	Asp	Ala	Ser	Arg	Gln	Ser	Leu	Arg	Arg	Asp	Leu	Asp	Ala
305					310					315					320
Ser	Arg	Glu	Ala	Lys	Lys	Gln	Val	Glu	Lys	Asp	Leu	Ala	Asn	Leu	Thr
				325					330					335	
Ala	Glu	Leu	Asp	Lys	Val	Lys	Glu	Asp	Lys	Gln	Ile	Ser	Asp	Ala	Ser
		340						345					350		
Arg	Gln	Gly	Leu	Arg	Arg	Asp	Leu	Asp	Ala	Ser	Arg	Glu	Ala	Lys	Lys
		355					360					365			
Gln	Val	Glu	Lys	Asp	Leu	Ala	Asn	Leu	Thr	Ala	Glu	Leu	Asp	Lys	Val
	370					375					380				
Lys	Glu	Glu	Lys	Gln	Ile	Ser	Asp	Ala	Ser	Arg	Gln	Gly	Leu	Arg	Arg

385		390		395		400									
Asp	Leu	Asp	Ala	Ser	Arg	Glu	Ala	Lys	Lys	Gln	Val	Glu	Lys	Ala	Leu
		405						410						415	
Glu	Glu	Ala	Asn	Ser	Lys	Leu	Ala	Ala	Leu	Glu	Lys	Leu	Asn	Lys	Glu
		420						425						430	
Leu	Glu	Glu	Ser	Lys	Lys	Leu	Thr	Glu	Lys	Glu	Lys	Ala	Glu	Leu	Gln
		435					440						445		
Ala	Lys	Leu	Glu	Ala	Glu	Ala	Lys	Ala	Leu	Lys	Glu	Gln	Leu	Ala	Lys
	450					455					460				
Gln	Ala	Glu	Glu	Leu	Ala	Lys	Leu	Arg	Ala	Gly	Lys	Ala	Ser	Asp	Ser
465				470					475						480
Gln	Thr	Pro	Asp	Thr	Lys	Pro	Gly	Asn	Lys	Ala	Val	Pro	Gly	Lys	Gly
			485					490						495	
Gln	Ala	Pro	Gln	Ala	Gly	Thr	Lys	Pro	Asn	Gln	Asn	Lys	Ala	Pro	Met
		500						505					510		
Lys	Glu	Thr	Lys	Arg	Gln	Leu	Pro	Ser	Thr	Gly	Glu	Thr	Ala	Asn	Pro
		515					520						525		
Phe	Phe	Thr	Ala	Ala	Ala	Leu	Thr	Val	Met	Ala	Thr	Ala	Gly	Val	Ala
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<210> SEQ ID NO 673

<211> LENGTH: 3546

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 673

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accgaacaag	ctgtagaaac	cccacaacca	acagcggttt	ctgaggaagc	accatcatca	180
aaggaaacca	aaacccca	aactcctgat	gacgcagaag	aaacaatagc	agatgacgct	240
aatgatctag	cccctcaagc	tcttgctaaa	actgctgata	caccagcaac	ctcaaaagcg	300
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gcggcagact	caacattgac	agttgcttct	tacagcccag	ataaacagct	cactgaaact	1020
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<210> SEQ ID NO 674

<211> LENGTH: 1181

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 674

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			35				40					45			
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			50				55				60				
Thr	Pro	Gln	Thr	Pro	Asp	Asp	Ala	Glu	Glu	Thr	Ile	Ala	Asp	Asp	Ala
65					70					75				80	
Asn	Asp	Leu	Ala	Pro	Gln	Ala	Pro	Ala	Lys	Thr	Ala	Asp	Thr	Pro	Ala
				85					90					95	
Thr	Ser	Lys	Ala	Thr	Ile	Arg	Asp	Leu	Asn	Asp	Pro	Ser	Gln	Val	Lys
			100						105					110	
Thr	Leu	Gln	Glu	Lys	Ala	Gly	Lys	Gly	Ala	Gly	Thr	Val	Val	Ala	Val
			115				120						125		
Ile	Asp	Ala	Gly	Phe	Asp	Lys	Asn	His	Glu	Ala	Trp	Arg	Leu	Thr	Asp
			130				135				140				
Lys	Thr	Lys	Ala	Arg	Tyr	Gln	Ser	Lys	Glu	Asp	Leu	Glu	Lys	Ala	Lys
145					150					155					160
Lys	Glu	His	Gly	Ile	Thr	Tyr	Gly	Glu	Trp	Val	Asn	Asp	Lys	Val	Ala

				165					170					175			
Tyr	Tyr	His	Asp	Tyr	Ser	Lys	Asp	Gly	Lys	Thr	Ala	Val	Asp	Gln	Glu		
			180					185					190				
His	Gly	Thr	His	Val	Ser	Gly	Ile	Leu	Ser	Gly	Asn	Ala	Pro	Ser	Glu		
		195					200					205					
Thr	Lys	Glu	Pro	Tyr	Arg	Leu	Glu	Gly	Ala	Met	Pro	Glu	Ala	Gln	Leu		
	210					215					220						
Leu	Leu	Met	Arg	Val	Glu	Ile	Val	Asn	Gly	Leu	Ala	Asp	Tyr	Ala	Arg		
225					230					235					240		
Asn	Tyr	Ala	Gln	Ala	Ile	Ile	Asp	Ala	Val	Asn	Leu	Gly	Ala	Lys	Val		
			245					250						255			
Ile	Asn	Met	Ser	Phe	Gly	Asn	Ala	Ala	Leu	Ala	Tyr	Ala	Asn	Leu	Pro		
			260					265					270				
Asp	Glu	Thr	Lys	Lys	Ala	Phe	Asp	Tyr	Ala	Lys	Ser	Lys	Gly	Val	Ser		
		275					280						285				
Ile	Val	Thr	Ser	Ala	Gly	Asn	Asp	Ser	Ser	Phe	Gly	Gly	Lys	Thr	Arg		
	290					295					300						
Leu	Pro	Leu	Ala	Asp	His	Pro	Asp	Tyr	Gly	Val	Val	Gly	Thr	Pro	Ala		
305					310					315					320		
Ala	Ala	Asp	Ser	Thr	Leu	Thr	Val	Ala	Ser	Tyr	Ser	Pro	Asp	Lys	Gln		
			325					330					335				
Leu	Thr	Glu	Thr	Ala	Thr	Val	Lys	Thr	Ala	Asp	Gln	Gln	Asp	Lys	Glu		
			340					345					350				
Met	Pro	Val	Leu	Ser	Thr	Asn	Arg	Phe	Glu	Pro	Asn	Lys	Ala	Tyr	Asp		
		355					360					365					
Tyr	Ala	Tyr	Ala	Asn	Arg	Gly	Met	Lys	Glu	Asp	Asp	Phe	Lys	Asp	Val		
	370					375					380						
Lys	Gly	Lys	Ile	Ala	Leu	Ile	Glu	Arg	Gly	Asp	Ile	Asp	Phe	Lys	Asp		
385					390					395					400		
Lys	Ile	Ala	Asn	Ala	Lys	Lys	Ala	Gly	Ala	Val	Gly	Val	Leu	Ile	Tyr		
			405					410					415				
Asp	Asn	Gln	Asp	Lys	Gly	Phe	Pro	Ile	Glu	Leu	Pro	Asn	Val	Asp	Gln		
			420					425					430				
Met	Pro	Ala	Ala	Phe	Ile	Ser	Arg	Lys	Asp	Gly	Leu	Leu	Leu	Lys	Glu		
		435					440						445				
Asn	Pro	Gln	Lys	Thr	Ile	Thr	Phe	Asn	Ala	Thr	Pro	Lys	Val	Leu	Pro		
	450					455						460					
Thr	Ala	Ser	Gly	Thr	Lys	Leu	Ser	Arg	Phe	Ser	Ser	Trp	Gly	Leu	Thr		
465					470					475					480		
Ala	Asp	Gly	Asn	Ile	Lys	Pro	Asp	Ile	Ala	Ala	Pro	Gly	Gln	Asp	Ile		
			485					490					495				
Leu	Ser	Ser	Val	Ala	Asn	Asn	Lys	Tyr	Ala	Lys	Leu	Ser	Gly	Thr	Ser		
			500					505					510				
Met	Ser	Ala	Pro	Leu	Val	Ala	Gly	Ile	Met	Gly	Leu	Leu	Gln	Lys	Gln		
		515					520						525				
Tyr	Glu	Thr	Gln	Tyr	Pro	Asp	Met	Thr	Pro	Ser	Glu	Arg	Leu	Asp	Leu		
	530					535					540						
Ala	Lys	Lys	Val	Leu	Met	Ser	Ser	Ala	Thr	Ala	Leu	Tyr	Asp	Glu	Asp		
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Glu	Lys	Ala	Tyr	Phe	Ser	Pro	Arg	Gln	Gln	Gly	Ala	Gly	Ala	Val	Asp		
			565					570					575				
Ala	Lys	Lys	Ala	Ser	Ala	Ala	Thr	Met	Tyr	Val	Thr	Asp	Lys	Asp	Asn		
			580					585					590				
Thr	Ser	Ser	Lys	Val	His	Leu	Asn	Val	Ser	Asp	Lys	Phe	Glu	Val			
		595					600					605					
Thr	Val	Thr	Val	His	Asn	Lys	Ser	Asp	Lys	Pro	Gln	Glu	Leu	Tyr	Tyr		
	610					615					620						